

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:04:52 ; Search time 154.853 Seconds
(without alignments)
8075.738 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22

Sequence: 1 ccategccaaggagatcgagct 22

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

GenBank:
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	48	6	I43071 Sequence 54
2	22	100.0	127	6	CQ816525 Sequence
3	22	100.0	127	6	CQ816526 Sequence
4	22	100.0	139	6	CQ816524 Sequence
5	22	100.0	161	6	CQ816521 Sequence
6	22	100.0	161	6	CQ816522 Sequence
7	22	100.0	231	6	CQ816511 Sequence
8	22	100.0	231	6	CQ816512 Sequence
9	22	100.0	231	6	CQ816513 Sequence
10	22	100.0	270	1	AF445452 Mycobacte
11	22	100.0	270	1	AF445453 Mycobacte
12	22	100.0	270	1	AF445454 Mycobacte
13	22	100.0	271	1	D16487 Mycobacteri
14	22	100.0	325	6	CQ816510 Sequence
15	22	100.0	381	1	AF271096 Mycobacte
16	22	100.0	381	1	AF271346 Mycobacte
17	22	100.0	386	1	AY943196 Mycobacte
18	22	100.0	397	1	AY341032 Mycobacte

19	22	100.0	397	1	AY341033 Mycobacte
20	22	100.0	409	1	AY943197 Mycobacte
21	22	100.0	417	1	AY856440 Mycobacte
22	22	100.0	418	1	AY911398 Propionib
23	22	100.0	421	1	AY255477 Mycobacte
24	22	100.0	422	1	DQ124111 Mycobacte
25	22	100.0	424	1	AF547802 Mycobacte
26	22	100.0	424	1	AF547803 Mycobacte
27	22	100.0	424	1	AF547804 Mycobacte
28	22	100.0	424	1	AF547805 Mycobacte
29	22	100.0	424	1	AF547806 Mycobacte
30	22	100.0	424	1	AF547807 Mycobacte
31	22	100.0	424	1	AF547808 Mycobacte
32	22	100.0	424	1	AF547809 Mycobacte
33	22	100.0	424	1	AF547810 Mycobacte
34	22	100.0	424	1	AF547811 Mycobacte
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47	22	100.0	424	1	AF547826 Mycobacte
48	22	100.0	424	1	AF547827 Mycobacte
49	22	100.0	424	1	AF547828 Mycobacte
50	22	100.0	424	1	AF547829 Mycobacte
51	22	100.0	424	1	AF547830 Mycobacte
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ALIGNMENTS

RESULT 1

I43071
LOCUS I43071 Sequence 54 from patent US 5631130. 48 bp DNA linear PAT 07-OCT-1997
DEFINITION I43071
ACCESSION I43071
VERSION I43071.1 GI:2468315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 48)
AUTHORS Leckie,G.W., Davis,A.H., Semple-Facey,I.E., Manlove,M.T. and Solomon,N.A.
TITLE Materials and methods for the detection of Mycobacterium tuberculosis
JOURNAL Patent: US 5631130-A 54 20-MAY-1997;
FEATURES Location/Qualifiers
source
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ORIGIN

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CCATCGCCCAAGGAGATCGAGCT 29

RESULT 2
LOCUS CQ816525 127 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 17 from Patent WO2004029296.
ACCESSION CQ816525
VERSION CQ816525.1 GI:48144801
KEYWORDS
SOURCE
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 17 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 17 CCATCGCCCAAGGAGATCGAGCT 38

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LOCUS CQ816526 127 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 18 from Patent WO2004029296.
ACCESSION CQ816526
VERSION CQ816526.1 GI:48144802
KEYWORDS
SOURCE
ORGANISM Mycobacterium simiae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 18 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 4
LOCUS CQ816524 139 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 16 from Patent WO2004029296.
ACCESSION CQ816524
VERSION CQ816524.1 GI:48144800
KEYWORDS
SOURCE
ORGANISM Mycobacterium chitae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 16 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
FEATURES
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    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 5
LOCUS CQ816521 161 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 13 from Patent WO2004029296.
ACCESSION CQ816521
VERSION CQ816521.1 GI:48144797
KEYWORDS
SOURCE
ORGANISM Mycobacterium xenopi
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Koeksalan,O.K. and Kocagoez,T.
TITLE Molecular size markers for species identification of mycobacteriae
JOURNAL Patent: WO 2004029296-A 13 08-APR-2004;
Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 6
LOCUS CQ816522 161 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 14 from Patent WO2004029296.
ACCESSION CQ816522
VERSION CQ816522.1 GI:48144798
KEYWORDS
SOURCE
ORGANISM Mycobacterium gallinarum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
```


AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 14 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
 FEATURES
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 Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:39689"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 161;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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 DB 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 7
 CQ816511
 LOCUS 231 bp DNA linear PAT 03-JUN-2004
 DEFINITION Sequence 3 from Patent WO2004029296.
 CQ816511
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium simiae
 Mycobacterium simiae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1
 AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 3 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
 FEATURES
 source
 Location/Qualifiers
 1. .231
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 /mol_type="unassigned DNA"
 /db_xref="taxon:1784"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 231;
 Best Local Similarity 100.0%; Pred. No. 52;
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 QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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 DB 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 8
 CQ816512
 LOCUS 231 bp DNA linear PAT 03-JUN-2004
 DEFINITION Sequence 4 from Patent WO2004029296.
 CQ816512
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium smegmatis
 Mycobacterium smegmatis
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1
 AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 4 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
 FEATURES
 source
 Location/Qualifiers
 1. .231
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Query Match 100.0%; Score 22; DB 6; Length 231;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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 DB 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 9
 CQ816513
 LOCUS 231 bp DNA linear PAT 03-JUN-2004
 DEFINITION Sequence 5 from Patent WO2004029296.
 CQ816513
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium intracellulare
 Mycobacterium intracellulare
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 avium complex (MAC).

REFERENCE 1
 AUTHORS Koeksalan,O.K. and Kocagoez,T.
 TITLE Molecular size markers for species identification of mycobacteriae
 JOURNAL Patent: WO 2004029296-A 5 08-APR-2004;
 Koeksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)
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 /db_xref="taxon:1767"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 231;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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 DB 17 CCATCGCCCAAGGAGATCGAGCT 38

RESULT 10
 AF445452
 LOCUS 270 bp DNA linear BCT 06-DEC-2001
 DEFINITION Mycobacterium simiae B Hsp65 (hsp65) gene, partial cds.
 AF445452
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium simiae
 Mycobacterium simiae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1
 AUTHORS El Sahly,H.M., Septimus,E., Soini,H., Septimus,J., Musser,J.M. and
 Graviss,E.A.
 TITLE Mycobacterium simiae pseudo-outbreak resulting from contaminated
 hospital water supply in Houston, Texas
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 270)
 AUTHORS El Sahly,H.M., Septimus,E., Soini,H., Septimus,J., Musser,J.M. and
 Graviss,E.A.
 TITLE Direct Submission
 JOURNAL Submitted (08-NOV-2001) Pathology, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
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 Location/Qualifiers
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/db_xref="GI:17386082"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
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DB 17 CCATCGCCAAGGAGATCGAGCT 38

RESULT 11
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LOCUS 270 bp DNA linear BCT 06-DEC-2001
DEFINITION Mycobacterium simiae A Hsp65 (hsp65) gene, partial cds.
ACCESSION AF445453
VERSION AF445453.1 GI:17386083
KEYWORDS
SOURCE
ORGANISM
Mycobacterium simiae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
El Sahly, H.M., Septimus, E., Soini, H., Septimus, J., Musser, J.M. and
Graviss, E.A.
TITLE
Mycobacterium simiae pseudo-outbreak resulting from contaminated
hospital water supply in Houston, Texas
JOURNAL
Unpublished
REFERENCE
AUTHORS
El Sahly, H.M., Septimus, E., Soini, H., Septimus, J., Musser, J.M. and
Graviss, E.A.
TITLE
Direct Submission
JOURNAL
Submitted (08-NOV-2001) Pathology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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/db_xref="GI:17386086"
/translations="TNDGVSIAKEIELEDPYEKIGAEIVKEVAKTDDVAGDGTATT
VLAQALVKEGLRNVAAGANPLGLKRGIEKAVEKVTETLLKSAKVE"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCGAGCT 22
|||||
DB 17 CCATCGCCAAGGAGATCGAGCT 38

RESULT 13
D16487
LOCUS 271 bp DNA linear BCT 20-AUG-1997
DEFINITION Mycobacterium intracellulare DNA for 65kD antigen, partial cds.
ACCESSION D16487 D16488 D16489 D16490
VERSION D16487.1 GI:2339963
KEYWORDS
SOURCE
ORGANISM
Mycobacterium intracellulare
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
avium complex (MAC).
REFERENCE
AUTHORS
Yamazaki, T. and Nakamura, R.M.
TITLE
Identification of Mycobacterium intracellulare by a polymerase
chain reaction using species-specific primers
JOURNAL
Tuber. Lung Dis. 76 (4), 330-335 (1995)
PUBMED
7579315
REFERENCE
AUTHORS
Yamazaki, T.
TITLE
Direct Submission
JOURNAL
Submitted (18-JUN-1993) Toshio Yamazaki, National Institute of
```

Health, Dept. Bacteriology; 1-23-1 Toyama, Shinjuku-ku, Tokyo 162,
Japan (Tel:03-5285-1111ex.2227), Fax:03-5285-1163)

FEATURES

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1. .271
/organism="Mycobacterium intracellulare"
/mol_type="genomic DNA"
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/db_xref="taxon:1767"
1. .20
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66. .70
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/product="65kD antigen"
/protein_id="BAA21830.1"
/db_xref="GI:2339964"
/translation="MAKTIAYDEEARRGLRGLNALADAVKVTLGPKGRNVVLEVG
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complement(262. .271)

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 241 CCATGCCCAAGGAGATCGAGCT 262

RESULT 14

LOCUS CQ816510 325 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 2 from Patent WO2004029296.
ACCESSION CQ816510
VERSION CQ816510.1 GI:48144786
KEYWORDS

SOURCE

Mycobacterium terrae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1
Köksalan,O.K. and Kocagoez,T.
Molecular size markers for species identification of mycobacteriae
Patent: WO 2004029296-A 2 08-APR-2004;
Köksalan, Orhan Kaya (TR); Kocagoez, Tanil (TR)

FEATURES

source
1. .325
/organism="Mycobacterium terrae"
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/db_xref="taxon:1788"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 17 CCATGCCCAAGGAGATCGAGCT 38

RESULT 15

LOCUS AF271096 381 bp DNA linear BCT 13-NOV-2000
DEFINITION Mycobacterium ulcerans putative 65 kDa heat shock protein (groEL)
gene, partial cds.
ACCESSION AF271096
VERSION AF271096.1 GI:11139537
KEYWORDS

SOURCE

Mycobacterium ulcerans

ORGANISM

Mycobacterium ulcerans
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 381)
Stinear,T.P., Jenkin,G.A., Johnson,P.D. and Davies,J.K.
Comparative genetic analysis of Mycobacterium ulcerans and
Mycobacterium marinum reveals evidence of recent divergence
J. Bacteriol. 182 (22), 6322-6330 (2000)

JOURNAL

PUBMED 11053375

REFERENCE

2 (bases 1 to 381)
Stinear,T.P., Jenkin,G.A., Johnson,P.D.R. and Davies,J.K.

AUTHORS

Direct Submission

TITLE

Submitted (16-MAY-2000) Microbiology, Monash University, Wellington

JOURNAL

Rd, Clayton, VIC 3168, Australia

FEATURES

Location/Qualifiers

1. .381

/organism="Mycobacterium ulcerans"

/mol_type="genomic DNA"

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/db_xref="ATCC:19423"

/db_xref="taxon:1809"

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/gene="groEL"

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/product="putative 65 kDa heat shock protein"

/protein_id="AAG31747.1"

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/translation="SIKRIELEDPEYKIGAEIVKEVAKTDDVAGDGTATVLAQA

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ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 2 CCATGCCCAAGGAGATCGAGCT 23

RESULT 16

LOCUS AF2711346 381 bp DNA linear BCT 03-NOV-2000
DEFINITION Mycobacterium marinum putative GroEL (groEL) gene, partial cds.
ACCESSION AF2711346
VERSION AF2711346.1 GI:9255843
KEYWORDS

SOURCE

Mycobacterium marinum
Mycobacterium marinum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 381)
Stinear,T.P., Jenkin,G.A., Johnson,P.D. and Davies,J.K.
Comparative genetic analysis of Mycobacterium ulcerans and
Mycobacterium marinum reveals evidence of recent divergence
J. Bacteriol. 182 (22), 6322-6330 (2000)

JOURNAL

PUBMED 11053375

REFERENCE

2 (bases 1 to 381)
Stinear,T.P., Jenkin,G.A., Johnson,P.D.R. and Davies,J.K.

AUTHORS

Direct Submission

TITLE

Submitted (24-MAY-2000) Microbiology, Monash University, Wellington

JOURNAL

Rd, Clayton, VIC 3168, Australia

FEATURES

Location/Qualifiers

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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DB 8 CCATCGCCCAAGGAGATCGAGCT 29
|||||

RESULT 20
AY943197
LOCUS
DEFINITION
Mycobacterium canariensis strain CIP 107998 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION
AY943197
VERSION
AY943197.1 GI:61200474
KEYWORDS
Mycobacterium canariensis
SOURCE
Mycobacterium canariensis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 409)
AUTHORS
Pichat,C. and Flandrois,J.P.
DIRECT SUBMISSION
Submitted (24-FEB-2005) Dynamique Des Populations Bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES
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/db_xref="taxon:228230"
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/db_xref="GI:61200475"
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QALVREGLRNVAAGANPLGKRGIEKVAATVRLSTAKEVTEKEQIAAATAGISAGD
QSIGDLIAEALDKVNGEVIIVTESNTFGL"

ORIGIN
Query Match 100.0%; Score 22; DB 1; Length 409;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCATCGCCCAAGGAGATCGAGCT 22

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Db
9 CCATCGCCCAAGGAGATCGAGCT 30
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RESULT 21
AY856440/c
LOCUS
DEFINITION
Mycobacterium sp. WJ-3 65 kDa heat shock protein (hsp65) gene,
partial cds.
ACCESSION
AY856440
VERSION
AY856440.1 GI:57235702
SOURCE
Mycobacterium sp. WJ-3
ORGANISM
Mycobacterium sp. WJ-3
Bacteria; Actinobacteridae; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 417)
AUTHORS
Wang,Y., Ogawa,M., Miyamoto,H. and Taniguti,H.
TITLE
Isolate novel Mycobacterium spp. from contaminant soil
JOURNAL
Unpublished
2 (bases 1 to 417)
REFERENCE
Wang,Y., Ogawa,M., Miyamoto,H. and Taniguti,H.
AUTHORS
Direct Submission
TITLE
Submitted (14-DEC-2004) Microbiology, School of Medicine,
University of Occupational and Environmental Health, Japan, 1-1,
Iseigaoka, Yahata-nishi-ku, Kitakyushu, Fukuoka 807-8555, Japan
JOURNAL
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 413 CCATCGCCCAAGGAGATCGAGCT 392
|||||

RESULT 22
AY911398
LOCUS
DEFINITION
Propionibacterium acnes 60kDa heat shock protein (hsp60) gene,
partial cds.
ACCESSION
AY911398
VERSION
AY911398.1 GI:59381105
SOURCE
Propionibacterium acnes
ORGANISM
Propionibacterium acnes
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium.
REFERENCE
1 (bases 1 to 418)
AUTHORS
Fardel,G.F. and Flandrois,J.P.F.
TITLE
Direct Submission
JOURNAL
Submitted (28-JAN-2005) Dynamique des Populations Bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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ORIGIN
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Db 5 CCATGCCCAAGGAGATCGAGCT 26
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RESULT 23
AY255477 421 bp DNA linear BCT 29-DEC-2004
LOCUS Mycobacterium canariense Hsp65 (hsp65) gene, partial cds.
DEFINITION Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
ACCESSION AY255477
VERSION AY255477.1 GI:30267690
KEYWORDS
SOURCE Mycobacterium canariense
ORGANISM Mycobacterium canariense
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Jimenez,M.S., Campos-Herrero,M.I., Garcia,D., Luquin,M., Herrera,L.
and Garcia,M.J.
TITLE Mycobacterium canariense sp. nov
JOURNAL Int. J. Syst. Evol. Microbiol. 54 (Pt 5), 1729-1734 (2004)
PUBMED 15388736
REFERENCE
AUTHORS Jimenez,M.S., Campos-Herrero,M.I., Garcia,D., Luquin,M., Herrera,L.
and Garcia,M.J.
Direct Submission
Submitted (13-MAR-2003) Bacteriologia (Mycobacterias), Instituto de
Salud Carlos III (CNM), Carretera Majadahonda-Pozuelo Km 2,
Majadahonda, Madrid 28220, Spain
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                TVGEIIAEALDKVGNVITVBSNTFGLQLELTGM"

ORIGIN
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    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 5 CCATGCCCAAGGAGATCGAGCT 26
    |||||

RESULT 24
DQ124111 422 bp DNA linear BCT 03-AUG-2005
LOCUS Mycobacterium cosmeticum strain DSM 44829 65 kDa heat shock protein
(hsp65) gene, partial cds.
DEFINITION Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
ACCESSION DQ124111
VERSION DQ124111.1 GI:71493337
KEYWORDS
SOURCE Mycobacterium cosmeticum
ORGANISM Mycobacterium cosmeticum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Erbilin,A.L. and Flandrois,J.-P.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2005) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyonl UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
Location/Qualifiers
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ORIGIN
    Query Match      100.0%; Score 22; DB 1; Length 422;
    Best Local Similarity 100.0%; Pred. No. 53;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 9 CCATGCCCAAGGAGATCGAGCT 30
    |||||

RESULT 25
AF547802 424 bp DNA linear BCT 18-JAN-2005
LOCUS Mycobacterium abscessus strain CIP 104536 65 kDa heat shock protein
(hsp65) gene, partial cds.
DEFINITION Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
ACCESSION AF547802
VERSION AF547802.1 GI:27502168
KEYWORDS
SOURCE Mycobacterium abscessus
ORGANISM Mycobacterium abscessus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

```

```

TITLE      A multigene approach to phylogenetic analysis using the genus
JOURNAL    Mycobacterium as a model
PUBMED     Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
AUTHORS     2 (bases 1 to 424)
DIRECT SUBMISSION
TITLE      Devulder,G., Pichat,C. and Flandrois,J.P.
JOURNAL     Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
            Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES    Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCGCCCAAGGAGATCGAGCT 22
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Db      10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 26
AF547803 LOCUS      424 bp      DNA      linear      BCT 18-JAN-2005
DEFINITION Mycobacterium africanum strain CIP 105147 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION AF547803
VERSION    AF547803.1 GI:27502170
KEYWORDS   Mycobacterium africanum
SOURCE     Mycobacterium africanum
ORGANISM   Mycobacterium africanum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            tuberculosis complex.
REFERENCE   1 (bases 1 to 424)
AUTHORS     Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE      A multigene approach to phylogenetic analysis using the genus
            Mycobacterium as a model
JOURNAL     Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED     15653890
AUTHORS     Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE      Direct Submission
JOURNAL     Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
            Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES    Location/Qualifiers
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Query Match      100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCGCCCAAGGAGATCGAGCT 22
        |||||
Db      10 CCATCGCCCAAGGAGATCGAGCT 31

TITLE      A multigene approach to phylogenetic analysis using the genus
JOURNAL    Mycobacterium as a model
PUBMED     Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
AUTHORS     2 (bases 1 to 424)
DIRECT SUBMISSION
TITLE      Devulder,G., Pichat,C. and Flandrois,J.P.
JOURNAL     Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
            Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES    Location/Qualifiers
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            QSIGDLIAEAMDKVGNEGVITVESNTFGLQLELTEGMR"
ORIGIN
Query Match      100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCGCCCAAGGAGATCGAGCT 22
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Db      10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 27
AF547804 LOCUS      424 bp      DNA      linear      BCT 18-JAN-2005
DEFINITION Mycobacterium aichiense strain DSM 44147 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION AF547804
VERSION    AF547804.1 GI:27502172
KEYWORDS   Mycobacterium aichiense
SOURCE     Mycobacterium aichiense
ORGANISM   Mycobacterium aichiense
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 424)
AUTHORS     Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE      A multigene approach to phylogenetic analysis using the genus
            Mycobacterium as a model
JOURNAL     Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED     15653890
AUTHORS     Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE      Direct Submission
JOURNAL     Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
            Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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            /product="65 kDa heat shock protein"
            /protein_id="AAO17448.1"
            /db_xref="GI:27502173"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCGCCCAAGGAGATCGAGCT 22
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Db      10 CCATCGCCCAAGGAGATCGAGCT 31

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PUBMED	15653890
REFERENCE	2 (bases 1 to 424)
AUTHORS	Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE	Direct Submission
JOURNAL	Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
	Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
	Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES	Location/Qualifiers
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	QSIGDLIAEMDKVNEGVIITVEESNTFGIQLLETGMR"
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Query Match	100.0%; Score 22; Length 424;
Best Local Similarity	100.0%; Pred.No. 53;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CCATCGCCCAAGGAGATCGAGCT 22
Db	10 CCATCGCCCAAGGAGATCGAGCT 31
RESULT 30	
AF547807	
LOCUS	AF547807 424 bp DNA linear BCT 18-JAN-2005
DEFINITION	Mycobacterium austroafricanum strain CIP 105395 65 kDa heat shock
	protein (hsp65) gene, partial cds.
ACCESSION	AF547807
VERSION	AF547807.1 GI:27502178
KEYWORDS	.
SOURCE	Mycobacterium austroafricanum
ORGANISM	Mycobacterium austroafricanum
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
	Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 424)
AUTHORS	Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE	A multigene approach to phylogenetic analysis using the genus
JOURNAL	Mycobacterium as a model
PUBMED	Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
REFERENCE	15653890
AUTHORS	2 (bases 1 to 424)
	Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE	Direct Submission
JOURNAL	Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
	Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
	Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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RESULT 28	
AF547805	
LOCUS	AF547805 424 bp DNA linear BCT 18-JAN-2005
DEFINITION	Mycobacterium alvei strain CIP 103464 65 kDa heat shock protein
	(hsp65) gene, partial cds.
ACCESSION	AF547805
VERSION	AF547805.1 GI:27502174
KEYWORDS	.
SOURCE	Mycobacterium alvei
ORGANISM	Mycobacterium alvei
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
	Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 424)
AUTHORS	Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE	A multigene approach to phylogenetic analysis using the genus
JOURNAL	Mycobacterium as a model
PUBMED	Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
REFERENCE	15653890
AUTHORS	2 (bases 1 to 424)
	Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE	Direct Submission
JOURNAL	Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
	Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
	Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES	Location/Qualifiers
source	1..424
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	/mol_type="genomic DNA"
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	/db_xref="taxon:67081"
	/note="type strain"
gene	<1..>424
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CDS	<1..>424
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	/protein_id="AAO17449.1"
	/db_xref="GI:27502175"
	/translation="GVSIAKEIELEDPEYKIGAEIVKEVAKTDDVAGDGTATVLA
	QALVREGUNVAAGNPLGKRGEIKAVKYVTTLKSACEVETKEQIAATAGISAGD
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ORIGIN	
Query Match	100.0%; Score 22; DB 1; Length 424;
Best Local Similarity	100.0%; Pred.No. 53;
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CCATCGCCCAAGGAGATCGAGCT 22
Db	10 CCATCGCCCAAGGAGATCGAGCT 31
RESULT 29	
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LOCUS	AF547806 424 bp DNA linear BCT 18-JAN-2005
DEFINITION	Mycobacterium asiaticum strain DSM 44297 65 kDa heat shock protein
	(hsp65) gene, partial cds.
ACCESSION	AF547806
VERSION	AF547806.1 GI:27502176
KEYWORDS	.
SOURCE	Mycobacterium asiaticum
ORGANISM	Mycobacterium asiaticum
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
	Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 424)
AUTHORS	Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE	A multi-gene approach to phylogenetic analysis using the genus
JOURNAL	Mycobacterium as a model
	Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

/product="65 kDa heat shock protein"
 /protein_id="AAO17451.1"
 /db_xref="GI:27502179"
 /translation="GVSTAKIELEDPEYKIGAEIVKEVAKTTDDVAGDGTATVLA
 QALVREGLRNVAAGANPLGKRGIEKAVEKVTETLLKSAKEVETKQDQAAATTAISAGD
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ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 424;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
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 Db 10 CCATGCCCAAGGAGATCGAGCT 31

RESULT 31

AF547808

LOCUS

AF547808 424 bp DNA linear BCT 18-JAN-2005
 Mycobacterium avium subsp. avium strain CIP 104244 65 kDa heat
 shock protein (hsp65) gene, partial cds.

ACCESSION

AF547808

VERSION

AF547808.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

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JOURNAL      Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED       15653890
REFERENCE    2 (bases 1 to 424)
AUTHORS      Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE        Direct Submission
JOURNAL      Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
              Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
              Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES     Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 34
AF547811
LOCUS
DEFINITION      Mycobacterium bohemicum strain CIP 105811 65 kDa heat shock protein
ACCESSION       AF547811
VERSION         AF547811.1 GI:27502186
KEYWORDS
SOURCE          Mycobacterium bohemicum
ORGANISM        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE       1 (bases 1 to 424)
AUTHORS         Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE           A multigene approach to phylogenetic analysis using the genus
                Mycobacterium as a model
JOURNAL         Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED         15653890
REFERENCE       2 (bases 1 to 424)
AUTHORS         Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE           Direct Submission
JOURNAL         Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
                Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
                Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES       Location/Qualifiers
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/db_xref="GI:27502191"
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QALVKEGLRNVAAGANPLAKRGIEKAVEKVTETLLKSAKVEVTEKQIAATAAISAGD
QSIGDLIAEAMDKVGNEGVIIVTESNTFGLQLELTEGMR"
ORIGIN
Query Match      100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 35
AF547813
LOCUS
DEFINITION      Mycobacterium bovis strain CIP 105234 65 kDa heat shock protein
ACCESSION       AF547813
VERSION         AF547813.1 GI:27502190
KEYWORDS
SOURCE          Mycobacterium bovis
ORGANISM        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                tuberculosis complex.
REFERENCE       1 (bases 1 to 424)
AUTHORS         Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE           A multigene approach to phylogenetic analysis using the genus
                Mycobacterium as a model
JOURNAL         Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED         15653890
REFERENCE       2 (bases 1 to 424)
AUTHORS         Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE           Direct Submission
JOURNAL         Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
                Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
                Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES       Location/Qualifiers
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QY 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

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RESULT 36
AF547814
LOCUS
DEFINITION
  Mycobacterium bovis strain CIP 105050 65 kDa heat shock protein
ACCESSION
  AF547814
VERSION
  AF547814.1 GI:27502192
KEYWORDS
  source
SOURCE
  Mycobacterium bovis
ORGANISM
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
  tuberculosis complex.
REFERENCE
  1 (bases 1 to 424)
  Devulder, G., de Montclos, M.P. and Flandrois, J.P.
  A multigene approach to phylogenetic analysis using the genus
  Mycobacterium as a model
  Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
FEATURES
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ORIGIN
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  LOCUS
  DEFINITION
    Mycobacterium branderi strain CIP 104592 65 kDa heat shock protein
  ACCESSION
    AF547815
  VERSION
    AF547815.1 GI:27502194
  KEYWORDS
    source
  SOURCE
    Mycobacterium branderi
  ORGANISM
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  REFERENCE
    1 (bases 1 to 424)
    Devulder, G., de Montclos, M.P. and Flandrois, J.P.
    A multigene approach to phylogenetic analysis using the genus
    Mycobacterium as a model
    Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
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  ORIGIN
    100.0%; Score 22; DB 1; Length 424;
    Best Local Similarity 100.0%; Pred. No. 53;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 1 CCATCGCCAGGAGATCGAGCT 22
    Db 10 CCATCGCCAGGAGATCGAGCT 31
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JOURNAL
  Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED
  15653890
REFERENCE
  2 (bases 1 to 424)
  Devulder, G., Pichat, C. and Flandrois, J.P.
  Direct Submission
  Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
  Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
  Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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ORIGIN
  100.0%; Score 22; DB 1; Length 424;
  Best Local Similarity 100.0%; Pred. No. 53;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 1 CCATCGCCAGGAGATCGAGCT 22
  Db 10 CCATCGCCAGGAGATCGAGCT 31
  |||||
  RESULT 38
  AF547817
  LOCUS
  DEFINITION
    Mycobacterium celatum strain CIP 106109 65 kDa heat shock protein
  ACCESSION
    AF547817
  VERSION
    AF547817.1 GI:27502198
  KEYWORDS
    source
  SOURCE
    Mycobacterium celatum
  ORGANISM
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  REFERENCE
    1 (bases 1 to 424)
    Devulder, G., de Montclos, M.P. and Flandrois, J.P.
    A multigene approach to phylogenetic analysis using the genus
    Mycobacterium as a model
    Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
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    Best Local Similarity 100.0%; Pred. No. 53;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 1 CCATCGCCAGGAGATCGAGCT 22
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ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 424;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGATCGAGCT 22
 |||||
 Db 10 CCATGCCCAAGGATCGAGCT 31

RESULT 39
 AF547818
 LOCUS AF547818 424 bp DNA linear BCT 18-JAN-2005
 DEFINITION Mycobacterium chelonae strain CIP 104535 65 kDa heat shock protein
 (hsp65) gene, partial cds.
 ACCESSION AF547818
 VERSION AF547818.1 GI:27502200
 KEYWORDS
 SOURCE Mycobacterium chelonae
 ORGANISM
 Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 424)
 AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.
 TITLE A multigenic approach to phylogenetic analysis using the genus
 Mycobacterium as a model
 JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
 PUBLISHED 15653890
 REFERENCE 2 (bases 1 to 424)
 AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source
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ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 424;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGATCGAGCT 22
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 Db 10 CCATGCCCAAGGATCGAGCT 31

RESULT 40
 AF547819
 LOCUS AF547819 424 bp DNA linear BCT 18-JAN-2005
 DEFINITION Mycobacterium chitae strain CIP 105383 65 kDa heat shock protein
 (hsp65) gene, partial cds.
 ACCESSION AF547819
 VERSION AF547819.1 GI:27502202
 KEYWORDS
 SOURCE Mycobacterium chitae
 ORGANISM

Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 424)
 AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.
 TITLE A multigenic approach to phylogenetic analysis using the genus
 Mycobacterium as a model
 JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
 PUBLISHED 15653890
 REFERENCE 2 (bases 1 to 424)
 AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source
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ORIGIN

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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGATCGAGCT 22
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 Db 10 CCATGCCCAAGGATCGAGCT 31

RESULT 41
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 LOCUS AF547820 424 bp DNA linear BCT 18-JAN-2005
 DEFINITION Mycobacterium chlorophenolicum strain CIP 104189 65 kDa heat shock
 protein (hsp65) gene, partial cds.
 ACCESSION AF547820
 VERSION AF547820.1 GI:27502204
 KEYWORDS
 SOURCE Mycobacterium chlorophenolicum
 ORGANISM

Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 424)
 AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.
 TITLE A multigenic approach to phylogenetic analysis using the genus
 Mycobacterium as a model
 JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
 PUBLISHED 15653890
 REFERENCE 2 (bases 1 to 424)

AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

TITLE Direct Submission

JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGAGATCGAGCT 22
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Db 10 CCATCGCCCAAGAGATCGAGCT 31
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RESULT 42

AF547821

LOCUS

DEFINITION Mycobacterium chubuense strain CIP 106810 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547821

VERSION AF547821.1 GI:27502206

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 15653890

2 (bases 1 to 424)

AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

TITLE Direct Submission

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Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source

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CDS

RESULT 44

AF547823

LOCUS

DEFINITION Mycobacterium confluentis strain CIP 105510 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547823

VERSION AF547823.1 GI:27502208

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 15653890

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AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

TITLE Direct Submission

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Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source

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CDS

RESULT 42

AF547821

LOCUS

DEFINITION Mycobacterium chubuense strain CIP 106810 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547821

VERSION AF547821.1 GI:27502206

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 15653890

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AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

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Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

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CDS

RESULT 44

AF547823

LOCUS

DEFINITION Mycobacterium confluentis strain CIP 105510 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547823

VERSION AF547823.1 GI:27502208

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

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AF547821

LOCUS

DEFINITION Mycobacterium chubuense strain CIP 106810 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547821

VERSION AF547821.1 GI:27502206

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

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AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

TITLE Direct Submission

JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,

Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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LOCUS

DEFINITION Mycobacterium confluentis strain CIP 105510 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547823

VERSION AF547823.1 GI:27502208

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

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AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

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Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

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AF547821

LOCUS

DEFINITION Mycobacterium chubuense strain CIP 106810 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547821

VERSION AF547821.1 GI:27502206

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 15653890

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AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

TITLE Direct Submission

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Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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CDS

RESULT 44

AF547823

LOCUS

DEFINITION Mycobacterium confluentis strain CIP 105510 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547823

VERSION AF547823.1 GI:27502208

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 15653890

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AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.

TITLE Direct Submission

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Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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gene

CDS

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AF547821

LOCUS

DEFINITION Mycobacterium chubuense strain CIP 106810 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547821

VERSION AF547821.1 GI:27502206

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

REFERENCE 15653890

DEFINITION Mycobacterium conspicuum strain CIP 105165 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547823

VERSION AF547823.1 GI:27502210

KEYWORDS

SOURCE Mycobacterium conspicuum

ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.

TITLE A multigene approach to phylogenetic analysis using the genus Mycobacterium as a model

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

PUBMED 15653890

REFERENCE 2 (bases 1 to 424)

AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.

TITLE Direct Submission

JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 53;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CCATCGCCAGGAGATCGAGCT 31

gene

CDS

RESULT 45

AF547824

LOCUS AF547824 424 bp DNA linear BCT 18-JAN-2005

DEFINITION Mycobacterium cookii strain CIP 105396 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547824

VERSION AF547824.1 GI:27502212

KEYWORDS

SOURCE Mycobacterium cookii

ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.

TITLE A multigene approach to phylogenetic analysis using the genus Mycobacterium as a model

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

PUBMED 15653890

REFERENCE 2 (bases 1 to 424)

AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.

TITLE Direct Submission

JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 424;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CCATCGCCAGGAGATCGAGCT 31

RESULT 46

AF547825

LOCUS AF547825 424 bp DNA linear BCT 18-JAN-2005

DEFINITION Mycobacterium diernhoferi strain CIP 105384 65 kDa heat shock protein (hsp65) gene, partial cds.

ACCESSION AF547825

VERSION AF547825.1 GI:27502214

KEYWORDS

SOURCE Mycobacterium diernhoferi

ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 424)

AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.

TITLE A multigene approach to phylogenetic analysis using the genus Mycobacterium as a model

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

PUBMED 15653890

REFERENCE 2 (bases 1 to 424)

AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.

TITLE Direct Submission

JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud, Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

Location/Qualifiers

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ORIGIN

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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 47

AF547826
LOCUS
DEFINITION Mycobacterium doricum strain DSM 44339 65 kDa heat shock protein
AF547826 (hsp65) gene, partial cds.
ACCESSION AF547826.1 GI:27502216
VERSION
KEYWORDS
SOURCE
ORGANISM Mycobacterium doricum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 424)
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
JOURNAL
PUBMED 15653890
2 (bases 1 to 424)
Devulder, G., Pichat, C. and Flandrois, J.P.
Direct Submission
TITLE
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

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gene

CDS

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 48

AF547827
LOCUS
DEFINITION Mycobacterium duvalii strain CIP 104539 65 kDa heat shock protein
AF547827 (hsp65) gene, partial cds.
ACCESSION AF547827.1 GI:27502218
VERSION

KEYWORDS
SOURCE
ORGANISM

Mycobacterium duvalii
Mycobacterium duvalii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 424)
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
JOURNAL
PUBMED 15653890
2 (bases 1 to 424)
Devulder, G., Pichat, C. and Flandrois, J.P.
Direct Submission
TITLE
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source

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ORIGIN

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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 49

AF547828
LOCUS
DEFINITION Mycobacterium elephantis strain CIP 106831 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION AF547828
VERSION AF547828.1 GI:27502220
KEYWORDS
SOURCE
ORGANISM Mycobacterium elephantis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE

1 (bases 1 to 424)
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
JOURNAL
PUBMED 15653890
2 (bases 1 to 424)
Devulder, G., Pichat, C. and Flandrois, J.P.
Direct Submission
TITLE
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES

source

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Db 10 CCATGCCCAAGGAGATCGAGCT 31
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ORIGIN
Query Match 100.0%; Score 22; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 10 CCATGCCCAAGGAGATCGAGCT 31
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RESULT 50
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Myobacterium fallax strain CIP 81.39 65 kDa heat shock protein
/db_xref="GI:27502221"
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LQIGDLIAEMDKVGNVGVITVEESNTFGLQLELTGMR"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 53;
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Db 10 CCATGCCCAAGGAGATCGAGCT 31
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Best Local Similarity 100.0%; Pred. No. 53;
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QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 10 CCATGCCCAAGGAGATCGAGCT 31
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RESULT 53
AF547830
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DEFINITION
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protein (hsp65) gene, partial cds.
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/translations="GVSIKAEILEDPEYKIGAEIVKEVAKTDDVAGDGTATVLA
QALVREGLRNVAAGANPLGKRGIEKAVEKVTETLLKSAKEVETKQIAATAISAGD
LQIGDLIAEMDKVGNVGVITVEESNTFGLQLELTGMR"

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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
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Db 10 CCATGCCCAAGGAGATCGAGCT 31
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RESULT 54
AF547832
LOCUS
DEFINITION
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Myobacterium fortuitum subsp. acetamidolyticum
Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED
15653890
REFERENCE
AUTHORS
Devulder, G., Pichat, C. and Flandrois, J.P.
TITLE
Direct Submission
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CCATGCCCAAGGAGATCGAGCT 31
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RESULT 55
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Db 10 CCATGCCCAAGGAGATCGAGCT 31
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RESULT 56
AF547832
LOCUS
DEFINITION
Myobacterium fortuitum subsp. acetamidolyticum
Myobacterium fortuitum subsp. acetamidolyticum
Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE
A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED
15653890
REFERENCE
AUTHORS
Devulder, G., Pichat, C. and Flandrois, J.P.
TITLE
Direct Submission
JOURNAL
Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22
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Db 10 CCATGCCAAGGAGATCGAGCT 31

RESULT 55
AF547835
LOCUS
DEFINITION Mycobacterium gadium strain CIP 105388 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION AF547835
VERSION AF547835.1 GI:27502234
KEYWORDS
SOURCE Mycobacterium gadium
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
REFERENCE
2 (bases 1 to 424)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 10 CCATGCCAAGGAGATCGAGCT 31

RESULT 57
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LOCUS
DEFINITION Mycobacterium gilvum strain DSM 44503 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION AF547838
VERSION AF547838.1 GI:27502240
KEYWORDS
SOURCE Mycobacterium gilvum
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 424)
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
REFERENCE
2 (bases 1 to 424)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 10 CCATGCCAAGGAGATCGAGCT 31

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AF547837
LOCUS
DEFINITION Mycobacterium genavense strain DSM 44424 65 kDa heat shock protein
(hsp65) gene, partial cds.
ACCESSION AF547837
VERSION AF547837.1 GI:27502238
KEYWORDS
SOURCE Mycobacterium genavense
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 58
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LOCUS 424 bp DNA linear BCT 18-JAN-2005
DEFINITION Mycobacterium goodii strain CIP 106349 65 kDa heat shock protein
ACCESSION (hsp65) gene, partial cds.
VERSION AF547839
KEYWORDS
SOURCE
ORGANISM Mycobacterium goodii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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RESULT 60
AF547841
LOCUS 424 bp DNA linear BCT 18-JAN-2005
DEFINITION Mycobacterium haemophilum strain CIP 105049 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION AF547841
VERSION AF547841.1 GI:27502246
KEYWORDS
SOURCE
ORGANISM Mycobacterium haemophilum
Mycobacterium haemophilum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

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RESULT 59
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LOCUS 424 bp DNA linear BCT 18-JAN-2005
DEFINITION Mycobacterium gordonae strain CIP 104529 65 kDa heat shock protein
(hsp65) gene, partial cds.
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VERSION AF547840.1 GI:27502244
KEYWORDS
SOURCE
ORGANISM Mycobacterium gordonae
Mycobacterium gordonae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
AUTHORS Devulder, G., Pichat, C. and Flandrois, J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Best Local Similarity 100.0%; Pred. No. 53;
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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

RESULT 60
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DEFINITION Mycobacterium haemophilum strain CIP 105049 65 kDa heat shock
protein (hsp65) gene, partial cds.
ACCESSION AF547841
VERSION AF547841.1 GI:27502246
KEYWORDS
SOURCE
ORGANISM Mycobacterium haemophilum
Mycobacterium haemophilum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Devulder, G., de Montclos, M.P. and Flandrois, J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)

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PUBMED 15653890
REFERENCE 2 (bases 1 to 424)
AUTHORS Devulder,G.; Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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gene
CDS

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 CCATCGCCCAAGGAGATCGAGCT 31

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 16:58:33 ; Search time 12.7069 Seconds
(without alignments)
3077.569 Million cell updates/sec

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Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 60 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	22	100.0	48	6	PCT-US95-05816-54
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6	22	100.0	647	2	US-08-997-362-115
7	22	100.0	647	3	US-09-095-855-115
8	22	100.0	647	3	US-09-324-542-115
9	22	100.0	647	3	US-09-205-426-115
10	22	100.0	888	3	US-09-613-303-32
11	22	100.0	888	3	US-10-267-311-32
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15	22	100.0	1569	3	US-09-324-542-113
16	22	100.0	1569	3	US-09-205-426-113
17	22	100.0	1623	3	US-09-613-303-3
18	22	100.0	1623	3	US-10-267-311-3
19	22	100.0	1623	3	US-09-712-363-23
20	22	100.0	1626	2	US-08-997-080-159
21	22	100.0	1626	2	US-08-997-362-159
22	22	100.0	1626	3	US-09-095-855-159
23	22	100.0	1626	3	US-09-324-542-159
24	22	100.0	1626	3	US-09-205-426-159

25	22	100.0	1920	3	US-09-613-303-16	Sequence 16, Appl
26	22	100.0	1920	3	US-10-267-311-16	Sequence 16, Appl
27	22	100.0	1947	3	US-09-613-303-28	Sequence 28, Appl
28	22	100.0	1947	3	US-10-267-311-28	Sequence 28, Appl
29	22	100.0	2073	3	US-10-068-059-9	Sequence 9, Appl
30	22	100.0	2130	3	US-10-068-059-7	Sequence 7, Appl
31	22	100.0	2175	3	US-10-068-059-11	Sequence 11, Appl
32	22	100.0	2241	3	US-10-068-059-5	Sequence 5, Appl
33	22	100.0	2847	3	US-09-613-303-20	Sequence 20, Appl
34	22	100.0	2847	3	US-10-267-311-20	Sequence 20, Appl
35	22	100.0	4380	3	US-08-955-565A-3	Sequence 3, Appl
36	22	100.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
37	22	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl
38	19.4	88.2	5275	2	US-08-485-588-1	Sequence 1, Appl
39	19.4	88.2	5275	2	US-08-484-565-1	Sequence 1, Appl
40	19.4	88.2	5275	2	US-08-480-751-1	Sequence 1, Appl
41	19.4	88.2	5275	2	US-08-943-986-1	Sequence 1, Appl
42	19.4	88.2	5275	3	US-08-353-784-1	Sequence 1, Appl
43	19.4	88.2	5275	3	US-08-484-719B-1	Sequence 1, Appl
44	19.4	88.2	5275	3	US-08-484-159-1	Sequence 1, Appl
45	19	86.4	1651	3	US-09-902-540-3255	Sequence 3255, Ap
46	19	86.4	4134	3	US-09-162-021B-1	Sequence 1, Appl
47	19	86.4	4134	3	US-09-687-477-17	Sequence 17, Appl
48	19	86.4	4134	3	US-09-687-476-17	Sequence 17, Appl
49	19	86.4	4134	3	US-09-687-372-17	Sequence 17, Appl
50	19	86.4	4134	3	US-09-975-553-17	Sequence 17, Appl
51	19	86.4	4134	3	US-10-270-795-17	Sequence 17, Appl
52	19	86.4	4134	3	US-10-270-876-17	Sequence 17, Appl
53	19	86.4	4134	3	US-10-268-051-7	Sequence 7, Appl
54	19	86.4	4134	3	US-10-411-076-23	Sequence 23, Appl
55	19	86.4	4134	3	US-10-125-772-1	Sequence 1, Appl
56	19	86.4	19954	3	US-09-902-540-1150	Sequence 1150, Ap
C 57	18.8	85.5	276	3	US-09-252-991A-10595	Sequence 10595, A
C 58	18.8	85.5	606	3	US-09-252-991A-10780	Sequence 10780, A
C 59	18.8	85.5	609	3	US-09-252-991A-7774	Sequence 7774, Ap
60	18.8	85.5	720	3	US-09-252-991A-10378	Sequence 10378, A

ALIGNMENTS

RESULT 1
US-08-242-403A-54
; Sequence 54, Application US/08242403A
; Patent No. 5631130
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
; APPLICANT: Semple-Pacey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; TITLE OF INVENTION: Mycobacteria tuberculosis
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,403A
; FILING DATE: May 13, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459

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/ REFERENCE/DOCKET NUMBER: 5370.US.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 708/937-4884
/ TELEFAX: 708/938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: Mycobacterium
/ US-08-242-403A-54

Query Match 100.0%; Score 22; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 8 CCATCGCCCAAGGAGATCGAGCT 29

RESULT 2
US-08-774-128-54
; Sequence 54, Application US/08774128
; Patent No. 5786149
; GENERAL INFORMATION:
; APPLICANT: Leckie, G. W.
; APPLICANT: Davis, A. H.
; APPLICANT: Sample-Facey, I. E.
; APPLICANT: Manlove, M. T.
; APPLICANT: Solomon, N. A.
; TITLE OF INVENTION: Materials and Methods for the Detection of
; MYCOBACTERIA TUBERCULOSIS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MSDOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,128
; FILING DATE: 23-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/242,403
; FILING DATE: May 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5370.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-4884
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium
/ PCT-US95-05602-54

Query Match 100.0%; Score 22; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 8 CCATCGCCCAAGGAGATCGAGCT 29

RESULT 4
PCT-US95-05816-54
; Sequence 54, Application PC/TUS9505816
; GENERAL INFORMATION:
; APPLICANT: Solomon, N.
; ORGANISM: Mycobacterium
/ US-08-774-128-54

Query Match 100.0%; Score 22; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 8 CCATCGCCCAAGGAGATCGAGCT 29
```

APPLICANT: Leckie, G.
APPLICANT: Kratochvil, J.
APPLICANT: O'Donnell, D.
TITLE OF INVENTION: Materials and Methods for the Detection of
MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05816
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5371.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-4884
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Mycobacterium
PCT-US95-05816-54

Query Match 100.0%; Score 22; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
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Db 8 CCATCGCCCAAGGAGATCGAGCT 29

RESULT 5
US-08-997-080-115
; Sequence 115, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; INDUCED ALLERGIC REACTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
; US-08-997-080-115

Query Match 100.0%; Score 22; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3; Length 647;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 6
US-08-997-362-115
; Sequence 115, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; THE TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563

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;
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 647 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Genomic RNA
;   US-08-997-362-115
;
Query Match      100.0%; Score 22; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 7
US-09-855-115
; Sequence 115, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 647 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Genomic RNA
;   US-09-855-115
;
Query Match      100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 8
US-09-324-542-115
; Sequence 115, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-115
;
Query Match      100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 9
US-09-205-426-115
; Sequence 115, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-205-426-115
;
Query Match      100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182
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Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 10
US-09-613-303-32
; Sequence 32, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-09-613-303-32

Query Match 100.0%; Score 22; DB 3; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
|||||

Db 161 CCATGCCCAAGGAGATCGAGCT 182
|||||

RESULT 11
US-10-267-311-32
; Sequence 32, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match 100.0%; Score 22; DB 3; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
|||||

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 12
US-08-997-080-113
; Sequence 113, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-080-113

Query Match 100.0%; Score 22; DB 2; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
|||||

Db 161 CCATGCCCAAGGAGATCGAGCT 182
|||||

RESULT 13
US-08-997-362-113
; Sequence 113, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-997-362-113
Query Match 100.0%; Score 22; DB 2; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182
RESULT 14
US-09-095-855-113
Sequence 113, Application US/09095855
Patent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-095-855-113
Query Match 100.0%; Score 22; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182
RESULT 15
US-09-324-542-113
Sequence 113, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
EARLIER FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 113
LENGTH: 1569
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-09-324-542-113
Query Match 100.0%; Score 22; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182
RESULT 16
US-09-205-426-113
Sequence 113, Application US/09205426
Patent No. 6406704
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and

;; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
;; FILE REFERENCE: 11000.1002c4
;; CURRENT APPLICATION NUMBER: US/09/205,426
;; CURRENT FILING DATE: 1998-12-04
;; EARLIER APPLICATION NUMBER: 09/095,855
;; EARLIER FILING DATE: 1998-06-11
;; EARLIER APPLICATION NUMBER: 08/997,362
;; EARLIER FILING DATE: 1997-12-23
;; EARLIER APPLICATION NUMBER: 08/873,970
;; EARLIER FILING DATE: 1997-06-12
;; EARLIER APPLICATION NUMBER: 08/705,347
;; EARLIER FILING DATE: 1996-08-29
;; NUMBER OF SEQ ID NOS: 208
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 113
;; LENGTH: 1569
;; TYPE: DNA
;; ORGANISM: Mycobacterium vaccae
US-09-205-426-113

Query Match 100.0%; Score 22; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 17
US-09-613-303-3
;; Sequence 3, Application US/09613303
;; Patent No. 6495347
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Marvin
;; APPLICANT: Chu, N. Randall
;; APPLICANT: Mizzen, Lee A.
;; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
;; FILE REFERENCE: 12071/002001
;; CURRENT APPLICATION NUMBER: US/09/613,303
;; CURRENT FILING DATE: 2000-07-10
;; PRIOR APPLICATION NUMBER: US 60/143,757
;; PRIOR FILING DATE: 1999-07-08
;; NUMBER OF SEQ ID NOS: 55
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 1623
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: fusion sequence
;; NAME/KEY: CDS
;; LOCATION: (1)...(1620)
US-09-613-303-3

Query Match 100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 18
US-10-267-311-3
;; Sequence 3, Application US/10267311
;; Patent No. 6657055
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Marvin
;; APPLICANT: Chu, N. Randall
;; APPLICANT: Mizzen, Lee A.
;; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

;; FILE REFERENCE: 12071/002001
;; CURRENT APPLICATION NUMBER: US/10/267,311
;; CURRENT FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: US/09/613,303
;; PRIOR FILING DATE: 2000-07-10
;; PRIOR APPLICATION NUMBER: US 60/143,757
;; PRIOR FILING DATE: 1999-07-08
;; NUMBER OF SEQ ID NOS: 55
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 1623
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: fusion sequence
;; NAME/KEY: CDS
;; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match 100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 19
US-09-712-363-23
;; Sequence 23, Application US/09712363
;; Patent No. 6892139
;; GENERAL INFORMATION:
;; APPLICANT: Eisenberg, David
;; APPLICANT: Rotstein, Sergio H.
;; APPLICANT: Marcotte, Edward M.
;; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
;; FILE REFERENCE: 07419-032001
;; CURRENT APPLICATION NUMBER: US/09/712,363
;; CURRENT FILING DATE: 2000-11-13
;; PRIOR APPLICATION NUMBER: PCT/US00/02246
;; PRIOR FILING DATE: 2000-01-28
;; PRIOR APPLICATION NUMBER: 60/179,531
;; PRIOR FILING DATE: 2000-02-01
;; PRIOR APPLICATION NUMBER: 60/117,844
;; PRIOR FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: 60/118,206,
;; PRIOR FILING DATE: 1999-02-01
;; PRIOR APPLICATION NUMBER: 60/126,593
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: 60/134,093
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/134,092
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/165,124
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/165,086
;; PRIOR FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 292
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 23
;; LENGTH: 1623
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match 100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22

Db 161 CCATGCCAAGGAGATCGAGCT 182
|||||
RESULT 20
US-08-997-080-159
; Sequence 159, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-080-159
Query Match 100.0%; Score 22; DB 2; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATGCCAAGGAGATCGAGCT 22
Db 161 CCATGCCAAGGAGATCGAGCT 182
|||||
RESULT 21
US-08-997-362-159
; Sequence 159, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-159
Query Match 100.0%; Score 22; DB 2; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATGCCAAGGAGATCGAGCT 22
Db 161 CCATGCCAAGGAGATCGAGCT 182
|||||
RESULT 22
US-09-095-855-159
; Sequence 159, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-095-855-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 23

US-09-324-542-159
Sequence 159, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 159
LENGTH: 1626
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-09-324-542-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 24

US-09-205-426-159
Sequence 159, Application US/09205426
Patent No. 6406704
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002c4

CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER FILING DATE: 1997-06-12
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 159
LENGTH: 1626
TYPE: DNA
ORGANISM: Mycobacterium vaccae
US-09-205-426-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 25

US-09-613-303-16
Sequence 16, Application US/09613303
Patent No. 6495347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1920
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(1917)
US-09-613-303-16

Query Match 100.0%; Score 22; DB 3; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 26

US-10-267-311-16
Sequence 16, Application US/10267311
Patent No. 6657055
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311

; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-267-311-16

Query Match 100.0%; Score 22; DB 3; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 27
US-09-613-303-28
; Sequence 28, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-09-613-303-28

Query Match 100.0%; Score 22; DB 3; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 28
US-10-267-311-28
; Sequence 28, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311

; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-267-311-28

Query Match 100.0%; Score 22; DB 3; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 29
US-10-068-059-9
; Sequence 9, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match 100.0%; Score 22; DB 3; Length 2073;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 611 CCATGCCCAAGGAGATCGAGCT 632

RESULT 30
US-10-068-059-7
; Sequence 7, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059

; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-7

Query Match 100.0%; Score 22; DB 3; Length 2130;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 668 CCATGCCCAAGGAGATCGAGCT 689
|||||

RESULT 31
US-10-068-059-11
; Sequence 11, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 22; DB 3; Length 2175;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 713 CCATGCCCAAGGAGATCGAGCT 734
|||||

RESULT 32
US-10-068-059-5
; Sequence 5, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 22; DB 3; Length 2241;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 779 CCATGCCCAAGGAGATCGAGCT 800
|||||

RESULT 33
US-09-613-303-20
; Sequence 20, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-09-613-303-20

Query Match 100.0%; Score 22; DB 3; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 221 CCATGCCCAAGGAGATCGAGCT 242
|||||

RESULT 34
US-10-267-311-20
; Sequence 20, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match      100.0%; Score 22; DB 3; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      221 CCATGCCCAAGGAGATCGAGCT 242

RESULT 35
US-08-955-565A-3
; Sequence 3, Application US/08955565A
; Patent No. 6331388
; GENERAL INFORMATION:
; APPLICANT: Malkovsky, Miroslav
; APPLICANT: Wells, Andrew
; TITLE OF INVENTION: Immune Response Enhancer Therapy
; FILE REFERENCE: WARP-02625
; CURRENT APPLICATION NUMBER: US/08/955,565A
; CURRENT FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4380
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-08-955-565A-3

Query Match      100.0%; Score 22; DB 3; Length 4380;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      412 CCATGCCCAAGGAGATCGAGCT 433

RESULT 36
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
```


;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below: 9
;; APPLICATION NUMBER: 08/353,784
;; FILING DATE: 9 December, 1994
;; APPLICATION NUMBER: PCT/US/94/12117
;; FILING DATE: 21 October, 1994
;; APPLICATION NUMBER: U.S. 08/292,827
;; FILING DATE: 23 August, 1994
;; APPLICATION NUMBER: U.S. 08/141,248
;; FILING DATE: 22 October, 1993
;; APPLICATION NUMBER: U.S. 08/009,389
;; FILING DATE: 23 February, 1993
;; APPLICATION NUMBER: U.S. 07/934,161
;; FILING DATE: 21 August, 1992
;; APPLICATION NUMBER: U.S. 07/834,044
;; FILING DATE: 11 February, 1992
;; APPLICATION NUMBER: U.S. 07/749,451
;; FILING DATE: 23 August, 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Heber, Sheldon O.
;; REGISTRATION NUMBER: 38,179
;; REFERENCE/DOCKET NUMBER: 213/005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5275 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 515..3769
;; OTHER INFORMATION:
US-08-485-588-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 39
US-08-484-565-1
; Sequence 1, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: FASTSEQ
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,565
;; FILING DATE: 7 June, 1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below: 9
;; APPLICATION NUMBER: 08/353,784
;; FILING DATE: 9 December, 1994
;; APPLICATION NUMBER: PCT/US/94/12117
;; FILING DATE: 21 October, 1994
;; APPLICATION NUMBER: U.S. 08/292,827
;; FILING DATE: 23 August, 1994
;; APPLICATION NUMBER: U.S. 08/141,248
;; FILING DATE: 22 October, 1993
;; APPLICATION NUMBER: U.S. 08/009,389
;; FILING DATE: 23 February, 1993
;; APPLICATION NUMBER: U.S. 08/017,127
;; FILING DATE: 12 February, 1993
;; APPLICATION NUMBER: U.S. 07/934,161
;; FILING DATE: 21 August, 1992
;; APPLICATION NUMBER: U.S. 07/834,044
;; FILING DATE: 11 February, 1992
;; APPLICATION NUMBER: U.S. 07/749,451
;; FILING DATE: 23 August, 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Heber, Sheldon O.
;; REGISTRATION NUMBER: 38,179
;; REFERENCE/DOCKET NUMBER: 213/006
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5275 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 515..3769
;; OTHER INFORMATION:
US-08-484-565-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 40
US-08-480-751-1
; Sequence 1, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-480-751-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 41
US-08-943-986-1
Sequence 1, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-943-986-1

Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 42
US-08-353-784-1
; Sequence 1, Application US/08353784
; Patent No. 6011068
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen, Manuel
; APPLICANT: F. Balandrin, Forrest H. Fuller,
; APPLICANT: Eric G. Delmar, and Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,784
; FILING DATE: 9 December, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 8
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hebert, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 209/069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
US-08-353-784-1

Query Match 88.2%; Score 19.4; DB 3; Length 5275;

Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAGCT 22
DB 2311 CATCGCCCAAGGAGATCGAGTT 2331

RESULT 43
US-08-484-719B-1
; Sequence 1, Application US/08484719B
; Patent No. 6031003
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen,
; APPLICANT: Manuel P. Balandrin,
; APPLICANT: Forrest H. Fuller, Eric G.
; APPLICANT: Delmar, Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Word
; SOFTWARE: FASTSEQ for Windows Version 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,719B
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Douglas C. Murdock
; REGISTRATION NUMBER: 37,549
; REFERENCE/DOCKET NUMBER: 213/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; US-08-484-719B-1

Query Match      88.2%; Score 19.4; DB 3; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
Db      2311 CATGCCAAGGAGATCGAGTT 2331

RESULT 44
US-08-484-159-1
; Sequence 1, Application US/08484159
; Patent No. 6313146
; GENERAL INFORMATION:
; APPLICANT: Bradford C. Van Wagenen
; APPLICANT: Manuel F. Balandrin
; APPLICANT: Eric G. Del Mar
; APPLICANT: Edward F. Nemeth
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,159
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 214/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; US-08-484-719B-1

Query Match      88.2%; Score 19.4; DB 3; Length 5275;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGAGCT 22
Db      2311 CATGCCAAGGAGATCGAGTT 2331

RESULT 45
US-09-902-540-3255
; Sequence 3255, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3255
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-3255

Query Match      86.4%; Score 19; DB 3; Length 1651;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TCGCCAAGGAGATCGAGCT 22
Db      164 TCGCCAAGGAGATCGAGCT 182

RESULT 46
US-09-162-021B-1
; Sequence 1, Application US/09162021B
; Patent No. 6337391
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/09/162,021B
; CURRENT FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 1
LENGTH: 4134
TYPE: DNA
ORGANISM: squalas acanthias
FEATURE:
NAME/KEY: CDS
LOCATION: (439)...(3522)
US-09-162-021B-1

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 47

US-09-687-477-17
Sequence 17, Application US/09687477
Patent No. 6463883
GENERAL INFORMATION:
APPLICANT: AquaBio Product Sciences, LLC
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.1004-000
CURRENT APPLICATION NUMBER: US/09/687,477
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-687-477-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 48

US-09-687-476-17
Sequence 17, Application US/09687476
Patent No. 6475792
GENERAL INFORMATION:
APPLICANT: AquaBio Product Sciences, LLC
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.2001-000
CURRENT APPLICATION NUMBER: US/09/687,476
CURRENT FILING DATE: 2000-10-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-687-476-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 49

US-09-687-372-17
Sequence 17, Application US/09687372
Patent No. 6481379
GENERAL INFORMATION:
APPLICANT: AquaBio Product Sciences, LLC
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.2002-000
CURRENT APPLICATION NUMBER: US/09/687,372
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-687-372-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 50

US-09-975-553-17
Sequence 17, Application US/09975553
Patent No. 6564747
GENERAL INFORMATION:
APPLICANT: Harris, H. William, Jr.
APPLICANT: Russell, David R.
APPLICANT: Nearing, Jacqueline
APPLICANT: Betka, Marlies
TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
FILE REFERENCE: 2213.1004-001
CURRENT APPLICATION NUMBER: US/09/975,553
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/687,477
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 09/687,476
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 09/687,372
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 4134
TYPE: DNA
ORGANISM: Dogfish Shark
US-09-975-553-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 51
US-10-270-795-17
; Sequence 17, Application US/10270795
; Patent No. 6637171
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/10/270,795
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,372
; PRIOR FILING DATE: 2000-10-12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 52
US-10-270-876-17
; Sequence 17, Application US/10270876
; Patent No. 6655318
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 53
US-10-268-051-7
; Sequence 7, Application US/10268051
; Patent No. 6748900
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A
; APPLICANT: Betka, Marlies
; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213.2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-268-051-7

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 54
US-10-411-076-23
; Sequence 23, Application US/10411076
; Patent No. 6854422
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Growing Marine Fish in Freshwater
; FILE REFERENCE: 2213.1003007
; CURRENT APPLICATION NUMBER: US/10/411,076
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US01/31625
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,373
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Mustelus canis
US-10-411-076-23

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 55
US-10-125-772-1
; Sequence 1, Application US/10125772
; Patent No. 6951739

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20
|||||
Db 2256 CATGCCAAGGAGATCGAG 2274

; GENERAL INFORMATION:

; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-006
; CURRENT APPLICATION NUMBER: US/10/125,772
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-772-1

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAG 20

Db 2256 CATGCCAAGGAGATCGAG 2274

RESULT 56

US-09-902-540-1150
; Sequence 1150, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1150
; LENGTH: 19954
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1150

Query Match 86.4%; Score 19; DB 3; Length 19954;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGCCAAGGAGATCGAGCT 22

Db 7764 TCGCCAAGGAGATCGAGCT 7782

RESULT 57

US-09-252-991A-10595/c
; Sequence 10595, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10595
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10595

Query Match 85.5%; Score 18.8; DB 3; Length 276;
Best Local Similarity 90.9%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22

Db 225 CCATGCCAAGGAGATCGAGCT 204

RESULT 58

US-09-252-991A-10780/c
; Sequence 10780, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10780
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10780

Query Match 85.5%; Score 18.8; DB 3; Length 606;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22

Db 109 CCATGCCAAGGAGATCGAGCT 88

RESULT 59

US-09-252-991A-7774/c
; Sequence 7774, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7774
; LENGTH: 609
; TYPE: DNA

Search completed: April 1, 2006, 17:06:14
Job time : 25.7069 secs

GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 21:55:10 ; Search time 44.7112 Seconds
(without alignments)
3279.340 Million cell updates/sec

Title: US-10-824-527-1
Perfect score: 22
Sequence: 1 ccacgcgaagagatcgagct 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001s.*
5: Geneseqn2002s.*
6: Geneseqn2003s.*
7: Geneseqn2004s.*
8: Geneseqn2005s.*
9: Geneseqn2006s.*
10: Geneseqn2007s.*
11: Geneseqn2008s.*
12: Geneseqn2009s.*
13: Geneseqn2010s.*
14: Geneseqn2011s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	22	100.0	22 14	ADV99121 groEL2 ge
2	22	100.0	45 4	Aah46029 BCG deriv
3	22	100.0	647 2	AAV34609 M. vaccae
4	22	100.0	647 2	AAZ11344 Nucleotid
5	22	100.0	647 6	ABL36250 M vaccae
6	22	100.0	647 8	ABL36250 M vaccae
7	22	100.0	888 5	ACC42532 Mycobacte
8	22	100.0	1496 13	AAZ25022 Nucleotid
9	22	100.0	1569 2	AAV34608 M. vaccae
10	22	100.0	1569 2	AAZ11343 Nucleotid
11	22	100.0	1569 6	ABL36249 M vaccae
12	22	100.0	1620 8	ACA38272 Prokaryot
13	22	100.0	1620 13	ADR12623 Gene vacc
14	22	100.0	1623 4	Aah51969 Mycobacte
15	22	100.0	1623 5	AAZ25002 Nucleotid
16	22	100.0	1623 8	ACA40326 Prokaryot
17	22	100.0	1623 8	ACA37725 Prokaryot
18	22	100.0	1623 12	ADN11336 Chapteroni
19	22	100.0	1626 2	AAZ11371 Nucleotid

20	22	100.0	1626	6	ABL36277	ABL36277 M vaccae
21	22	100.0	1626	8	ACC42531	ACC42531 Mycobacte
22	22	100.0	1626	8	ACA39632	ACA39632 Prokaryot
23	22	100.0	1626	9	ACC70275	ACC70275 Nucleotid
24	22	100.0	1632	13	ADT46122	ADT46122 Bacterial
25	22	100.0	1701	9	AAZ57198	AAZ57198 Mycobacte
26	22	100.0	1752	8	ACC49833	ACC49833 Human rec
27	22	100.0	1761	14	ADX05272	ADX05272 HSP65-MUC
28	22	100.0	1800	10	ADK68629	ADK68629 HSP65-MUC
29	22	100.0	1914	8	ACC49834	ACC49834 Human rec
30	22	100.0	1920	5	AAF25012	AAF25012 Nucleotid
31	22	100.0	1947	5	AAF25019	AAF25019 Nucleotid
32	22	100.0	1965	13	ADM23606	ADM23606 Hepatite
33	22	100.0	1980	12	ADN00588	ADN00588 BCG vacci
34	22	100.0	2016	12	ADK72374	ADK72374 BCG-HER-2
35	22	100.0	2073	6	ABS54448	ABS54448 BCG Hsp65
36	22	100.0	2130	6	ABS54447	ABS54447 BCG Hsp65
37	22	100.0	2175	6	ABS54449	ABS54449 BCG Hsp65
38	22	100.0	2241	6	ABS54446	ABS54446 His tagge
39	22	100.0	2585	13	ADR30583	ADR30583 Arthrobac
40	22	100.0	2847	5	AAF25014	AAF25014 Nucleotid
41	22	100.0	3613	1	AAH80339	AAH80339 Clone Y31
42	22	100.0	4260	1	AAH81768	AAH81768 Sequence
43	22	100.0	4380	1	AAH80222	AAH80222 Sequence
44	22	100.0	4380	2	AAV05708	AAV05708 Mycobacte
45	22	100.0	4380	6	AAH99141	AAH99141 hsp65 enc
46	22	100.0	13380	4	AAH59637	AAH59637 Propionib
47	22	100.0	13380	8	ACF64566	ACF64566 Propionib
48	22	100.0	86114	6	ABX09143	ABX09143 Mycobacte
49	22	100.0	110000	4	AAI99682_05	Continuation (6 of
50	22	100.0	110000	4	AAI99682_05	Continuation (6 of
51	21	95.5	48	2	AAI06825	AAI06825 65 KD hea
52	21	95.5	48	2	AAI06825	AAI06825 65 KD hea
53	20.4	92.7	1728	13	ADS56335	ADS56335 Bacterial
54	20.4	92.7	99090	12	ADM72250	ADM72250 O. minuta
55	20	90.9	20	9	ACF04316	ACF04316 Mycobacte
56	19.4	88.2	5275	2	AAV28962	AAV28962 Bovine pa
57	19.4	88.2	5275	2	AAI95857	AAI95857 Bovine pa
58	19.4	88.2	5275	2	AAZ25053	AAZ25053 Bovine pa
59	19.4	88.2	5275	2	AAV82483	AAV82483 Bovine pa
60	19.4	88.2	5275	3	AAZ89296	AAZ89296 Bovine Ca

ALIGNMENTS

RESULT 1
ADV99121
ID ADV99121 standard; DNA; 22 BP.

XX	AC	ADV99121;
XX	DT	24-MAR-2005 (first entry)
XX	DE	groEL2 gene forward primer, STGROF1, SEQ ID 1.
XX	DE	Microorganism identification; microorganism detection; groEL2;
XX	KW	potato scab; PCR; primer; ss.
XX	OS	Streptomyces sp.
XX	PN	US2004265873-A1.
XX	PD	30-DEC-2004.
XX	PF	15-APR-2004; 2004US-00824527.
XX	PR	18-APR-2003; 2003KR-00024656.
XX	PR	14-NOV-2003; 2003KR-00080580.
XX	PA	(KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX	PI	Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

```

XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
XX Claim 1; SEQ ID NO 1; 34pp; English.
XX
XX The present invention relates to novel primers STGR0F1 (ADV99121) and
CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
XX Sequence 22 BP; 6 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
SQ
    Query Match      100.0%; Score 22; DB 14; Length 22;
    Best Local Similarity 100.0%; Pred. No. 2.3;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 1 CCATCGCCCAAGGAGATCGAGCT 22

RESULT 2
AAH46029
ID AAH46029 standard; DNA; 45 BP.
XX
XX AAH46029;
XX
DT 12-SEP-2001 (first entry)
XX
DE BCG derived synthetic oligonucleotide 3.
XX
XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
XX tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
XX lymphoma; ss; BCG.
XX
XX Mycobacterium bovis.
XX Synthetic.
XX
XX WO200144465-A2.
XX
XX 21-JUN-2001.
XX
XX 12-DEC-2000; 2000WO-CA001467.
XX
XX 13-DEC-1999; 99US-0170325P.
XX
XX 29-AUG-2000; 2000US-0228925P.
XX
XX (BION-) BIONICHE LIFE SCI INC.
XX
XX Phillips NC, Fillion MC;
XX
XX WPI; 2001-398150/42.
XX
XX Composition comprising synthetic oligonucleotides which comprise multiple
PT repeats of dinucleotides such as GT, TG useful for treating cancer by
PT inducing cell cycle arrest, inhibiting proliferation, activating
PT caspases.
XX
XX Example 20; Page 33; 77pp; English.
XX
XX The present sequence is that of a synthetic BCG (Bacillus Calmette-
CC Guerin) derived oligonucleotide useful to the invention. The invention
CC

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CC relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH
CC synthetic oligonucleotide which comprises multiple repeats of
CC dinucleotides such as GT, TG, etc., according to specific formula and
CC having cytostatic activity. The oligonucleotide compositions are useful
CC for inducing cell cycle arrest, inhibition of proliferation, activation
CC of caspases and induction of apoptosis or production of cytokines such as
CC interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor
CC (TNF)-alpha by immune system cells, in an animal having cancer such as
CC primary carcinoma, secondary carcinoma, primary sarcoma and secondary
CC sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal,
CC ovarian or bone cancer. The compositions induce apoptosis independent of
CC Fas, p53/p21, p21/waf-1/CIP, p15(ink4b), p16(ink4), drug resistance,
CC caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone
CC dependence
XX
XX Sequence 45 BP; 13 A; 11 C; 14 G; 7 T; 0 U; 0 Other;
SQ
    Query Match      100.0%; Score 22; DB 4; Length 45;
    Best Local Similarity 100.0%; Pred. No. 2.4;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 2 CCATCGCCCAAGGAGATCGAGCT 23

RESULT 3
AAV34609
ID AAV34609 standard; RNA; 647 BP.
XX
XX AAV34609;
XX
DT 25-AUG-1998 (first entry)
XX
DE M. vaccae antigen GV-27A encoding DNA.
XX
XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
XX M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
XX mycobacteria infection; vaccine; cancer; ss.
XX
XX Mycobacterium vaccae.
XX
XX Key      Location/Qualifiers
XX CDS      1..645
XX          /tag= a
XX          /product= "GV-27A antigen"
XX          /note= "the stop codon is not indicated"
XX
XX WO9808542-A2.
XX
XX 05-MAR-1998.
XX
XX 28-AUG-1997; 97WO-NZ000105.
XX
XX 29-AUG-1996; 96US-00705347.
XX
XX 12-JUN-1997; 97US-00873970.
XX
XX (GENE-) GENESIS RES & DEV CORP.
XX
XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
XX
XX P-PSDB; AAW60145.
XX
XX Mycobacterium vaccae polypeptides - used to develop products for use in
PT detection, therapy and prevention of mycobacteria infections or as immune
PT response enhancers.
XX
XX Example 6; Page 116; 153pp; English.
XX
XX This RNA encodes a Mycobacterium vaccae antigen GV-27A. The invention
CC provides M. vaccae polypeptides that comprise an immunogenic portion of a
CC soluble M. vaccae antigen, or a variant, where the antigen induces an

```

CC immune response in patients previously exposed to a mycobacterium. Such
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific
 CC immune response. The methods and products can be used for the detection,
 CC treatment and prevention of infectious diseases caused by mycobacteria
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
 CC the ability to induce cell proliferation and cytokine production (e.g.
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells, B
 CC cells, or macrophages. They can be used for enhancing immune responses
 CC for use in vaccines or immunotherapy of infectious diseases and cancers

SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 647;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 4

AAZ11344

ID AAZ11344 standard; DNA; 647 BP.

XX

AC AAZ11344;

XX

XX

DT 25-OCT-1999 (first entry)

XX

DE Nucleotide sequence of M. vaccae antigen GV-27A.

XX

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 KW squamous cell carcinoma; melanoma; sb.

XX

OS Mycobacterium vaccae.

XX

PN WO9932634-A2.

XX

XX

PD 01-JUL-1999.

XX

PF 23-DEC-1998; 98WO-NZ000189.

XX

PR 23-DEC-1997; 97US-00996624.

XX

PR 23-DEC-1997; 97US-00997080.

XX

PR 23-DEC-1997; 97US-00997382.

XX

PR 11-JUN-1998; 98US-00095855.

XX

PR 17-SEP-1998; 98US-00156181.

XX

PR 04-DEC-1998; 98US-00205426.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX

PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;

XX

DR WPI; 1999-430163/36.

XX

DR P-PSDB; RAY14892.

XX

XX Enhancing immune response to an antigen.

XX

PS Example 14; Page 190-191; 243pp; English.

XX

CC The invention provides heat-killed Mycobacterium vaccae, or recombinant
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
 CC cells and natural killer cells, to stimulate the production of cytokines,
 CC to enhance the expression of co-stimulatory molecules on dendritic cells
 CC and monocytes, and to enhance dendritic cell maturation and function. The
 CC proteins can be expressed by standard recombinant methodology.
 CC Pharmaceutical compositions comprising the proteins or nucleic acid
 CC sequences encoding the proteins can be used for the treatment,
 CC prevention, and detection of disorders including infectious diseases,

CC immune disorders and cancer. In particular, the compounds and methods are
 CC used for treatment of diseases of the respiratory system, such as
 CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
 CC sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma

SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 647;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 5

ABL36250

ID ABL36250 standard; DNA; 647 BP.

XX

AC ABL36250;

XX

XX

DT 08-APR-2002 (first entry)

XX

XX

DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 115.

XX

KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
 KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
 KW antipruritic; dermatological; antiinflammatory; antiallergic;
 KW Th2 immune response; immunomodulatory; gene; ds.

XX

OS Mycobacterium vaccae.

XX

PN US6328978-B1.

XX

PD 11-DEC-2001.

XX

PF 02-JUN-1999; 99US-00324542.

XX

PR 23-DEC-1997; 97US-00997080.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX

PI Watson JD, Tan PLJ, Prestidge R;

XX

DR WPI; 2002-138361/18.

XX

DR P-PSDB; ABB73498.

XX

PT Inhibiting skin inflammation associated with skin disorder e.g.

XX

PT psoriasis, by administering composition comprising delipidated and

XX

PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae

XX

PT culture filtrate.

XX

PS Example 4; Col 125-126; 116pp; English.

XX

CC The present invention relates to a method of inhibiting skin inflammation
 CC associated with a skin disorder selected from psoriasis, atopic
 CC dermatitis and allergic contact dermatitis, which involves administering
 CC a composition containing delipidated and deglycolipidated Mycobacterium
 CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
 CC treated may also include alopecia areata, and skin cancers such as basal
 CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
 CC acts by inhibiting the Th2 immune response. The present sequence is a
 CC coding sequence described in the exemplification of the invention

SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 647;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 6
ACC42532
ID ACC42532 standard; DNA; 647 BP.
XX
AC ACC42532;
XX
DT 26-AUG-2003 (first entry)
XX
DE Mycobacterium vaccae antigen GV-27A coding sequence, SEQ ID 15.
XX
KW Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
KW antidiabetic; antipsoriatic; dermatological; anti-inflammatory;
KW immune response; Notch signalling pathway; autoimmune disorder;
KW Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
KW apoptotic cell death; cell proliferation; gene; ds.
XX
OS Mycobacterium vaccae.
XX
FH Key Location/Qualifiers
FT CDS 1..645
FT /tag= a
FT /partial
FT /product= "Antigen GV-27A"
FT /note= "No stop codon given"
XX
PN WO2003013595-A1.
XX
PD 20-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-NZ000135.
XX
PR 26-JUL-2001; 2001US-0308446P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Abernethy N;
XX
DR WPI; 2003-239567/23.
DR P-PSDB; ABP70892.
XX
PT Methods for modulating immune responses by modulating the Notch signaling
PT and Toll-like receptor signaling pathways, and treating e.g. autoimmune
PT disorders.
XX
PS Claim 7; Page 109; 136pp; English.
XX
CC The present invention relates to methods for modulating immune responses
CC by modulating the Notch signalling and Toll-like receptor signalling
CC pathways using compositions comprising mycobacteria antigens (ACC42518-
CC ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
CC immune responses and treating e.g. autoimmune disorders (such as multiple
CC sclerosis, rheumatoid arthritis, Type I diabetes mellitus, psoriasis,
CC systemic lupus erythematosus, scleroderma), allergic disease and graft
CC rejection and also disorders characterised by undesired apoptotic cell
CC death or undesired cell proliferation
XX
SQ Sequence 647 BP; 136 A; 204 C; 215 G; 92 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 8; Length 647;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 7
AAF25022
ID AAF25022 standard; DNA; 888 BP.
XX
AC AAF25022;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of Hsp65-E7 fusion protein.
XX
KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KW E7 protein; ss.
XX
OS Synthetic.
OS Mycobacterium bovis.
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT CDS 1..888
FT /tag= a
FT /product= "Hsp65-E7 fusion protein"
XX
PN WO200104344-A2.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018828.
XX
PR 08-JUL-1999; 99US-0143757P.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Siegel M, Chu NR, Mizzen LA;
XX
DR WPI; 2001-138361/14.
DR P-PSDB; AAB31615.
XX
PT Screening for compounds that stimulate Th1-like responses in CD4+ T
PT lymphocyte cells.
XX
PS Example 12; Fig 11; 88pp; English.
XX
CC The present sequence encodes a fusion protein comprising a Mycobacterium
CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7
CC protein. The fusion protein is used in the method of the invention. The
CC specification describes a method of determining whether a compound
CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
CC lymphocyte cells. The method comprises contacting naive lymphocytes in
CC vitro with a fusion protein comprising at least a fragment of Hsp, and
CC then detecting the Th1-like response exhibited by the cell sample. The
CC proteins which may be used in the method of the invention are Hsp65,
CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
CC compounds that stimulate Th1-like responses in response to microbial
CC pathogens
XX
SQ Sequence 888 BP; 224 A; 235 C; 272 G; 157 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 5; Length 888;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 8
ADW23618
ID ADW23618 standard; DNA; 1496 BP.
XX
AC ADW23618;
XX
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DT 10-MAR-2005 (first entry)
DE HSP65 DNA.
KW recombinant protein; vaccine; fusion protein; HSP65; ds.
OS Unidentified.
XX CN1462636-A.
XX 24-DEC-2003.
XX 30-MAY-2002; 2002CN-00122116.
XX 30-MAY-2002; 2002CN-00122116.
XX (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX Wang L, Sun M, Yu Y;
XX WPI; 2004-239553/23.
XX Vaccine of recombinated albumen for preventing and treating infection of
XX human hepatitis C virus.
XX Example 1; Page 14; 54pp; Chinese.
XX The invention relates to a recombinant protein vaccine which is a fusion
XX protein of BCG vaccine's heat shock protein 65 and the core antigen of
XX multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
XX and nucleotide sequence for coding it, the expression carrier containing
XX nucleotide sequence, the host cell containing expression carrier, the
XX preparing process of recombinant protein vaccine, the vaccine containing
XX recombinant protein for preventing and treating hepatitis C and a method
XX for detecting the activity of specifically killing T-lymphocytes by the
XX hepatitis C induced by vaccine and its cell model are disclosed. The
XX present sequence represents a HSP65 DNA.
XX Sequence 1496 BP; 300 A; 456 C; 523 G; 217 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 13; Length 1496;
XX Best Local Similarity 100.0%; Pred. No. 3.2;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 163 CCATCGCCCAAGGAGATCGAGCT 184

RESULT 9
AAV34608
ID AAV34608 standard; DNA; 1569 BP.
XX
XX AAV34608;
XX
XX 25-AUG-1998 (first entry)
XX M. vaccae antigen GV-27 encoding DNA.
XX
XX Mycobacterium vaccae; antigen; prevention; cytokine production;
XX M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
XX mycobacteria infection; vaccine; cancer; ss.
XX
XX Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
XX CDS 1..1569
XX /*tag= a
XX /product= "GV-27 antigen"
XX /note= "the stop codon is not indicated"
XX
XX WO9808542-A2.

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PD 05-MAR-1998.
XX
XX 28-AUG-1997; 97WO-NZ000105.
XX
XX 29-AUG-1996; 96US-00705347.
XX 12-JUN-1997; 97US-00873970.
XX
XX (GENE-) GENESIS RES & DEV CORP.
XX
XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX
XX WPI; 1998-216926/19.
XX P-FSDB; AAW60144.
XX
XX Mycobacterium vaccae polypeptides - used to develop products for use in
XX detection, therapy and prevention of mycobacteria infections or as immune
XX response enhancers.
XX
XX Example 6; Page 114; 153pp; English.
XX
XX This DNA encodes a Mycobacterium vaccae antigen GV-27. The invention
XX provides M. vaccae polypeptides that comprise an immunogenic portion of a
XX soluble M. vaccae antigen, or a variant, where the antigen induces an
XX immune response in patients previously exposed to a mycobacterium. Such
XX M. vaccae polypeptides can be used in methods for enhancing non-specific
XX immune response. The methods and products can be used for the detection,
XX treatment and prevention of infectious diseases caused by mycobacteria
XX such as M. vaccae, M. avium or M. tuberculosis. The products also have
XX the ability to induce cell proliferation and cytokine production (e.g.
XX interferon-gamma and interleukin-12 production) in T cells, NK cells, B
XX cells, or macrophages. They can be used for enhancing immune responses
XX for use in vaccines or immunotherapy of infectious diseases and cancers
XX
XX Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 2; Length 1569;
XX Best Local Similarity 100.0%; Pred. No. 3.2;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 10
AAZ11343
ID AAZ11343 standard; DNA; 1569 BP.
XX
XX AAZ11343;
XX
XX 25-OCT-1999 (first entry)
XX
XX Nucleotide sequence of M. vaccae antigen GV-27.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
XX dendritic cell maturation; infectious disease; immune disorder; cancer;
XX respiratory system; mycobacterial infection; allergy; tuberculosis;
XX leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
XX dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
XX squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
XX
XX WO9932634-A2.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
XX 23-DEC-1997; 97US-00997080.
XX 23-DEC-1997; 97US-00997362.
XX 11-JUN-1998; 98US-00095855.
XX

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PR 17-SEP-1998; 98US-00156181.
PR 04-DEC-1998; 98US-00205426.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX PI
XX WPI; 1999-430163/36.
XX P-PSDB; AAY14891.
XX Enhancing immune response to an antigen.
XX Example 14; Page 188-189; 243pp; English.
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC to enhance the expression of co-stimulatory molecules on dendritic cells
CC and monocytes, and to enhance dendritic cell maturation and function. The
CC proteins can be expressed by standard recombinant methodology.
CC Pharmaceutical compositions comprising the proteins or nucleic acid
CC sequences encoding the proteins can be used for the treatment,
CC prevention, and detection of disorders including infectious diseases,
CC immune disorders and cancer. In particular, the compounds and methods are
CC used for treatment of diseases of the respiratory system, such as
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma
XX
SQ Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 2; Length 1569;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182
RESULT 11
ABL36249
ID ABL36249 standard; DNA; 1569 BP.
XX AC
XX ABL36249;
XX 08-APR-2002 (first entry)
XX DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 113.
XX KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
XX KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
XX KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
XX KW Th2 immune response; immunomodulatory; gene; ds.
XX OS Mycobacterium vaccae.
XX PN US6328978-B1.
XX PD 11-DEC-2001.
XX PF 02-JUN-1999; 99US-00324542.
XX PR 23-DEC-1997; 97US-00997080.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Watson JD, Tan PLJ, Prestidge R;
XX WPI; 2002-138361/18.
XX P-PSDB; ABB73497.
us-10-824-527-1.rng
XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX Example 4; Col 121-124; 116pp; English.
XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC coding sequence described in the exemplification of the invention
XX
SQ Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 6; Length 1569;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182
RESULT 12
ACA38272
ID ACA38272 standard; DNA; 1620 BP.
XX AC
XX ACA38272;
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #19929.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW drug design; gene.
XX OS Mycobacterium bovis.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX P-PSDB; ABU34402.
XX DR New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX Claim 14; SEQ ID NO 26142; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1620;
 Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGATCGAGCT 22
 DB 161 CCATCGCCCAAGGATCGAGCT 182

RESULT 13

ADRI12623
 ID ADRI12623 standard; DNA; 1620 BP.

AC ADRI12623;

DT 04-NOV-2004 (first entry)

DE Gene vaccine nucleic acid #41.

KW ds; gene; antimalarial; antitubercular; tuberculostatic; anti-HIV;
 KW antibacterial; haemostatic; protozoacide; antiinflammatory;
 KW neuroprotective; virucide; gene vaccine; ubiquitin; antigen;
 KW intracellular parasite; protozoan parasite infection; malaria;
 KW tuberculosis; toxoplasmosis; trypanosomiasis; AIDS;
 KW cytomegalovirus infection; achiomydia disease; Rickettsia; leishmaniasis;
 KW Ebola hemorrhagic fever; Trypanosoma; Chagas disease;
 KW Japanese encephalitis; influenza; rubeola; dengue virus; poliomyelitis;
 KW Herpes virus; severe acute respiratory syndrome.

OS Unidentified.

PN WO2004067040-A1.

PD 12-AUG-2004.

XX 30-JAN-2004; 2004WO-JP000975.

PF 31-JAN-2003; 2003JP-00023507.

XX (KYUS-) KYUSHU TLO CO LTD.

XX Himeno K, Ishii K;

XX

DR WPI; 2004-594036/57.

DR P-PSDB; ADR12624.

XX Gene vaccine having nucleic acids encoding ubiquitin and antigen protein
 PT of intracellular parasite, useful for treating parasite infections such
 PT as malaria, tuberculosis, toxoplasmosis.

XX Disclosure; SEQ ID NO 90; 266pp; Japanese.

XX A gene vaccine (1) comprises nucleic acid sequence encoding ubiquitin,
 CC and a nucleic acid sequence encoding the antigen protein of an
 CC intracellular parasite containing T-cell target sequence. (1) is useful
 CC for preventing or treating the disease resulting from intracellular
 CC protozoan parasite infection such as malaria, tuberculosis,
 CC toxoplasmosis, trypanosomiasis, AIDS, cytomegalovirus infection,
 CC achiomydia disease, infections caused by Rickettsia, leishmaniasis,
 CC Ebola hemorrhagic fever, Trypanosoma infections, Chagas disease, Japanese
 CC encephalitis, influenza, rubeola and dengue viral infections,
 CC poliomyelitis, Herpes virus (alpha) infections, or severe acute
 CC respiratory syndrome. This sequence represent a nucleic acid used in the
 CC method of the invention.

SQ Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 13; Length 1620;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGATCGAGCT 22

DB 161 CCATCGCCCAAGGATCGAGCT 182

RESULT 14

ADRI12623
 ID ADRI12623 standard; DNA; 1623 BP.

AC ADRI12623;

DT 04-SEP-2001 (first entry)

DE Mycobacterium tuberculosis potential drug target gene SEQ ID 23.

KW Drug target; growth; organism viability; characterisation; ds.

OS Mycobacterium tuberculosis.

PN WO200135317-A1.

PD 17-MAY-2001.

XX 13-NOV-2000; 2000WO-US031152.

XX 12-NOV-1999; 99US-0165086P.

PR 12-NOV-1999; 99US-0165124P.

PR 01-FEB-2000; 2000US-0179531P.

XX (REGC) UNIV CALIFORNIA.

XX Eisenberg D, Rotstein SH, Marcotte EM;

XX WPI; 2001-329193/34.

DR P-PSDB; AAG81118.

XX Identifying nucleotide or polypeptide sequence for use as drug target,
 PT involves providing algorithm that analyzes a functional relationship
 PT between nucleotide or polypeptide sequences, and comparing the sequences.

XX Disclosure; Page 63-64; 207pp; English.

XX This invention relates to a method for identifying a nucleotide or
 CC polypeptide sequence that may be a drug target, or essential for growth

or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241. Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism

XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 1623;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 15
AAF25002
ID AAF25002 standard; DNA; 1623 BP.

XX AC AAF25002;

XX DT 30-APR-2001 (first entry)

XX DE Nucleotide sequence of M. bovis BCG heat shock protein 65 (Hsp65).

XX KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen; ss.

XX OS Mycobacterium bovis.

XX FH Key Location/Qualifiers
FT CDS 1..1623
FT /*tag= a
FT /product= "Hsp65"

XX PN WO200104344-A2.

XX PD 18-JAN-2001.

XX PF 10-JUL-2000; 2000WO-US018828.

XX PR 08-JUL-1999; 99US-0143757P.

XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX PI Siegel M, Chu NR, Mizzen LA;

XX DR WPI; 2001-138361/14.

XX DR P-PSDB; AAB31606.

XX Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.

XX Example 2; Fig 1A-B; 88pp; English.

XX The present sequence encodes the Mycobacterium bovis BCG heat shock protein (Hsp) 65. Hsp65 is used in the course of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial

CC pathogens

XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 1623;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 16

ACAA0326
ID ACAA0326 standard; DNA; 1623 BP.

XX AC ACAA0326;

XX DT 19-JUN-2003 (first entry)

XX DE Prokaryotic essential gene #21983.

XX KW Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

XX OS Mycobacterium tuberculosis.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX DR F-PSDB; ABU36456.

XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 28196; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies on a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1623;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 17

ACA37725

ID ACA37725 standard; DNA; 1623 BP.

AC ACA37725;

DT 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #19382.

DE Antisense; ds; prokaryotic essential gene; cell proliferation;

KW drug design; gene.

XX Mycobacterium avium.

OS WO200277183-A2.

PN 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR P-PSDB; ABU33855.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 25595; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1623 BP; 304 A; 545 C; 566 G; 208 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1623;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 18

ADN11336

ID ADN11336 standard; DNA; 1623 BP.

XX AC ADN11336;

XX 17-JUN-2004 (first entry)

DE Chaperonin 60.2 coding sequence.

XX Analgesic; heat shock protein; pain relief; chaperonin 60.2; gene; ds.

XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers

FT 1..1623

FT /*tag= a

FT /product= "Chaperonin 60.2"

XX GB2391477-A.

XX 11-FEB-2004.

XX 05-NOV-2003; 2003GB-00025782.

XX 08-NOV-2002; 2002GB-00026105.

XX (HELP-) HELPERBY THERAPEUTICS LTD.

XX Coates ARM;

XX WPI; 2004-159054/16.

DR P-PSDB; ADN11337.

XX Use of heat shock polypeptide and/or encoding nucleic acid sequence, in

PT manufacture of medicament for use in relief of pain such as headache,

PT headache, or earache.

XX

PS Claim 6; Fig 2; 39pp; English.

XX The present invention relates to heat shock proteins (I) and their coding
CC sequences (II), which are useful in the manufacture of a medicament for
CC use in pain relief. (I) is a chaperonin derived from Mycobacterium
CC tuberculosis (ADN1335, ADN1337 or ADN1339). (I) and (II) are useful in
CC the manufacture of a medicament used as a pain relief, where the pain is
CC at least one chosen from backache, headache, toothache, earache,
CC arthritis, Gout, soft tissue trauma, ligament/tendon traumatic damage,
CC broken bones, cancer, post operative pain, menstrual pain, obstetric
CC pain, renal tract pain, visceral pain, burns, abscesses and other
CC infections. The present sequence is a coding sequence for one such
CC chaperonin.

XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 1623;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

|||||

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 19

AAZ11371

ID AAZ11371 standard; DNA; 1626 BP.

XX AC AAZ11371;

XX DT 25-OCT-1999 (first entry)

XX DE Nucleotide sequence of M. vaccae antigen GV-27.

XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; ss.

XX OS Mycobacterium vaccae.

XX PN W09932634-A2.

XX PD 01-JUL-1999.

XX PF 23-DEC-1998; 98WO-NZ000189.

XX PR 23-DEC-1997; 97US-00996624.

XX PR 23-DEC-1997; 97US-00997080.

XX PR 11-JUN-1998; 98US-00095855.

XX PR 17-SEP-1998; 98US-00156181.

XX PR 04-DEC-1998; 98US-00205426.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;

XX WPI; 1999-430163/36.

XX DR P-PSDB; AAY14909.

XX PT Enhancing immune response to an antigen.

XX PS Claim 3; Page 212-213; 243pp; English.

XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC to enhance the expression of co-stimulatory molecules on dendritic cells
CC and monocytes, and to enhance dendritic cell maturation and function. The

CC proteins can be expressed by standard recombinant methodology.
CC Pharmaceutical compositions comprising the proteins or nucleic acid
CC sequences encoding the proteins can be used for the treatment,
CC prevention, and detection of disorders including infectious diseases,
CC immune disorders and cancer. In particular, the compounds and methods are
CC used for treatment of diseases of the respiratory system, such as
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma

XX SQ Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 1626;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22

|||||

Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 20

ABL36277

ID ABL36277 standard; DNA; 1626 BP.

XX AC ABL36277;

XX DT 08-APR-2002 (first entry)

XX DE M vaccae GroEL homologue GV-27 coding sequence SEQ ID NO: 159.

XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; gene; ds.

XX OS Mycobacterium vaccae.

XX PN US6328978-B1.

XX PD 11-DEC-2001.

XX PF 02-JUN-1999; 99US-00324542.

XX PR 23-DEC-1997; 97US-00997080.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Watson JD, Tan PLJ, Prestidge R;

XX WPI; 2002-138361/18.

XX DR P-PSDB; ABB73515.

XX PT Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX Example 4; Col 167-170; 116pp; English.

XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC coding sequence described in the exemplification of the invention
XX SQ Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 21
ACC42531
ID ACC42531 standard; DNA; 1626 BP.
XX AC ACC42531;
XX DT 26-AUG-2003 (first entry)
XX DE Mycobacterium vaccae antigen GV-27 coding sequence, SEQ ID 14.
XX KW Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
XX KW antidiabetic; antipsoriatic; dermatological; anti-inflammatory;
XX KW immune response; Notch signalling pathway; autoimmune disorder;
XX KW Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
XX KW apoptotic cell death; cell proliferation; gene; ds.
XX OS Mycobacterium vaccae.
XX FH Key Location/Qualifiers
XX CDS 1..1626
FT /*tag=a
FT /product= "Antigen GV-27"
XX PN WO2003013595-A1.
XX PD 20-FEB-2003.
XX PF 26-JUL-2002; 2002WO-NZ000135.
XX PR 26-JUL-2001; 2001US-0308446P.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Watson JD, Tan PLJ, Abernethy N;
XX DR WPI; 2003-239567/23.
XX DR P-PSDB; ABP70891.
XX PT Methods for modulating immune responses by modulating the Notch signaling
XX PT and Toll-like receptor signaling pathways, and treating e.g. autoimmune
XX PT disorders.
XX PS Claim 7; Page 108-109; 136pp; English.
XX CC The present invention relates to methods for modulating immune responses
XX CC by modulating the Notch signaling and Toll-like receptor signalling
XX CC pathways using compositions comprising mycobacteria antigens (ACC42518-
XX CC ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
XX CC immune responses and treating e.g. autoimmune disorders (such as multiple
XX CC sclerosis, rheumatoid arthritis, Type I diabetes mellitus, psoriasis,
XX CC systemic lupus erythematosus, scleroderma), allergic disease and graft
XX CC rejection and also disorders characterised by undesired apoptotic cell
XX CC death or undesired cell proliferation
XX SQ Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 22
ACA39632
ID ACA39632 standard; DNA; 1626 BP.
XX AC ACA39632;
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #21289.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW drug design; gene.
XX OS Mycobacterium leprae.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX DR P-PSDB; ABU35762.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 14; SEQ ID NO 27502; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids
XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
XX CC prokaryotic essential genes. Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1626 BP; 352 A; 450 C; 540 G; 284 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGATCGAGCT 182

RESULT 23
ACCT0275
ID ACC70275 standard; DNA; 1626 BP.
XX
AC ACC70275;
XX
DT 11-AUG-2003 (first entry)
XX
DE Nucleotide sequence of the Rhodococcus equi GroEL2 protein.
XX
KW GroEL protein; protein aggregation; protein folding; immune response;
KW antigen; pathogenic infection; gene; ss.
XX
OS Rhodococcus equi.
XX
FH Key Location/Qualifiers
FT CDS 1
FT /*tag= a
FT /product= "GroEL2"
XX
PN WO2003035676-A1.
XX
PD 01-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-AU001460.
XX
PR 26-OCT-2001; 2001AU-00008523.
XX
PA (UYSA-) UNIV SOUTH AUSTRALIA.
PA (MEDV-) MEDVET SCI PTY LTD.
PA (RURA-) RURAL IND RES & DEV CORP.
XX
PI Vamiasinkam T, Barton M, Heuzenroeder MW;
XX
WPI; 2003-482030/45.
DR P-PSDB; ABR55530.
XX
PT New GroEL protein, useful for preparing a composition for preventing or
PT treating pathogenic infections.
XX
PS Disclosure; Fig 1; 77pp; English.
XX
CC The present sequence encodes a GroEL protein. The groEL2 gene is highly
CC conserved between species, and the protein facilitates the correct
CC folding of various bacterial proteins as well as prevent the aggregation
CC of denatured proteins by an ATP-dependent mechanism. The specification
CC describes a chimeric protein, consisting of a GroEL protein which has a
CC modification or analogue comprising a surface exposed exogenous amino
CC acid sequence inserted to it. The exogenous amino acid sequence is
CC configured to elicit an immune response specifically reactive to the
CC antigenic determinant. The chimeric protein is useful for preparing a
CC composition for preventing or treating pathogenic infections
XX
SQ Sequence 1626 BP; 300 A; 544 C; 549 G; 233 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 9; Length 1626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGATCGAGCT 182

RESULT 24
ADT46122
ID ADT46122 standard; cDNA; 1632 BP.
XX
AC ADT46122;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #20873.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOX/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 44560; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX

```
SQ Sequence 1632 BP; 356 A; 514 C; 507 G; 255 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 13; Length 1632;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 25
AAD57198
ID AAD57198 standard; DNA; 1701 BP.
XX
AC AAD57198;
XX
DT 06-NOV-2003 (first entry)
XX
DE Mycobacterium avium subspecies paratuberculosis protein gene #11.
XX
KW Immunogenic fragment; vaccine; Map infection; wild-type infection;
KW antibacterial; gene; ds.
XX
OS Mycobacterium avium.
XX
FH Key Location/Qualifiers
CDS 76..1701
FT /*tag= a
FT /product= "Protein"
XX
PN WO2003058248-A2.
XX
PD 17-JUL-2003.
XX
PF 13-JAN-2003; 2003WO-NL000020.
XX
PR 11-JAN-2002; 2002EP-00075089.
XX
PA (IDLE-) ID-LELYSTAD INST DIERHOUDRIJ EN DIERGEZ.
XX
PI Willemsen PTJ, Westerveen SP, Bakker D, Van Zijderveld FG;
PI Thole JER;
XX
DR WPI; 2003-598398/56.
DR P-PSDB; AAE37881.
XX
PT Novel Mycobacterium avium subspecies paratuberculosis protein, useful as
PT vaccine for combating the bacterial infection, and for diagnosing the
PT infection.
XX
PS Disclosure; Page 84-86; 88pp; English.
XX
CC The invention relates to Mycobacterium avium subspecies paratuberculosis
CC protein or an immunogenic fragment of the protein. The invention is
CC useful in the manufacture of a vaccine for combating Map infection. The
CC nucleic acids, the proteins and antibodies are also useful in
CC diagnostics. The vaccines are also suitable as marker vaccines, in that
CC it allows discrimination of vaccinated and field-infected mammals on the
CC basis of characteristic antibody panel induced by wild-type infection.
CC The present sequence is Mycobacterium avium subspecies paratuberculosis
CC protein gene
XX
SQ Sequence 1701 BP; 318 A; 569 C; 591 G; 223 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 236 CCATCGCCCAAGGAGATCGAGCT 257

RESULT 26
ACC49833
ID ACC49833 standard; DNA; 1752 BP.
XX
AC ACC49833;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human recombinant protein vaccine gene.
XX
KW Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
KW antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
CDS 1..1752
FT /*tag= a
FT
XX
PN CN1362263-A.
XX
PD 07-AUG-2002.
XX
PF 15-NOV-2001; 2001CN-00134935.
XX
PR 04-JAN-2001; 2001CN-00100380.
XX
PA (BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
XX
PI Wang L, Li D, Yu Y;
XX
DR WPI; 2003-230415/23.
DR P-PSDB; ABR40246.
XX
PT Recombinant protein vaccine for preventing and treating human prostate
PT cancer.
XX
PS Claim 7; Page 15-19; 35pp; Chinese.
XX
CC The invention relates to a novel recombinant protein vaccine, a fusion
CC protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of
CC human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The
CC vaccine of the invention is useful for treating and preventing carcinoma
CC of prostate. The invention also discloses the genes encoding the
CC recombinant protein vaccines. The present sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 1752 BP; 356 A; 535 C; 595 G; 266 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 8; Length 1752;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 27
ADX05272
ID ADX05272 standard; DNA; 1761 BP.
XX
AC ADX05272;
XX
DT 21-APR-2005 (first entry)
XX
DE HSP65-MUC1-ME fusion protein coding sequence, SEQ ID 1.
XX
KW Fusion protein; Cytostatic; Gene Therapy; heat shock protein 65; HSP65;
KW mucin; MUC1; carcinoma; gene; ds.
XX
```


XX Claim 7; Page 23-26; 35pp; Chinese.

XX The invention relates to a novel recombinant protein vaccine, a fusion

CC protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of

CC human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The

CC vaccine of the invention is useful for treating and preventing carcinoma

CC of prostate. The invention also discloses the genes encoding the

CC recombinant protein vaccines. The present sequence is used in the

CC exemplification of the invention

XX

SQ Sequence 1914 BP; 397 A; 576 C; 633 G; 308 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1914;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGATCGAGCT 22

DB 161 CCATCGCCCAAGGATCGAGCT 182

RESULT 30

AAF25012

ID AAF25012 standard; DNA; 1920 BP.

XX

AC AAF25012;

XX

DT 30-APR-2001 (first entry)

XX

DE Nucleotide sequence of Hsp65-E7 fusion protein.

XX

KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

KW E7 protein; ss.

XX

OS Synthetic.

OS Mycobacterium bovis.

OS Human papillomavirus.

XX

PH Key Location/Qualifiers

FT CDS 1..1920

FT /*tag= a

FT /product= "Hsp65-E7 fusion protein"

XX

PN WO200104344-A2.

XX

PD 18-JAN-2001.

XX

PF 10-JUL-2000; 2000WO-US018828.

XX

PR 08-JUL-1999; 99US-0143757P.

XX

PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX

PI Siegel M, Chu NR, Mizzen LA;

XX

DR WPI; 2001-138361/14.

DR P-PSDB; AAB31609.

XX

PT Screening for compounds that stimulate Th1-like responses in CD4+ T

PT lymphocyte cells.

XX

PS Example 5; Fig 4A-B; 88pp; English.

XX

CC The present sequence encodes a fusion protein comprising a Mycobacterium

CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a Hpv16 E7

CC protein. The fusion protein is used in the method of the invention. The

CC specification describes a method of determining whether a compound

CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T

CC lymphocyte cells. The method comprises contacting naive lymphocytes in

CC vitro with a fusion protein comprising at least a fragment of Hsp, and

CC then detecting the Th1-like response exhibited by the cell sample. The

CC proteins which may be used in the method of the invention are Hsp65,

CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify

CC compounds that stimulate Th1-like responses in response to microbial

CC pathogens

XX

SQ Sequence 1920 BP; 415 A; 551 C; 638 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 1920;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGATCGAGCT 22

DB 161 CCATCGCCCAAGGATCGAGCT 182

RESULT 31

AAF25019

ID AAF25019 standard; DNA; 1947 BP.

XX

AC AAF25019;

XX

DT 30-APR-2001 (first entry)

XX

DE Nucleotide sequence of Hsp65-E7 fusion protein.

XX

KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;

KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;

KW E7 protein; ss.

XX

OS Synthetic.

OS Mycobacterium bovis.

OS Human papillomavirus.

XX

PH Key Location/Qualifiers

FT CDS 1..1947

FT /*tag= a

FT /product= "Hsp65-E7 fusion protein"

XX

PN WO200104344-A2.

XX

PD 18-JAN-2001.

XX

PF 10-JUL-2000; 2000WO-US018828.

XX

PR 08-JUL-1999; 99US-0143757P.

XX

PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX

PI Siegel M, Chu NR, Mizzen LA;

XX

DR WPI; 2001-138361/14.

DR P-PSDB; AAB31614.

XX

PT Screening for compounds that stimulate Th1-like responses in CD4+ T

PT lymphocyte cells.

XX

PS Example 11; Fig 10A-B; 88pp; English.

XX

CC The present sequence encodes a fusion protein comprising a Mycobacterium

CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a Hpv16 E7

CC protein. The fusion protein is used in the method of the invention. The

CC specification describes a method of determining whether a compound

CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T

CC lymphocyte cells. The method comprises contacting naive lymphocytes in

CC vitro with a fusion protein comprising at least a fragment of Hsp, and

CC then detecting the Th1-like response exhibited by the cell sample. The

CC proteins which may be used in the method of the invention are Hsp65,

CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify

CC compounds that stimulate Th1-like responses in response to microbial

CC pathogens

XX

SQ Sequence 1947 BP; 417 A; 557 C; 653 G; 320 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 1947;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 32
 ADW23606
 ID ADW23606 standard; DNA; 1965 BP.
 XX
 AC ADW23606;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Hepatitis C virus related DNA SEQ ID NO 6.
 XX
 KW recombinant protein; vaccine; fusion protein; hepatitis C; ds; gene.
 XX
 OS Synthetic.
 XX
 PN CN1462636-A.
 XX
 XX 24-DEC-2003.
 XX
 XX 30-MAY-2002; 2002CN-00122116.
 XX
 XX 30-MAY-2002; 2002CN-00122116.
 XX
 PA (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
 XX
 PI Wang L, Sun M, Yu Y;
 XX
 DR WPI; 2004-239553/23.
 DR P-PSDB; ADW23607.
 XX
 PT Vaccine of recombinated albumen for preventing and treating infection of
 PT human hepatitis C virus.
 XX
 PS Claim 9; SEQ ID NO 6; 54pp; Chinese.
 XX
 CC The invention relates to a recombinant protein vaccine which is a fusion
 CC protein of BCG vaccine's heat shock protein 65 and the core antigen of
 CC multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
 CC and nucleotide sequence for coding it, the expression carrier containing
 CC nucleotide sequence, the host cell containing expression carrier, the
 CC preparing process of recombinant protein vaccine, the vaccine containing
 CC recombinant protein for preventing and treating hepatitis C and a method
 CC for detecting the activity of specifically killing T-lymphocytes by the
 CC hepatitis C induced by vaccine and its cell model are disclosed. The
 CC present sequence represents a hepatitis C virus related DNA.
 XX
 SQ Sequence 1965 BP; 405 A; 593 C; 658 G; 309 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 13; Length 1965;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 33
 ADN00588
 ID ADN00588 standard; DNA; 1980 BP.
 XX
 AC ADN00588;
 XX
 DT 17-JUN-2004 (first entry)

XX BCG vaccine HSP65-MOMP fusion protein coding sequence, SEQ ID 3.
 DE
 XX Antibacterial; gynaecological; protein vaccine;
 KW BCG vaccine heat shock protein 65; major outer membrane protein; MOMP;
 KW Chlamydia infection; urogenital infection; gene; ds.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1980
 FT /*tag= a
 FT /product= "BCG vaccine HSP65-MOMP fusion protein"
 XX
 XX WO2004020471-A1.
 PN
 XX 11-MAR-2004.
 PD
 XX
 PF 03-JUN-2003; 2003WO-CN000430.
 XX
 PR 29-AUG-2002; 2002CN-00141977.
 XX
 PA (BEIJ-) BEIJING HYDVAX BIOTECHNOLOGY CO LTD.
 XX
 PI Wang L, Yang S, Yu Y;
 XX
 DR WPI; 2004-248232/23.
 DR P-PSDB; ADN00589.
 XX
 PT Heat shock protein-based recombinant protein for vaccines against human
 PT Chlamydia trachomatis, applicable in preventing or/and treating human
 PT Chlamydia infections.
 XX
 PS Claim 7; SEQ ID NO 3; 49pp; Chinese.
 XX
 CC The present invention relates to a recombinant protein vaccine
 CC (ADN00589), which is a fusion protein of BCG vaccine heat shock protein
 CC (HSP) 65 with the major outer membrane protein (MOMP) of Chlamydia
 CC trachomatis (ADN00587). The fusion protein comprises the BCG vaccine HSP
 CC 65 at the amino-end, with the MOMP protein at the carboxy-end. The
 CC vaccine is capable of activating cytotoxic T-lymphocytes and can be used
 CC for preventing or/and treating human Chlamydia infections, particularly
 CC urogenital infections. The present sequence is the coding sequence for
 CC the fusion protein, used to illustrate the invention.
 XX
 SQ Sequence 1980 BP; 407 A; 595 C; 653 G; 325 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 1980;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 34
 ADK72374
 ID ADK72374 standard; DNA; 2016 BP.
 XX
 AC ADK72374;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE BCG-HER-2 fusion gene construct for breast cancer vaccine treatment.
 XX
 KW vaccine; fusion protein; BCG; heat-shock protein 65; HSP65; HER-2;
 KW antigen; breast cancer; gene; ds.
 XX
 OS Homo sapiens.
 OS Bacillus sp.
 OS Chimeric.
 XX


```

FT CDS 1. .2130
FT /*tag= a
FT /product= "HisHepCorT(149/87S97F)Hsp65"
XX
XX WO200262959-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX
XX 05-FEB-2001; 2001US-0266733P.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Mizzen L, Liu H, Siegel M;
XX
XX WPI; 2002-706903/76.
XX
XX P-PSDB; ABG70776.
XX
XX Novel isolated fusion protein useful for treating hepatitis B virus
XX infection in a subject, comprises a stress protein or its portion, and a
XX hepatitis B virus core antigen.
XX
XX Example 1; Fig 7; 58pp; English.
XX
XX The invention discloses an isolated fusion protein, and the
XX polynucleotide encoding it, that comprises a stress protein (e.g.
XX Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
XX hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
XX when administered to an individual, induces or enhances an immune
XX response against the HBV core antigen. HBV is a non-cytopathic DNA virus
XX against which a vaccine has been developed. However, due to the morbidity
XX and mortality arising from chronic HBV infection occurring over a period
XX of decades, the impact of vaccinations will not be apparent for some time
XX yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
XX therapy and as a pharmaceutical composition for inducing or enhancing an
XX immune response against an HBV core antigen in a subject for treating an
XX HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
XX The sequence presented is the DNA encoding the truncated hepatitis B
XX virus core antigen fused to the N-terminus of the M. bovis variant
XX Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65,
XX HisHepCorT(149/87S97F)Hsp65. The core antigen the DNA encodes has been
XX truncated to include residues 1 to 149, had an N-terminal histidine tag
XX added, had two amino acids changed from the wild-type sequence and there
XX has been an additional residue added between the HBV core protein and the
XX Hsp65 protein. (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 2130 BP; 444 A; 616 C; 681 G; 389 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 6; Length 2130;
XX Best Local Similarity 100.0%; Pred. NO. 3.3;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCATGCCCAAGGAGATCGAGCT 22
XX 668 CCATGCCCAAGGAGATCGAGCT 689
XX
XX RESULT 37
XX ABS54449
XX ID ABS54449 standard; DNA; 2175 BP.
XX
XX AC ABS54449;
XX
XX 07-AUG-2003 (revised)
XX 09-DEC-2002 (first entry)
XX
XX BCG Hsp65/mutant HBV core antigen, HepCor(97F)Hsp65, DNA.
XX
XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
XX Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity;
XX mortality; infection; gene therapy; hepatitis; cirrhosis;
XX hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
XX

```

```

KW antiinflammatory; BCG; chimera; mutant.
XX
XX Hepatitis B virus.
XX Mycobacterium bovis.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..2175
XX /*tag= a
XX /*product= "HepCor(97F)Hsp65"
XX
XX WO200262959-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX
XX 05-FEB-2001; 2001US-0266733P.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Mizzen L, Liu H, Siegel M;
XX
XX WPI; 2002-706903/76.
XX
XX P-PSDB; ABG70778.
XX
XX Novel isolated fusion protein useful for treating hepatitis B virus
XX infection in a subject, comprises a stress protein or its portion, and a
XX hepatitis B virus core antigen.
XX
XX Example 1; Fig 11; 58pp; English.
XX
XX The invention discloses an isolated fusion protein, and the
XX polynucleotide encoding it, that comprises a stress protein (e.g.
XX Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
XX hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
XX when administered to an individual, induces or enhances an immune
XX response against the HBV core antigen. HBV is a non-cytopathic DNA virus
XX against which a vaccine has been developed. However, due to the morbidity
XX and mortality arising from chronic HBV infection occurring over a period
XX of decades, the impact of vaccinations will not be apparent for some time
XX yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
XX therapy and as a pharmaceutical composition for inducing or enhancing an
XX immune response against an HBV core antigen in a subject for treating an
XX HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
XX The sequence presented is the DNA encoding the hepatitis B virus core
XX antigen fused to the N-terminus of the M. bovis variant Bacille-Calmette-
XX Guerin (BCG) heat shock protein (Hsp) 65, HepCor(97F)Hsp65. The core
XX antigen the DNA encodes has had an amino acid changed from the wild-type
XX sequence. (Updated on 07-AUG-2003 to correct OS field.)
XX
XX Sequence 2175 BP; 459 A; 628 C; 691 G; 397 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 6; Length 2175;
XX Best Local Similarity 100.0%; Pred. NO. 3.3;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCATGCCCAAGGAGATCGAGCT 22
XX 713 CCATGCCCAAGGAGATCGAGCT 734
XX
XX RESULT 38
XX ABS54446
XX ID ABS54446 standard; DNA; 2241 BP.
XX
XX AC ABS54446;
XX
XX 07-AUG-2003 (revised)
XX 09-DEC-2002 (first entry)
XX
XX His tagged BCG Hsp65/mutant HBV core antigen, hisHepCor(97F)Hsp65, DNA.

```

XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein; Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity; KW mortality; infection; gene therapy; hepatitis; cirrhosis; KW hepatocellular carcinoma; virucide; immunostimulant; hepatotropic; KW antiinflammatory; BCG; chimera; mutant.

XX Hepatitis B virus.

OS Mycobacterium bovis.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

XX CDS 1..2241

XX /tag= a

XX /product= "HisHepCor(97F)Hsp65"

XX WO200262959-A2.

XX 15-AUG-2002.

XX 05-FEB-2002; 2002WO-US003460.

XX 05-FEB-2001; 2001US-0266733P.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

XX Mizzen L, Liu H, Siegel M;

XX WPI: 2002-706903/76.

XX P-PSDB; ABG70775.

XX Novel isolated fusion protein useful for treating hepatitis B virus infection in a subject, comprises a stress protein or its portion, and a hepatitis B virus core antigen.

XX Example 1; Fig 5; 59pp; English.

XX The invention discloses an isolated fusion protein, and the CC polynucleotide encoding it, that comprises a stress protein (e.g. CC Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a CC hepatitis B virus (HBV) core antigen (HBe), where the fusion protein, CC when administered to an individual, induces or enhances an immune CC response against the HBV core antigen. HBV is a non-cytopathic DNA virus CC against which a vaccine has been developed. However, due to the morbidity CC and mortality arising from chronic HBV infection occurring over a period CC of decades, the impact of vaccinations will not be apparent for some time CC yet. The polynucleotide and polypeptide can be used as a vaccine, in gene CC therapy and as a pharmaceutical composition for inducing or enhancing an CC immune response against an HBV core antigen in a subject for treating an CC HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma. CC The sequence presented is the DNA encoding the full length hepatitis B CC virus core antigen fused to the N-terminus of the M. bovis variant CC Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65, had an N- CC hisHepCor(97F)Hsp65. The core antigen the DNA encodes has had an N- CC terminal histidine tag added and had an amino acid changed from the wild- CC type sequence. Two additional residues have also been added between the CC HBV core protein and the Hsp65 protein. (Updated on 07-AUG-2003 to CC correct OS field.)

XX Sequence 2241 BP; 474 A; 650 C; 709 G; 408 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 22; DB 6; Length 2241;

XX Best Local Similarity 100.0%; Pred. No. 3.3;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGAGATCGAGCT 22

Db 779 CCATGCCCAAGAGATCGAGCT 800

RESULT 39

ADR30583

ID ADR30583 standard; DNA; 2585 BP.

XX ADR30583;

XX 18-NOV-2004 (first entry)

XX Arthrobacter heat shock protein 60 (hsp60) encoding DNA SEQ ID NO:1.

XX Arthrobacter; heat shock protein 60; hsp60; antibacterial; virucide; KW vaccine; bacterial kidney disease; salmonid rickettsial septicemia; KW infectious salmonia anaemia virus; infectious pancreatic necrosis virus; KW infectious disease; environmental stress; gene; ds.

XX Arthrobacter sp.

XX Key Location/Qualifiers

XX CDS 953..2578

XX /tag= a

XX /product= "heat shock protein 60 (hsp60)"

XX WO2004071387-A2.

XX 26-AUG-2004.

XX 13-FEB-2004; 2004WO-EP001368.

XX 14-FEB-2003; 2003GB-00003507.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS PHARMA GMBH.

XX Griffiths SG, Ritchie RJ, Simard NC;

XX WPI: 2004-625750/60.

XX P-PSDB; ADR30584.

XX New Arthrobacter hsp60 gene, useful in preparing a vaccine for treating or preventing Bacterial Kidney Disease, Salmonid Rickettsial Septicemia, Infectious Salmonia Anemia Virus or Infectious Pancreatic Necrosis Virus.

XX Claim 3; SEQ ID NO 1; 33pp; English.

XX The present sequence encodes Arthrobacter heat shock protein 60 (hsp60) (I). The present invention describes: (1) a chimeric nucleic acid sequence comprising (I) fused in-frame to a heterologous coding sequence encoding an antigen from an animal pathogen; (2) a DNA expression vector (II) comprising (I) operably linked to a transcriptional regulatory sequence; (3) a host cell transformed with (II); (4) an isolated Arthrobacter hsp60 amino acid sequence (III) or its fragment, derivative or homologue; (5) an antibody raised against (III); (6) a vaccine composition comprising (I)-(III) or an Arthrobacter cell extract enriched in hsp60 and a carrier; (7) a kit comprising the vaccine composition and a heterologous antigen or a nucleic acid sequence encoding the antigen for separate, sequential or simultaneous administration; (8) a method of inducing or enhancing an immune response to an immunogen or a hapten in an animal; (9) a method of treating or preventing infectious disease in fish; and (10) a method of preparing a vaccine composition. Hsp60 has antibacterial and virucide activities, and can be used in vaccines. The Arthrobacter hsp60 amino acid or nucleic acid sequence can be used as a non-specific vaccine adjuvant. The Arthrobacter hsp60 amino acid or nucleic acid sequence, DNA expression vector or an Arthrobacter cell extract enriched in hsp60 is useful in the manufacture of a vaccine for treating or preventing bacterial kidney disease, salmonid rickettsial septicemia, infectious salmonia anaemia virus or infectious pancreatic necrosis virus or for diagnosing infectious diseases or environmental stresses. The promoter sequence of Arthrobacter hsp60 gene is useful in expressing a heterologous gene. The antibody is useful in the manufacture of a medicament for the treatment or diagnosis of infectious disease.

XX Sequence 2585 BP; 515 A; 781 C; 824 G; 465 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 22; DB 13; Length 2585;

XX Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 1113 CCATGCCCAAGGAGATCGAGCT 1134

RESULT 40
AAP25014
ID AAF25014 standard; DNA; 2847 BP.
XX AC AAF25014;
XX 30-APR-2001 (first entry)
XX Nucleotide sequence of Hsp65-ovalbumin fusion protein.
XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KW ovalbumin; ss.
XX Synthetic.
OS Mycobacterium bovis.
OS Gallus sp.
XX Key Location/Qualifiers
XX CDS 1..2847
FT /*tag= a
FT /product= "Hsp65-ovalbumin fusion protein"
XX WO200104344-A2.
XX 18-JAN-2001.
XX 10-JUL-2000; 2000MO-US018828.
XX 08-JUL-1999; 99US-0143757P.
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX Siegel M, Chu NR, Mizzen LA;
XX WPI; 2001-138361/14.
DR P-PSDB; AAB31611.
XX Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.
XX Example 8; Fig 7A-B; 88pp; English.
XX The present sequence encodes a fusion protein comprising a Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to an ovalbumin protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial pathogens

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 221 CCATGCCCAAGGAGATCGAGCT 242

Query Match 100.0%; Score 22; DB 5; Length 2847;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 221 CCATGCCCAAGGAGATCGAGCT 242

RESULT 41
AAN80339
ID AAN80339 standard; DNA; 3613 BP.
XX AC AAN80339;
XX 25-MAR-2003 (revised)
DT 10-OCT-1990 (first entry)
XX Clone Y3178 insert contg. M. leprae 65kD antigen gene.
DE Leprosy; antigen; vaccine; armadillo; ss.
KW Mycobacterium leprae.
OS
XX Key Location/Qualifiers
XX CDS 56..1832
FT /*tag= a
FT /product= "61,856 dalton protein"
FT misc_RNA 207..1832
FT /*tag= b
FT /product= "56,686 dalton protein"
XX WO8800974-A.
XX 11-FEB-1988.
XX 28-JUL-1987; 87WO-US001825.
XX 31-JUL-1986; 86US-00892095.
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX Young RA;
XX WPI; 1988-049978/07.
DR P-PSDB; AAP80364.
XX DNA encoding antigens of mycobacterium leprae - used for producing immuno-determinant protein antigen for prevention diagnosis and treatment of leprosy.
XX Claim 7; Fig 1; 46pp; English.
XX The gene was isolated by probing a lambda gt11 library of M. leprae DNA with MBAs directed against M. leprae specific antigens. The sequences were determined with a rapid primer extension method. The antigen appears as a doublet on SDS PAGE with mol. wt. 55-65 kD so translation may initiate at the start of either CDS in the feature table, producing two polypeptides. The sequence can be used in the development of highly specific serological tests for screening populations for individuals producing Abs to M. leprae, in the development of vaccines and in the assessment of efficacy of treatment. (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 3613 BP; 724 A; 960 C; 1183 G; 746 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 22; DB 1; Length 3613;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 367 CCATGCCCAAGGAGATCGAGCT 368

RESULT 42
AAN81768
ID AAN81768 standard; DNA; 4260 BP.
XX AC AAN81768;

```

XX 25-MAR-2003 (revised)
DT 29-DEC-1990 (first entry)
XX
DE Sequence encoding Mycobacterium tuberculosis 540 and 517 AA residue
DE proteins.
XX
KW Diagnosis; assay; M.bovis; vaccine; ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT CDS 252..1874
FT /tag= a
FT /label= 540 AA protein
FT /note= "AAP81351"
FT CDS complement(3948..2395)
FT /tag= b
FT /label= 517 AA protein
FT /note= "AAP81868"
XX
PN WO8806591-A.
XX
XX
XX 07-SEP-1988.
XX
XX 25-FEB-1988; 88WO-US000598.
XX
XX 26-FEB-1987; 87US-00019529.
XX 24-FEB-1988; 88US-000159667.
XX
XX (SRI ) SCRIPPS CLINIC & RE.
XX
XX Shinnick T, Houghten R;
XX
XX WPI; 1988-271136/38.
XX
XX P-PSDB; AAP81351, AAP81868.
XX
XX Recombinant mycobacterial peptide(s) - used in assays for diagnosis of
XX infection, for producing vaccines and for producing antibodies.
XX
XX Disclosure; Fig 2a-2d; 117pp; English.
XX
XX An isolated DNA molecule that consists essentially of the nucleotide
XX sequence that corresponds to the sequence represented by position 3950 to
XX about 2390 and from position 3948 through position 2398 of AAN81768 is
XX claimed. Also claimed is a peptide sequence that consists of a 5-40 AA
XX residue sequence that corresponds to a sequence of the 540 AA residue
XX protein (AAP81351) or the 517 AA residue protein (AAP81868) coded for by
XX the DNA sequence. The proteins can be used for determining previous
XX immunological exposure of a mammal to M.tuberculosis or M.bovis and for
XX producing a vaccine. (Updated on 25-MAR-2003 to correct PR field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 4260 BP; 733 A; 1332 C; 1481 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 1; Length 4260;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 43
AAN80222
ID AAN80222 standard; DNA; 4380 BP.
XX
XX AAN80222;
XX
XX 25-MAR-2003 (revised)
DT 19-MAR-1991 (first entry)
XX

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DE Sequence of Mycobacterium tuberculosis DNA contg. gene encoding 65
DE protein.
XX
XX Antigen; vaccine; ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT CDS 192..1874
FT /tag= a
FT CDS complement(2398..4101)
FT /tag= b
XX
XX WO8805823-A.
XX
XX 11-AUG-1988.
XX
XX 01-FEB-1988; 88WO-US000281.
XX
XX 02-FEB-1987; 87US-00010007.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Husson RN, Young RA, Nick TM;
XX
XX WPI; 1988-235175/33.
XX
XX P-PSDB; AAP80215, AAP80216.
XX
XX Genes encoding Mycobacterium tuberculosis protein antigens - useful for
XX developing reagents for diagnosis, prevention and treatment of
XX tuberculosis.
XX
XX Claim 12; Fig 8; 82pp; English.
XX
XX The gene was isolated by probing a lambda gt11 expression library of
XX M.tuberculosis DNA with monoclonal antibodies directed against
XX M.tuberculosis-specific antigens. The 19KD, 71kd and the 65KD proteins
XX and genes are claimed, and so is a vaccine comprising DNA encoding
XX M.tuberculosis protein in a recombinant vaccine vector. AAP80216 is
XX encoded on the complementary strand. (Updated on 25-MAR-2003 to correct
XX PA field.)
XX
SQ Sequence 4380 BP; 757 A; 1373 C; 1512 G; 738 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 1; Length 4380;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
Db 412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 44
AAV05708
ID AAV05708 standard; DNA; 4380 BP.
XX
XX AAV05708;
XX
XX 22-JUN-1998 (first entry)
XX
XX Mycobacterium tuberculosis 65 kDa heat shock protein gene.
XX
XX Heat shock protein; Mt Hsp65; autoimmune disease; immunotherapy;
XX gene therapy; rheumatoid arthritis; multiple sclerosis; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
XX CDS 252..1874
XX /tag= a
XX /product= "65 kDa heat shock protein"
XX

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PN WO9746253-A2.
XX
XX
PD 11-DEC-1997.
XX
XX PF 03-JUN-1997; 97WO-US009427.
XX
XX PF 03-JUN-1996; 96US-0019100P.
XX
XX PF 03-JUN-1997; 97US-00019100.
XX
XX
XX (AURA-) AURAGEN INC.
XX
XX Haynes JR, Prayaga SK, Ramshaw IA;
XX
XX WPI; 1998-041892/04.
XX
XX P-PSDB; AA44702.
XX
XX
XX Treatment of auto-immune diseases - by administering auto-antigen-coated
XX particles or auto-antigen-encoding nucleic acid construct.
XX
XX Example 2; Page 55-59; 72pp; English.
XX
XX This DNA sequence encodes the 65 kDa heat shock protein (see AA44702),
XX designated Mt Hsp65, of Mycobacterium tuberculosis. This protein cross-
XX reacts with a component of articular cartilage, human Hsp60, that is up-
XX regulated in the joints of arthritic patients. A claimed method for
XX treating or preventing an autoimmune disease in a mammal comprises: (a)
XX providing a particle coated with an antigen against which an immune
XX response is mounted in the autoimmune disease; (b) delivering the
XX particle into the recipient cell of the mammal; and (c) repeating step
XX (b) until either a reduction in a cytotoxic immune response or a
XX desensitizing immune response is induced in the mammal. Alternatively,
XX step (a) comprises providing a nucleic acid construct comprising a coding
XX sequence for the antigen, operably linked to control elements such that
XX the coding sequence can be transcribed and translated in a recipient
XX cell, and delivering the construct to the recipient cell using a gene
XX gun. The antigen of step (a) is selected from collagen, Mt Hsp65, myelin
XX basic protein, myelin oligodendrocyte glycoprotein, proteolipid protein,
XX and epitopes thereof. These antigens mitigate cytotoxic responses and
XX elicit antigen desensitization. The method is used especially for
XX treating rheumatoid arthritis or multiple sclerosis. It represents a
XX novel use for the known Mt Hsp65 gene
XX
XX Sequence 4380 BP; 757 A; 1371 C; 1514 G; 738 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 22; DB 2; Length 4380;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 45
ABA99141
ID ABA99141 standard; DNA; 4380 BP.
XX
XX ABA99141;
XX
XX 23-MAY-2002 (first entry)
XX
XX hap65 encoding sequence.
XX
XX hap65; heat shock protein; cytosolic; antibacterial; antiparasitic;
XX MHC class I; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX US6331388-B1.
XX
XX 18-DEC-2001.
XX
XX 17-OCT-1997; 97US-00955565.
XX

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XX
XX 17-OCT-1997; 97US-00955565.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Malkovsky M, Wells AD;
XX
XX WPI; 2002-138381/18.
XX
XX Increasing expression of an MHC class I molecule in a cell, useful in
XX increasing antigen presentation and enhancing immune recognition of cells
XX infected with pathogens, by expressing a heat shock protein introduced by
XX a vector.
XX
XX Example 5; Fig 9; 89pp; English.
XX
XX This invention relates to increasing expression of an MHC class I
XX molecule in a target cell, infected with a pathogen that is processed by
XX the MHC class I endogenous pathway. The method of expressing a HSP is
XX achieved by the introduction of an expression vector encoding HSP to
XX produce a transfected cell with increased expression of at least one MHC
XX class I molecule. The method is cytostatic, antibacterial and
XX antiparasitic. The method can be used to increase expression of an MHC
XX class I molecule in a target cell and to increase presentation of an
XX antigen on a cell surface by an MHC class I molecule. The method can
XX enhance the immunogenicity of the endogenous antigen in vivo, by
XX enhancing the generation of antibodies to an otherwise poorly immunogenic
XX antigen or cell. The method can be used in the immunotherapy of cancer
XX and pathogen infections, and for enhancing or reducing radiation
XX resistance of cells. The expression of the heat shock protein in a cell
XX enhances the presentation of endogenous antigens by MHC class I molecules
XX onto the cell surface in vitro, and can enhance the immunogenicity of the
XX endogenous antigen in vivo, by enhancing the generation of antibodies to
XX an otherwise poorly immunogenic antigen or cell. This sequence represents
XX hsp65 encoding sequence
XX
XX Sequence 4380 BP; 757 A; 1372 C; 1513 G; 738 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 22; DB 6; Length 4380;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
DB 412 CCATCGCCCAAGGAGATCGAGCT 433

RESULT 46
AAS59637
ID AAS59637 standard; DNA; 13380 BP.
XX
XX AAS59637;
XX
XX 13-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein encoding DNA #132.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant; ds.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208941P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX

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XX (CORI-) CORIXA CORP.
 PA Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 XX L'Maisonneuve J, Zhang Y, Jen S, Carter D;
 PI WPI; 2001-616774/71.
 XX
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 XX Claim 1; SEQ ID NO 132; 1069pp; English.
 XX
 XX Sequences AAS59506-AAS59804 represent DNA molecules encoding
 CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
 CC associated DNA sequences are used in the treatment, prevention and
 CC diagnosis of medical conditions caused by P. acnes. The disorders include
 CC SAPHO syndrome (synovitis, acne, pustulosis, hypertonosis and
 CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
 CC infections of bone, joints and the central nervous system, however it is
 CC particularly involved in the inflammatory lesions associated with acne
 CC vulgaris. A method for detecting the presence or absence of P. acnes in a
 CC patient comprises contacting a sample with a binding agent that binds to
 CC the proteins of the invention and determining the amount of bound protein
 CC in the sample. The polypeptides may be used as antigens in the production
 CC of antibodies specific for P. acnes proteins. These antibodies can be
 CC used to downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
 CC polypeptides shown in AAU63485-AAU64031 and AAU67712. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13380 BP; 2486 A; 3689 C; 4274 G; 2930 T; 0 U; 1 Other;
 Query Match 100.0%; Score 22; DB 4; Length 13380;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCAGAGATCGAGCT 22
 |||||
 DB 4674 CCATCGCCAGAGATCGAGCT 4695
 |||||
 RESULT 47
 ACF64566
 ID ACF64566 standard; DNA; 13380 BP.
 XX
 AC ACF64566;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes DNA contig sequence #132.
 XX
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine; ds.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallie-Douglass J;
 XX WPI; 2003-381789/36.
 XX
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 XX Claim 1; SEQ ID NO 132; 1481pp; English.
 XX
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a P. acnes DNA contig which is specifically claimed
 CC in the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13380 BP; 2486 A; 3689 C; 4274 G; 2930 T; 0 U; 1 Other;
 Query Match 100.0%; Score 22; DB 8; Length 13380;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCATCGCCAGAGATCGAGCT 22
 |||||
 DB 4674 CCATCGCCAGAGATCGAGCT 4695
 |||||
 RESULT 48
 ABX09143
 ID ABX09143 standard; DNA; 86114 BP.
 XX
 AC ABX09143;
 XX
 DT 08-APR-2003 (first entry)
 XX
 DE Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv265.
 XX
 KW Mycobacteriosis; survival; virulence; protective antigen; vaccine;
 KW mycobacterial disease; tuberculosis; leprosy; ds; cosmid.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200274903-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-IB001973.
 XX
 PR 22-FEB-2001; 2001US-0270123P.
 XX
 PA (INSP) INST PASTEUR.

XX Cole S;
PI WPI; 2002-759885/82.
XX
XX Identifying and selecting genes for survival or virulence of mycobacteria
PT by a comparative genomic analysis of the sequences of Mycobacterium
PT tuberculosis and M. leprae.
XX
XX Disclosure; Fig 7; 874pp; English.
XX
XX This invention relates to a novel method for identifying essential genes
CC for survival or virulence of mycobacteria species. The method comprises
CC aligning the genomic sequence of a first mycobacterium species on a
CC genomic sequence of a second mycobacterium species and selecting a
CC polynucleotide sequence that is highly conserved in both genomes with no
CC counterparts in other bacterial genomic sequences and that corresponds to
CC an essential gene for the survival or virulence of mycobacterium species.
CC The method of the invention is useful for detecting M. tuberculosis or M.
CC leprae infection. The method reduces the number of potential new targets
CC and protective antigens for new drugs and vaccine compositions to treat
CC and prevent mycobacterial diseases, particularly tuberculosis and
CC leprosy. The present sequence represents a Mycobacterium cosmid DNA
CC sequence used in the method of the invention
XX

SQ Sequence 86114 BP; 14693 A; 27103 C; 28984 G; 15334 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 86114;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGATCGAGCT 22
DB 15365 CCATCGCCCAAGGATCGAGCT 15386
|||||

RESULT 49

AAI99682_05
Continuation (6 of 45) of AAI99682 from base 500001 (Mycobacterium tuberculosis strain H
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682

WP	Fragment Name	Begin	End
WP	AAI99682_00	1	110000
WP	AAI99682_01	100001	210000
WP	AAI99682_02	200001	310000
WP	AAI99682_03	300001	410000
WP	AAI99682_04	400001	510000
WP	AAI99682_05	500001	610000
WP	AAI99682_06	600001	710000
WP	AAI99682_07	700001	810000
WP	AAI99682_08	800001	910000
WP	AAI99682_09	900001	1010000
WP	AAI99682_10	1000001	1110000
WP	AAI99682_11	1100001	1210000
WP	AAI99682_12	1200001	1310000
WP	AAI99682_13	1300001	1410000
WP	AAI99682_14	1400001	1510000
WP	AAI99682_15	1500001	1610000
WP	AAI99682_16	1600001	1710000
WP	AAI99682_17	1700001	1810000
WP	AAI99682_18	1800001	1910000
WP	AAI99682_19	1900001	2010000
WP	AAI99682_20	2000001	2110000
WP	AAI99682_21	2100001	2210000
WP	AAI99682_22	2200001	2310000
WP	AAI99682_23	2300001	2410000
WP	AAI99682_24	2400001	2510000
WP	AAI99682_25	2500001	2610000
WP	AAI99682_26	2600001	2710000
WP	AAI99682_27	2700001	2810000
WP	AAI99682_28	2800001	2910000
WP	AAI99682_29	2900001	3010000
WP	AAI99682_30	3000001	3110000
WP	AAI99682_31	3100001	3210000

WP	AAI99682_32	3200001	3310000
WP	AAI99682_33	3300001	3410000
WP	AAI99682_34	3400001	3510000
WP	AAI99682_35	3500001	3610000
WP	AAI99682_36	3600001	3710000
WP	AAI99682_37	3700001	3810000
WP	AAI99682_38	3800001	3910000
WP	AAI99682_39	3900001	4010000
WP	AAI99682_40	4000001	4110000
WP	AAI99682_41	4100001	4210000
WP	AAI99682_42	4200001	4310000
WP	AAI99682_43	4300001	4410000
WP	AAI99682_44	4400001	4411529

Query Match 100.0%; Score 22; DB 4; Length 110000;

Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGATCGAGCT 22
DB 28765 CCATCGCCCAAGGATCGAGCT 28787
|||||

RESULT 50

AAI99683_05
Continuation (6 of 44) of AAI99683 from base 500001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession AAI99683

WP	Fragment Name	Begin	End
WP	AAI99683_00	1	110000
WP	AAI99683_01	100001	210000
WP	AAI99683_02	200001	310000
WP	AAI99683_03	300001	410000
WP	AAI99683_04	400001	510000
WP	AAI99683_05	500001	610000
WP	AAI99683_06	600001	710000
WP	AAI99683_07	700001	810000
WP	AAI99683_08	800001	910000
WP	AAI99683_09	900001	1010000
WP	AAI99683_10	1000001	1110000
WP	AAI99683_11	1100001	1210000
WP	AAI99683_12	1200001	1310000
WP	AAI99683_13	1300001	1410000
WP	AAI99683_14	1400001	1510000
WP	AAI99683_15	1500001	1610000
WP	AAI99683_16	1600001	1710000
WP	AAI99683_17	1700001	1810000
WP	AAI99683_18	1800001	1910000
WP	AAI99683_19	1900001	2010000
WP	AAI99683_20	2000001	2110000
WP	AAI99683_21	2100001	2210000
WP	AAI99683_22	2200001	2310000
WP	AAI99683_23	2300001	2410000
WP	AAI99683_24	2400001	2510000
WP	AAI99683_25	2500001	2610000
WP	AAI99683_26	2600001	2710000
WP	AAI99683_27	2700001	2810000
WP	AAI99683_28	2800001	2910000
WP	AAI99683_29	2900001	3010000
WP	AAI99683_30	3000001	3110000
WP	AAI99683_31	3100001	3210000
WP	AAI99683_32	3200001	3310000
WP	AAI99683_33	3300001	3410000
WP	AAI99683_34	3400001	3510000
WP	AAI99683_35	3500001	3610000
WP	AAI99683_36	3600001	3710000
WP	AAI99683_37	3700001	3810000
WP	AAI99683_38	3800001	3910000
WP	AAI99683_39	3900001	4010000
WP	AAI99683_40	4000001	4110000
WP	AAI99683_41	4100001	4210000
WP	AAI99683_42	4200001	4310000
WP	AAI99683_43	4300001	4403765

Query Match 100.0%; Score 22; DB 4; Length 110000;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 30208 CCATGCCCAAGGAGATCGAGCT 30229

RESULT 51

AAT06825
 ID AAT06825 standard; DNA; 48 BP.
 XX AC AAT06825;
 XX DT 03-JUL-1996 (first entry)
 XX DE 65 kD heat shock gene nucleotides 405-452, target sequence.
 XX KW probe; modified ligase chain reaction; Mycobacterium tuberculosis;
 XX KW M. avium; M. intracellulare; M. kansasii; detection; diagnosis; ss.
 XX OS Mycobacterium tuberculosis.
 XX PN WO9531571-A2;
 XX PD 23-NOV-1995.
 XX PF 04-MAY-1995; 95WO-US005816.
 XX PR 13-MAY-1994; 94US-00223330.
 XX PA (ABBO) ABBOTT LAB.
 XX PI Kratochvil JD, Leckie GW, Odonnell DL, Solomon NA;
 XX DR WPI; 1996-010956/01.

New probes for detection of Mycobacterium species - derived from the 16S ribosomal RNA gene, the protein antigen b gene and the 65 kD and 10 kD heat shock protein genes of M. tuberculosis.

Claim 1; Page 43; 60pp; English.

The present sequence is a target DNA sequence of the 65 kD heat shock protein gene (nucleotides 405-452) of M. tuberculosis. Probe set 12 (AAT06826-829) were utilised to detect bacteria of the genus Mycobacteria. The probes were labelled with biotin and fluorescein. A modified ligase chain reaction was utilised which uses two pairs of probes designated A, B (primary probes) and A', B' (secondary probes). Probe pairs were directed to the same target strand and ultimately ligated to one another after annealing to the target strand. At least one of the probes of a pair had a modified end with respect to the point of ligation. The modified end had bases omitted to create a gap between one probe terminus and the next probe terminus when the pair was annealed to the target sequence. Other modified ends include a base mismatched with the target sequence. The presence of modified ends reduced the falsely positive signal created by blunt-end ligation of the complementary probe duplexes to one another in the absence of target. "Correction" of the modification, in a target dependent manner, was subsequently carried out to render the probes ligatable. Once ligated, the fused (reorganised) probe was dissociated (e.g. melted) from the target and, as with conventional LCR, the process was repeated for several cycles

Sequence 48 BP; 12 A; 10 C; 18 G; 8 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 8 CATGCCCAAGGAGATCGAGCT 28

RESULT 52

AAT06550
 ID AAT06550 standard; DNA; 48 BP.
 XX AC AAT06550;
 XX DT 25-MAR-2003 (revised)
 XX DT 03-JUL-1996 (first entry)
 XX DE 65 kD heat shock gene nucleotides 405-452, target sequence.
 XX KW probe; modified ligase chain reaction; Mycobacterium tuberculosis;
 XX KW M. avium; M. intracellulare; M. kansasii; detection; diagnosis; ss.
 XX OS Mycobacterium tuberculosis.
 XX PN WO9531570-A1.
 XX PD 23-NOV-1995.
 XX PF 04-MAY-1995; 95WO-US005602.
 XX PR 13-MAY-1994; 94US-00242403.
 XX PA (ABBO) ABBOTT LAB.
 XX PI Leckie GW, Davis AH, Semplefacey IE, Manlove MT, Solomon NA;
 XX DR WPI; 1996-010955/01.

New probes for detection of M. tuberculosis - derived from e.g. the gene coding for protein antigen b and from the insertion-like element IS6110 of M. tuberculosis.

Example 10; Page 43; 60pp; English.

The present sequence is a target DNA sequence of the 65 kD heat shock protein gene (nucleotides 405-452) of M. tuberculosis. Probe set 12 (AAT06551-554) were utilised to detect bacteria of the genus Mycobacteria. The probes were labelled with biotin and fluorescein. A modified ligase chain reaction was utilised which uses two pairs of probes designated A, B (primary probes) and A', B' (secondary probes). Probe pairs were directed to the same target strand and ultimately ligated to one another after annealing to the target strand. At least one of the probes of a pair had a modified end with respect to the point of ligation. The modified end had bases omitted to create a gap between one probe terminus and the next probe terminus when the pair was annealed to the target sequence. Other modified ends include a base mismatched with the target sequence. The presence of modified ends reduced the falsely positive signal created by blunt-end ligation of the complementary probe duplexes to one another in the absence of target. "Correction" of the modification, in a target dependent manner, was subsequently carried out to render the probes ligatable. Once ligated, the fused (reorganised) probe was dissociated (e.g. melted) from the target and, as with conventional LCR, the process was repeated for several cycles. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 48 BP; 12 A; 10 C; 18 G; 8 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 8 CATGCCCAAGGAGATCGAGCT 28

RESULT 53

ADS56335
 ID ADS56335 standard; cDNA; 1728 BP.

XX AC ADS56335;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polynucleotide #8322.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KW pathogen tolerance; pest tolerance; plant disease resistance;
XX KW cell cycle pathway modification; plant growth regulator;
XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KW bacterial polynucleotide; gene; ss.
XX OS Bacteria.
XX US2003233675-A1.
XX PN 18-DEC-2003.
XX PD 20-FEB-2003; 2003US-00369493.
XX PF 21-FEB-2002; 2002US-0360039P.
XX PR (CAOY/) CNO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX PT New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 32009; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polynucleotide used in
XX CC the scope of the invention. Note: The sequence data for this patent did
XX CC not form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 1728 BP; 335 A; 570 C; 579 G; 244 T; 0 U; 0 Other;
Query Match 92.7%; Score 20.4; DB 13; Length 1728;
Best Local Similarity 95.5%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22

Db 269 CCATCGCTAAGGAGATCGAGCT 290
||||| |||||||
RESULT 54
ID ADM72250/c
AD 72250 standard; DNA; 99090 BP.
XX ADM72250;
XX AC ADM72250;
XX DT 03-JUN-2004 (first entry)
XX DE O. minuta Pi2 region contiguous sequence.
XX DE O. minuta Pi2 region contiguous sequence.
XX KW Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance;
XX KW gene; db.
XX OS Oryza minuta.
XX PN WO2004022715-A2.
XX PD 18-MAR-2004.
XX PF 08-SEP-2003; 2003WO-US027913.
XX PR 09-SEP-2002; 2002US-0409216P.
XX PR 18-MAR-2003; 2003US-0455713P.
XX PR 05-SEP-2003; 2003US-00656394.
XX PA (OHIS) UNIV OHIO STATE.
XX PI Wang G;
XX WPI; 2004-257576/24.
XX PT New rice Pi2-like disease resistance nucleic acid molecule that confers
XX PT disease resistance in plants, useful for creating or enhancing disease
XX PT resistance in plants.
XX PS Example 3; SEQ ID NO 13; 120pp; English.
XX CC The invention relates to novel broad-spectrum resistance gene Pi2 and the
XX CC NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
XX CC disease resistance nucleic acid molecules are useful for enhancing
XX CC disease resistance in plants. The present sequence represents a Pi2
XX CC region contiguous sequence
XX SQ Sequence 99090 BP; 28990 A; 20403 C; 21246 G; 28450 T; 0 U; 1 Other;
Query Match 92.7%; Score 20.4; DB 12; Length 99090;
Best Local Similarity 95.5%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
||||| |||||||
Db 38860 CCATCGCCCAAGGAGATCGAGCT 38839
RESULT 55
ID ACF04316
AD ACF04316 standard; DNA; 20 BP.
XX ACF04316;
XX AC ACF04316;
XX DT 06-NOV-2003 (first entry)
XX DE Mycobacterium hsp65 gene PCR primer #1.
XX KW Mycobacterium; hsp65; heat shock protein 65; identification;
XX KW tuberculosis; PCR; primer; ss.
XX OS Mycobacterium sp.
XX

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PN WO2003062470-A1.
XX
PD 31-JUL-2003.
XX
PF 21-JAN-2003; 2003WO-KR000131.
XX
XX 24-JAN-2002; 2002KR-00004297.
PR 05-MAR-2002; 2002KR-00011648.
XX
XX (BIOM-) BIOMEDLAB CORP.
PA (KIME/) KIM B.
XX
XX Kim B, Kook Y, Kim J;
XX
XX WPI; 2003-598757/56.
XX
XX Primers for amplifying a heat shock protein 65-gene fragment of
PT mycobacterial species, useful for identifying and diagnosing
PT mycobacterial species in tuberculosis infection.
XX
XX Claim 1; Page 100; 102pp; English.
XX
XX The present invention provides a pair of primers for specifically
CC amplifying a heat shock protein 65 (hsp 65) gene fragment of
CC mycobacterial species comprising those sequences shown in ACF04316-
CC ACF04317. Also provided are a number of hsp65 gene fragments, mainly from
CC mycobacterial species. The methods and compositions of the present
CC invention are useful for amplifying hsp 65 gene of mycobacterial species,
CC and identifying and diagnosing mycobacterial species in tuberculosis
CC infection. The present sequence is a PCR primer of the invention
XX
XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 90.9%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ATCGCCCAAGGAGATCGAGCT 22
DB 1 ATCGCCCAAGGAGATCGAGCT 20
RESULT 56
AAV26962
ID AAV26962 standard; cDNA to mRNA; 5275 BP.
XX
AC AAV26962;
XX
XX 01-SEP-1998 (first entry)
XX
XX Bovine parathyroid calcium receptor 1 gene 5Kb fragment.
XX
XX ss; calcium ion concentration; parathyroid hormone; homeostasis; kidney;
XX calcium receptor; detection.
XX
XX Bos sp.
XX
XX Key Location/Qualifiers
XX CDS 515..3772
XX /*tag= a
XX /product= "BopCar 1 5Kb fragment"
XX
XX US5763569-A.
XX
XX 09-JUN-1998.
XX
XX 07-JUN-1995; 95US-00484565.
XX
XX 23-AUG-1991; 91US-00749451.
XX 11-FEB-1992; 92US-00834044.
PR 21-AUG-1992; 92US-00934161.
XX 12-FEB-1993; 93US-00017127.
PR 23-FEB-1993; 93US-00009389.
XX
PR 22-OCT-1993; 93US-00141248.
XX
PR 22-OCT-1993; 93US-00141248.
PR 19-AUG-1994; 94US-00292827.
PR 21-OCT-1994; 94WO-US012117.
PR 08-DEC-1994; 94US-00353784.
XX
XX (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Hebert SC, Brown EM, Garrett JE;
XX
XX WPI; 1998-347412/30.
DR P-PSDB; AAW54844.
XX
XX Calcium receptor poly:peptide(s) - useful for drug screening or antibody
PT production.
XX
XX Example 25; Fig 47; 174pp; English.
XX
XX The bovine parathyroid calcium receptor gene encodes a 1085 amino acid
CC protein. The tissue from which this receptor and receptors from human
CC parathyroid and rat kidney are derived, respond to changes, and control
CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates
CC Ca2+ homeostasis in blood and extracellular fluid, and kidney function
CC alters through changes in Ca2+ levels in juxtaglomerular and proximal
CC tubule cells in the kidney. The purified receptors (produced
CC recombinantly) can be used to screen for compounds that modulate calcium
CC receptor activity, especially those that can be used to treat diseases
CC associated with the receptors in these tissues. They can also be used to
CC raise antibodies for use in detection assays
XX
XX Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T; 0 U; 0 Other;
SQ
Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CATGCCCAAGGAGATCGAGCT 22
DB 2311 CATGCCCAAGGAGATCGAGTT 2331
RESULT 57
AAT95857
ID AAT95857 standard; cDNA to mRNA; 5275 BP.
XX
AC AAT95857;
XX
XX 08-MAY-1998 (first entry)
XX
XX Bovine parathyroid cell calcium receptor 1 (BopCar 1) cDNA.
XX
XX Bovine parathyroid cell calcium receptor 1; BopCar 1;
XX calcium homeostasis; hyperparathyroidism; osteoporosis; ss.
XX
XX Bos sp.
XX
XX Key Location/Qualifiers
XX CDS 515..3772
XX /*tag= a
XX /product= "parathyroid_cell_calcium_receptor_1"
XX
XX US5688938-A.
XX
XX 18-NOV-1997.
XX
XX 07-JUN-1995; 95US-00485588.
XX
XX 23-AUG-1991; 91US-00749451.
XX 11-FEB-1992; 92US-00834044.
PR 21-AUG-1992; 92US-00934161.
XX 12-FEB-1993; 93US-00017127.
PR 23-FEB-1993; 93US-00009389.
XX
PR 22-OCT-1993; 93US-00141248.
XX

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PR 19-AUG-1994; 94US-00292827.
PR 21-OCT-1994; 94WO-US012117.
PR 08-DEC-1994; 94US-00353784.
XX
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (NPSP-) NPS PHARM INC.
XX
PI Garrett JE, Fuller FH, Brown EM, Hebert SC;
XX
DR WPI; 1998-008040/01.
DR P-PSDB; AAW38272.
XX
XX DNA encoding calcium receptor polypeptide(s) - useful for therapeutic
PT purposes, e.g. hyperparathyroidism and osteoporosis.
PT
XX Claim 1; Col 107-116; 174pp; English.
XX
XX The present sequence encodes bovine parathyroid cell calcium receptor 1
CC (BoPCar 1). The specification includes details of molecules that can
CC modulate one or more inorganic ion receptor activities, and antibodies
CC and antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat disorders by
CC modulating one or more inorganic ion receptor activities, preferably
CC disorders of calcium homeostasis, e.g. hyperparathyroidism and
CC osteoporosis
XX
XX Sequence 5275 BP; 1277 A; 1476 C; 1315 G; 1207 T; 0 U; 0 Other;
SQ
Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 58
AAZ25053
ID AAZ25053 standard; cDNA to mRNA; 5275 BP.
XX
AC AAZ25053;
XX
DT 08-DEC-1999 (first entry)
XX
DE Bovine parathyroid calcium receptor 1 nucleotide sequence.
XX
KW Parathyroid; calcium receptor; inorganic ion receptor; modulator;
KW receptor expression; detection; ss.
XX
OS Bos taurus.
XX
XX Key Location/Qualifiers
FH 515..3772
FT CDS /*tag= a
FT /product= "BoPCar 1"
FT /note= "parathyroid calcium receptor"
XX
XX US5962314-A.
XX
XX 05-OCT-1999.
XX
XX 03-OCT-1997; 97US-00943986.
XX
XX 23-FEB-1993; 93US-00009389.
XX
XX 22-OCT-1993; 93US-00141248.
XX
XX 19-AUG-1994; 94US-00292827.
XX
XX 21-OCT-1994; 94WO-US012117.
XX
XX 08-DEC-1994; 94US-00353784.
XX
XX 07-JUN-1995; 95US-00484565.
XX
XX (NPSP-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.

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XX Brown EM, Hebert SC, Garrett JE;
XX WPI; 1999-571274/48.
XX P-PSDB; AAY41778.
XX
XX Nucleic acids encoding protein calcium receptors useful for identifying
PT modulators of receptor expression and activity and for the production of
PT antigens specific for calcium receptors.
XX
XX Claim 5; Fig 47; 174pp; English.
XX
XX The present sequence encodes bovine parathyroid calcium receptor 1
CC (BoPCar 1). Calcium receptor polynucleotides may be used: (i) for
CC producing receptor proteins (or fragments) useful for determining
CC structure and activity relationships, for assaying molecular activity on
CC the receptor (i.e. identifying modulators of receptor function) and for
CC producing antibodies specific for the receptor; (ii) for sequencing the
CC normal form of the nucleic acids (the derived sequence may be compared
CC with other receptors to identify conserved sequences, mutations and
CC variations that may influence calcium receptor activity and to determine
CC target sites for antisense molecules, ribozymes, hybridization probes and
CC polymerase chain reaction (PCR) amplification primers; (iii) as
CC hybridization probes to detect the presence of similar sequences in
CC samples; and (iv) as PCR primers to generate particular nucleic acid
CC sequence regions; (e.g. to generate regions to be probes by hybridization
CC detection probes)
XX
XX Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T; 0 U; 0 Other;
SQ
Query Match 88.2%; Score 19.4; DB 2; Length 5275;
Best Local Similarity 95.2%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 2311 CATGCCCAAGGAGATCGAGTT 2331

RESULT 59
AAV82483
ID AAV82483 standard; cDNA to mRNA; 5275 BP.
XX
AC AAV82483;
XX
DT 19-MAR-1999 (first entry)
XX
DE Bovine parathyroid calcium receptor BoPCar 1 encoding cDNA.
XX
KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
KW depression; anxiety; ss.
XX
XX Bos sp.
XX
XX Key Location/Qualifiers
FH 515..3772
FT CDS /*tag= a
XX
XX US5858684-A.
XX
XX 12-JAN-1999.
XX
XX 07-JUN-1995; 95US-00480751.
XX
XX 23-AUG-1991; 91US-00749451.
XX
XX 11-FEB-1992; 92US-00834044.
XX
XX 21-AUG-1992; 92US-00934161.
XX
XX 12-FEB-1993; 93US-00017127.
XX
XX 23-FEB-1993; 93US-00009389.

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Search completed: April 1, 2006, 22:21:34
Job time : 50.7112 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:06:31 ; Search time 303.022 Seconds
(without alignments)
3396.840 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22

Sequence: 1 ccacgcgaagagatcgagct 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	100.0	828	10	CL693779 PRI0162C
2	21	95.5	539	7	CR928307
3	21	95.5	1319	8	DN666868
4	21	95.5	1370	8	DN666868 CFW34-F12
5	20.4	92.7	916	10	AG859232
6	19.4	88.2	340	1	AG859232 Cryza sat
7	19.4	88.2	588	2	AG859232 Cryza sat
8	19.4	88.2	649	7	CG503864
9	19.4	88.2	658	9	BZ566239
10	19.4	88.2	815	8	DR424057
11	19.4	88.2	840	9	CC475958
12	19.4	88.2	1402	8	DN737348
13	19.4	88.2	1480	8	DN721479
14	18.8	85.5	123	8	CV849414
15	18.8	85.5	180	7	CV849414
16	18.8	85.5	308	7	CV849414
17	18.8	85.5	308	10	CV849414
18	18.8	85.5	312	8	CV836743
19	18.8	85.5	312	8	CV836743
20	18.8	85.5	316	7	CV836743
21	18.8	85.5	317	7	CV836743
22	18.8	85.5	318	8	CV836743

23	18.8	85.5	319	7	CN755308
24	18.8	85.5	319	7	CN755404
25	18.8	85.5	323	10	CZ112870
26	18.8	85.5	332	8	CV828800
27	18.8	85.5	332	8	CV828800
28	18.8	85.5	332	8	CV829374
29	18.8	85.5	332	8	CV830911
30	18.8	85.5	332	8	CV831091
31	18.8	85.5	332	8	CV832760
32	18.8	85.5	332	8	CV838428
33	18.8	85.5	340	7	CN764316
34	18.8	85.5	407	7	CN750782
35	18.8	85.5	414	6	CN999580
36	18.8	85.5	424	6	CN999580
37	18.8	85.5	436	5	C25159
38	18.8	85.5	471	3	BM087289
39	18.8	85.5	483	7	CN750359
40	18.8	85.5	484	7	CN749153
41	18.8	85.5	492	6	CD451510
42	18.8	85.5	523	3	BJ645375
43	18.8	85.5	534	10	CW768437
44	18.8	85.5	551	6	CF292206
45	18.8	85.5	569	7	CN583982
46	18.8	85.5	570	6	CF292207
47	18.8	85.5	572	7	CN585977
48	18.8	85.5	581	6	CB087986
49	18.8	85.5	599	6	CD450119
50	18.8	85.5	612	7	CN584119
51	18.8	85.5	629	10	CL612592
52	18.8	85.5	640	6	CB690026
53	18.8	85.5	646	6	CF587912
54	18.8	85.5	656	9	AQ257000
55	18.8	85.5	665	6	CB000900
56	18.8	85.5	671	7	CN755289
57	18.8	85.5	671	9	AQ576753
58	18.8	85.5	672	10	CN775708
59	18.8	85.5	673	10	CW506965
60	18.8	85.5	684	9	AQ287315
			696	6	CF588105

ALIGNMENTS

RESULT 1

CL693779/c

LOCUS

DEFINITION

PR10162C_A12.2 - PRI0162C.BR (828) Mixed stage foetid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

CL693779

VERSION

CL693779.1

GI:50215687

KEYWORDS

GSS.

SOURCE

Pristionchus pacificus

ORGANISM

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE

1 (bases 1 to 828)

AUTHORS

Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE

AppaDB: an Acedb database for the nematode satellite organism Pristionchus pacificus

JOURNAL

Nucleic Acids Res. 32 (1), D421-D422 (2004)

PUBMED

14681447

COMMENT

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@uebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: foetid ends.

CL693779 828 bp DNA linear GSS 10-JUL-2004
PR10162C_A12.2 - PRI0162C.BR (828) Mixed stage foetid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

CL693779

CL693779.1

GI:50215687

KEYWORDS

GSS.

SOURCE

Pristionchus pacificus

ORGANISM

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE

1 (bases 1 to 828)

AUTHORS

Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE

AppaDB: an Acedb database for the nematode satellite organism Pristionchus pacificus

JOURNAL

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COMMENT

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Evolutionary Biology

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Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@uebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: foetid ends.


```

VERSION DN665225.1 GI:61985281
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

REFERENCE 1 (bases 1 to 1370)
AUTHORS Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,
Schmutz, J., and Myers, R.M.
TITLE Expressed sequence tags from Gasterosteus aculeatus
JOURNAL Unpublished (2003)
COMMENT Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 24
High quality sequence start: 30
High quality sequence stop: 872.

FEATURES
source
1..1370
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
/clone="CFW24-H08"
/sex="mixed male and female"
/tissue_type="gills"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CFW"
/note="Vector: Express 1; Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceded by a synthetic NotI site (first strand primer:
5'-GACTAGTCTAGATCGCAGCGGCCCT(25-3')). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5 prime end of mRNA, and
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
in the blunt end cloning, leaving a junction of the form
'xxxATC' (where is ATC is the second half of the EcoRV
site, and xxx is derived from the cDNA sequence). A map of
the Express 1 vector is available at:
http://www.openbiosystems.com/cdna library construction fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
http://www.openbiosystems.com/stickleback"

ORIGIN
Query Match 95.5%; Score 21; DB 8; Length 1370;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCGCAAGAGATCGAGC 21
|||||
Db 186 CCATCGCAAGAGATCGAGC 206

RESULT 5
AG859232
LOCUS AG859232
DEFINITION Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence,
BAC clone:K0172D09_F, genomic survey sequence.
ACCESSION AG859232
VERSION AG859232.1 GI:55325467

GSS.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1
AUTHORS Katagiri, S., Wu, J., Ito, Y., Karasawa, W., Shibata, M., Kanamori, H.,
Katayose, Y., Nani, N., Matsumoto, T. and Sasaki, T.
TITLE End Sequencing and Chromosomal in silico Mapping of BAC Clones
Derived from an indica Rice Cultivar, Kasalath
JOURNAL Breeding Science 54, 273-279 (2004)
REFERENCE 2 (bases 1 to 916)
AUTHORS Sasaki, T., Matsumoto, T. and Wu, J.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2004) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2 Tsukuba, Ibaraki 305-8602, Japan
(E-mail: taasakia@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
COMMENT The orientation of the sequence is from T7 side of the BAC clone.
FEATURES
source
1..916
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Kasalath"
/db_xref="taxon:39946"
/clone="K0172D09_F"

ORIGIN
Query Match 92.7%; Score 20.4; DB 10; Length 916;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCGCCAGGAGATCGAGCT 22
|||||
Db 387 CCATCGCCAGGAGATCGAGCT 408

RESULT 6
AW281326
LOCUS AW281326
DEFINITION fJ53e02.y1 zebrafish adult brain Danio rerio cDNA 5' similar to
TT:016732 Q16732 NA+/K+ ATPase ALPHA SUBUNIT ; mRNA sequence.
ACCESSION AW281326
VERSION AW281326.1 GI:6669875
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 340)
AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbratfish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and

```

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)

Trace considered overall poor quality

Seq primer: T7

High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1. .340

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/sex="mixed male and female"

/tissue_type="brain"

/dev stage="adult"

/lab_host="E. coli DH10B"

/clone_lib="zebrafish adult brain"

/note="Vector: pZiPlox; Site 1: NotI; Site 2: SalI;
Original library was constructed in lambdaZiPlox. Mass
excision of the cDNA library was performed to yield
pZiPlox plasmids. Insert check was done in original
library."

ORIGIN

Query Match 88.2%; Score 19.4; DB 1; Length 340;

Best Local Similarity 95.2%; Pred. No. 4.4e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGC 21

Db 66 CCATGCCCAAGGAGATCGAGC 86

RESULT 7

BG729640

LOCUS

DEFINITION

649 bp mRNA linear EST 09-MAY-2001
f081h07.y1 zebrafish gridded kidney Danio rerio cDNA clone
IMAGE:4726525 5' similar to SW:ATN3 RAT P06687
SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-3 CHAIN ; mRNA
sequence.

ACCESSION BG729640

VERSION BG729640.1 GI:114014715

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 588)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Edy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swallet, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Other ESTs: f081h07.x1

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address:
www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)

Seq primer: T3 ET from Amersham

High quality sequence stop: 462.

Location/Qualifiers

FEATURES

source

source

1. .588

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:4726525"

/sex="mixed"

/tissue_type="kidney pooled from 300 wild type adults"

/lab_host="XL0LR"

/clone_lib="zebrafish gridded kidney"

/note="Organ: kidney; Vector: pBK-CMV; Site 1: EcoRI;
Site 2: XhoI; Oligo dr cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."

ORIGIN

Query Match 88.2%; Score 19.4; DB 2; Length 588;

Best Local Similarity 95.2%; Pred. No. 4.6e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGC 21

Db 290 CCATGCCCAAGGAGATCGAGC 310

RESULT 8

CO503864

LOCUS

DEFINITION

649 bp mRNA linear EST 13-JUL-2004
GGEZCB1010E10.g chicken breast muscle - CBI Gallus gallus CDNA
clone GGEZCB1010E10, mRNA sequence.

ACCESSION CO503864

VERSION CO503864.1 GI:50274050

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 649)

Alves, H.J., Jorge, E.C., Marchesin, M.L., Monteiro-Vitorello, C.B.,

Patricio, M., Ledur, M.C. and Coutinho, L.L.

Discovery of new genes expressed in the chicken breast muscle

Unpublished (2004)

Contact: Helena J. Alves

Laboratory of Animal Biotechnology, Dep. of Animal Production

ESALQ - University of Sao Paulo

Av. Padowa Dias, 11, Piracicaba, SP, 13418-900, Brazil

Tel: 55 19 3429 4434

Fax: 55 19 3429 4285

Email: hjalves@esalq.usp.br and llicoutin@esalq.usp.br

PCR Primers

BACKWARD: T7.

Location/Qualifiers

1. .649

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="GGEZCB1010E10"

/tissue_type="breast muscle"

/dev stage="1 and 21 days old"

/lab_host="DH5 alpha"

/clone_lib="chicken breast muscle - CBI"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This

cDNA library was constructed with the SuperScript Plasmid

System with Gateway Technology kit (Invitrogen), following a

manufacturer's protocols. Plasmid DNA was purified using a

modified alkaline lysis method. Sequencing reactions were

conducted using the DYEnamic Cycle Sequencing Kit for

MegabAC (Amersham Biosciences) according to the

manufacturer's recommendations. Clones were sequenced by

the 5' end with T7 primer. Sequencing reactions were

analyzed on MegabAC1000 DNA Sequencer (Amersham

Biosciences). The quality and clustering of the ESTs were

analyzed using the softwares Phred/cap3. Only EST

sequences with Phred quality greater than 20 and at least 150 bp were considered for clustering."

ORIGIN

Query Match 88.2%; Score 19.4; DB 7; Length 649;
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCATCGCCCAAGGAGATCGAGC 21
 |||||
 Db 182 CCATCGCCCAAGGAGATCGAGC 202

RESULT 9

BZ566239 658 bp DNA linear GSS 17-DEC-2002
 LOCUS pac2-164_5975.y2 pac2-164_pseudomonas aeruginosa genomic clone
 DEFINITION pac2-164_5975, genomic survey sequence.

ACCESSION

BZ566239 BZ566239.1 GI:27195398

VERSION

KEYWORDS

SOURCE

ORGANISM

Pseudomonas aeruginosa

REFERENCE

Bacteria: Proteobacteria; Gammaproteobacteria; Pseudomonadales;

AUTHORS

Pseudomonadaceae; Pseudomonas.

TITLE

1 (bases 1 to 658)

JOURNAL

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,

COMMENT

Burns, J.L., Kaul, R. and Olsen, M.V.

Whole-Genome-Sequence variation among multiple isolates of

Pseudomonas aeruginosa library

J. Bacteriol. (2002) In press

Contact: Chris K. Raymond

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 2062216954

Fax: 2066857244

Email: craymond@u.washington.edu

Class: shotgun.

Location/Qualifiers

1. 658

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="2-164"

/db_xref="taxon:287"

/clone="pac2-164_5975"

/clone_lib="pac2-164"

/note="clinical isolate 2-164 whole genomic shotgun library."

ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 658;
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21

|||||

Db 131 CCATCGCCCAAGGAGATCGTGC 151

RESULT 10

DR424057 815 bp mRNA linear EST 29-JUN-2005
 LOCUS nwo02f12.y1 Chicken eye (hatched). Unnormalized (naw) Gallus gallus
 DEFINITION cDNA clone naw02f12 5', mRNA sequence.

ACCESSION

DR424057 DR424057.1 GI:68326073

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE

AUTHORS Wislow, G., Peterson, K. and McMurtry, J.

TITLE

NEIBank analysis of 15day post-hatched chicken eye

JOURNAL

Unpublished (2005)

COMMENT

Contact: Wislow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 02 row: f column: 12

Seq primer: Universal M13 Reverse.

Location/Qualifiers

1. 815

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="naw02f12"

/tissue_type="Whole eye"

/dev_stage="15d post-hatched"

/lab_host="EMDH108"

/clone_lib="Chicken eye (hatched). Unnormalized (naw)"

/note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted

from pooled 15day post-hatched chicken eye. A

directionally cloned cDNA library in the pCMVSPORT6 vector

(Invitrogen) was constructed at Bioserve Biotechnology

(Laurel MD) essentially following the protocols of the

SuperScript Plasmid System, full details of which are

contained in the manufacturer's instruction manual

(http://www.lifetech.com/). First strand synthesis was

carried out using a Not I primer-adaptor

[5'-pGACTAGTCTAGATCGAGCGCCGCTT15-3']. cDNA was

cloned in Not I/Sal I sites. EST analysis was performed at

the NIH Intramural Sequencing Center (NISC). Analyzed data

available through http://neibank.nei.nih.gov."

ORIGIN

Query Match 88.2%; Score 19.4; DB 8; Length 815;
 Best Local Similarity 95.2%; Pred. No. 4.7e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21

|||||

Db 508 CCATCGCCCAAGGAGATCGAGC 528

RESULT 11

CC475958 840 bp DNA linear GSS 16-JUN-2003
 LOCUS CH240_301N21.T7 CHORI-240 Bos taurus genomic clone CH240_301N21,
 DEFINITION genomic survey sequence.

ACCESSION

CC475958

VERSION CC475958.1 GI:31753167

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 840)

Holt, R., Stott, J., Yang, G., Barber, S., Small, D., Prabhu, A.-L.,

Tsai, M., Cloutier, A., Lee, D., Girm, N., Olson, T., Mayo, M.,

Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,

Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,

Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,

Dalrymple, B.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Unpublished (2003)

Other_GSSs: CH240_301N21.TARBAC13P2

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Sciences Centre, Canada.

Plate: 301 row: N column: 21
 Seq primer: T7

Class: BAC ends.

FEATURES

Location/Qualifiers
 1. .840
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="broad: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_301N21"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /notes="Vector: PTARBAC1.3; Site 1: MbolI; Site 2: MbolI;
 Hereford bull LI Domino 9375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 840;
 Best Local Similarity 95.2%; Pred. No. 4.7e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22

Db 751 CATGCCCAAGGAGATCGAGTT 771

RESULT 12

DN737348
 LOCUS
 DEFINITION CNB92-C09.y1d-s SHGC-CNB Gasterosteus aculeatus cDNA clone
 CNB92-C09 5', mRNA sequence.

ACCESSION DN737348

VERSION DN737348.1 GI:62113709

KEYWORDS EST.

SOURCE Gasterosteus aculeatus (three spined stickleback)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.

REFERENCE

1 (bases 1 to 1402)
 Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
 Schmutz,J. and Myers,R.M.

TITLE

Expressed sequence tags from Gasterosteus aculeatus

JOURNAL

Unpublished (2003)

COMMENT

Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@shgc.stanford.edu

Plate: 92

High quality sequence stop: 804.

FEATURES

Location/Qualifiers
 1. .1402
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"

/clone="CNB92-C09"
 /sex="mixed male and female"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHGC-CNB"

/notes="Vector: Express 1; Total and poly A+ RNA was
 isolated from the indicated stickleback tissue, and a cDNA
 library was constructed in the Express 1 plasmid vector by
 Open Biosystems. First strand cDNA synthesis was primed
 with an 54 bp linker primer containing an oligodT sequence
 preceded by a synthetic NotI site (first strand primer:
 5'-GACTAGTCTAGATCGGCGCGCCG(T)25-3'). Following

second strand synthesis, cDNAs were made blunt at the end
 corresponding to the original 5 prime end of mRNA, and
 cloned directionally into the NotI and EcoRV sites of
 Express 1. Note that the EcoRV site is typically destroyed
 in the blunt end cloning, leaving a junction of the form
 'xxxATC' (where is ATC is the second half of the EcoRV
 site, and xxx is derived from the cDNA sequence). A map of
 the Express 1 vector is available at:

http://www.openbiosystems.com/cdna_library_construction_fa
 q.php#8 The primary library was transformed and amplified
 in DH10B (T1 phage resistant) bacteria. Clones available
 from Open Biosystems:

http://www.openbiosystems.com/stickleback"

ORIGIN

Query Match 88.2%; Score 19.4; DB 8; Length 1402;
 Best Local Similarity 95.2%; Pred. No. 4.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGC 21

Db 828 CCATGCCCAAGGAGATCGAGC 848

RESULT 13

DN721479

LOCUS

DEFINITION

CNB139-F07.y1d-s SHGC-CNB Gasterosteus aculeatus cDNA clone

CNB139-F07 5', mRNA sequence.

ACCESSION DN721479

VERSION DN721479.1 GI:62097715

KEYWORDS EST.

SOURCE Gasterosteus aculeatus (three spined stickleback)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.

REFERENCE

1 (bases 1 to 1480)
 Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
 Schmutz,J. and Myers,R.M.

AUTHORS

Expressed sequence tags from Gasterosteus aculeatus

TITLE

Unpublished (2003)

COMMENT

Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@shgc.stanford.edu

Plate: 139

High quality sequence stop: 757.

FEATURES

Location/Qualifiers
 1. .1480
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"
 /clone="CNB139-F07"
 /sex="mixed male and female"

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/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CNB"
/notes="Vector: Express 1; Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceded by a synthetic NotI site (first strand primer:
5'-GACTAGTCTAGATCGGAGCGCGCC(T)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5' prime end of mRNA, and
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
in the blunt end cloning, leaving a junction of the form
'xxxATC' (where ATC is the second half of the EcoRV
site, and xxx is derived from the cDNA sequence). A map of
the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
http://www.openbiosystems.com/stickleback"

```

ORIGIN

```

Query Match      88.2%; Score 19.4; DB 8; Length 1480;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCATCGCCCAAGGAGATCGAGC 21
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```

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Db 414 CCATCGCCCAAGGAGATCGAGC 434
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```

RESULT 14

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CV849414
LOCUS ID0AEE8BA06RM1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AEE8BA06
5', mRNA sequence.
ACCESSION CV849414
VERSION CV849414.1 GI:55815097
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclert,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
Annotated ESTs of the pea aphid
Unpublished (2004)
Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Plate: 8B row: A column: 6.
Location/Qualifiers
1..123
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="vr2"
/db_xref="taxon:7029"
/clone="ID0AEE8BA06"
/tissue_type="antennae"
/dev_stage="L3"
/lab_host="XL1-Blue"

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FEATURES source

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1..123
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="vr2"
/db_xref="taxon:7029"
/clone="ID0AEE8BA06"
/tissue_type="antennae"
/dev_stage="L3"
/lab_host="XL1-Blue"

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```

/clone_lib="ID0AEE"
/notes="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AEE ; Plant growth place: INRA Rennes, UMR
Bio3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 15/04/2004 ; Harvesting
date: 15/04/2004 ; Description: Aphids inoculated on
one-week old Vicia faba under non-sterile conditions. A.
pisum VR2 is holocyclic, i.e. able to change its
reproductive mode under short photoperiods (sexual) versus
long photoperiods (clonal). experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 degC)"

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ORIGIN
Query Match      85.5%; Score 18.8; DB 8; Length 123;
Best Local Similarity 90.9%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||

```

```

Db 23 CCAAGGCCAAGGAGATCGAGCT 44
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RESULT 15

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CN758177
LOCUS ID0AAA21CA12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA21CA12
5', mRNA sequence.
ACCESSION CN758177
VERSION CN758177.1 GI:47532100
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
Unpublished (2004)
Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchner) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Plate: 21 row: A column: 12.
Location/Qualifiers
1..180
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA21CA12"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
/clone_lib="ApMS"

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FEATURES source

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1..180
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA21CA12"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
/clone_lib="ApMS"
/notes="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long

```

photoperiod (16-hr light/8-hr dark at 18 c)

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 180;
Best Local Similarity 90.9%; Pred. No. 7.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22
Db 80 CCAAGCCCAAGGATCGAGCT 101

RESULT 16

CN764299 308 bp mRNA linear EST 20-MAY-2004
LOCUS ID0AAA9CB05RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA9CB05 5',
DEFINITION mRNA sequence.

ACCESSION CN764299

VERSION 1

KEYWORDS

SOURCE

ORGANISM

Acyrthosiphon pisum (pea aphid)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 308)

AUTHORS Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

JOURNAL Unpublished (2004)

COMMENT Contact: D. Tagu

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Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts. These sequences were

obtained in the frame of the International Consortium of Aphid

Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAAACACGCTATGACC

Plate: 9

TOW: B

column: 5.

Location/Qualifiers

1. .308

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA9CB05"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/notes="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA; Plant growth place: Department of

Ecology & Evolutionary Biology, Princeton University;

Soil conditions: Soil; Sowing date: 01/06/1999;

Harvesting date: 01/06/1999; Stress date: no stress;

Description: Aphids inoculated on one-week old Vicia faba

under non-sterile conditions. All parthenogenetic stages

and both winged and wingless adults were collected for

library construction; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 308;
Best Local Similarity 90.9%; Pred. No. 8.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22

Db 208 CCAAGCCCAAGGATCGAGCT 229

RESULT 17

CW773364

LOCUS

DEFINITION

5', genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza glaberrima (African rice)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartioideae; Oryzoaceae; Oryza.

1 (bases 1 to 308)

AUTHORS Kim, H., Yu, Y., Wissotski, M., Byrne, M., Stum, D., Smart, D., Rao, K.,
Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C.
and Wing, R.

TITLE OMAP

JOURNAL Unpublished (2004)

COMMENT Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Plate: 0091

row: C

column: 22

Seq primer: TAA TAC GAC TCA CTA TAG GG

Class: BAC ends.

Location/Qualifiers

1. .308

/organism="Oryza glaberrima"

/mol_type="genomic DNA"

/db_xref="taxon:4538"

/clone="OG_BBa0091C22"

/tissue_type="young leaves"

/lab_host="DH10B T1 phage resistant"

/clone_lib="OG_BBa"

/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 85.5%; Score 18.8; DB 10; Length 308;

Best Local Similarity 90.9%; Pred. No. 8.1e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGATCGAGCT 22

Db 186 CCATGCCCAAGGATCGAGCT 207

RESULT 18

CV836743

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Acyrthosiphon pisum (pea aphid)

Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 312)

AUTHORS Sabater-Munoz, B., Legeai, F., Bonhomme, J., Dang, P., Dossat, C.,
Duclet, A., Gauthier, J.P., Hunter, W., Martinez-Torres, D., Moya, A.,
Nakabachi, A., Prunier-Leterme, N., Rahbe, Y., Shigenobu, S.,
Simon, J.C., Stern, D., Wincker, P. and Tagu, D.

TITLE Annotated ESTs of the pea aphid
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 3A row: G column: 6.
Location/Qualifiers

1. 312
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="P123"
/db_xref="taxon:7029"
/clone="ID0ACC3AG06"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 312;
Best Local Similarity 90.9%; Pred. NO. 8.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 212 CCAAGCCCAAGGAGATCGAGCT 233

RESULT 19

CV837906
LOCUS ID0ACCBHI0RM1 ID0ACC Acyrthosiphon pisum cdna clone ID0ACCBHI0
5', mRNA sequence.
DEFINITION CV837906.1 GI:55803589
ACCESSION
VERSION
KEYWORDS
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM

Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 312)
Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

REFERENCE
AUTHORS
TITLE Annotated ESTs of the pea aphid
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 6B row: H column: 10.
Location/Qualifiers

1. 312
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="P123"

FEATURES
source

/db_xref="taxon:7029"
/clone="ID0ACCBHI0"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 312;
Best Local Similarity 90.9%; Pred. No. 8.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATGCCCAAGGAGATCGAGCT 22
Db 212 CCAAGCCCAAGGAGATCGAGCT 233

RESULT 20

CV837906
LOCUS ID0AAA9CD12RM1 ApMS Acyrthosiphon pisum cdna clone ID0AAA9CD12 5',
mRNA sequence.
DEFINITION CN764328.1 GI:47538251
ACCESSION
VERSION
KEYWORDS
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM

Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 316)
Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.

REFERENCE
AUTHORS

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

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UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
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Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope

PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 9 row: D column: 12.
Location/Qualifiers

1. 316
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA9CD12"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old Vicia faba

DESCRIPTION: Aphids inoculated on one-week old Vicia faba

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

AUTHORS

1 (bases 1 to 319)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.

TITLE

An expressed sequence tags database for the pea aphid *Acyrthosiphon pisum*

JOURNAL

Unpublished (2004)

COMMENT

Contact: D. Tagu

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Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 15 row: H column: 11.

FEATURES

source

Location/Qualifiers

1..319

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA15BH11"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old *Vicia faba* under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 C)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 319;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATGCCAAGGAGATCGAGCT 22

Db 219 CCAAGCCAGGAGATCGAGCT 240

RESULT 24

CN755404

LOCUS

DEFINITION ID0AAA15DA07RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA15DA07

5', mRNA sequence.

ACCESSION CN755404

VERSION CN755404.1 GI:47520440

KEYWORDS EST.

SOURCE Acyrthosiphon pisum (pea aphid)

ORGANISM Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 319)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid *Acyrthosiphon*

pisum

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 15 row: A column: 7.

FEATURES

source

Location/Qualifiers

1..319

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA15DA07"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old *Vicia faba* under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 C)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 319;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATGCCAAGGAGATCGAGCT 22

Db 219 CCAAGCCAGGAGATCGAGCT 240

RESULT 25

CN755404

LOCUS

DEFINITION OM_Ba0154L01.f OM_Ba Oryza minuta genomic clone OM_Ba0154L01 5',

genomic survey sequence.

ACCESSION CN755404

VERSION CN755404.1 GI:57697153

KEYWORDS GSS.

SOURCE Oryza minuta

ORGANISM Oryza minuta

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 323)

Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,

Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and

Wing, R.

OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute

Unpublished (2005)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

Plate: 0154 row: L column: 01

Class: BAC ends.

Location/Qualifiers

1..323

FEATURES

source

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/organism="Oryza minuta"
/mol_type="genomic DNA"
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/clone="OM_Ba0154L01"
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/clone_lib="OM_Ba"
/notes="Vector: pCUGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      85.5%; Score 18.8; DB 10; Length 323;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 160 CCATCTCCAAGGAGATCGAGTT 181

RESULT 26
CV828800
LOCUS
DEFINITION      332 bp mRNA linear EST 17-NOV-2004
ID0ACC10DH01RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC10DH01
5', mRNA sequence.
ACCESSION      CV828800
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE      1 (bases 1 to 332)
AUTHORS
Sabater-Munoz,B., Leggai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rabbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
Annotated ESTs of the pea aphid
Unpublished (2004)
Contact: D. Tagu
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UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
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Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 10D row: H column: 1.
Location/Qualifiers
1. .332
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="P123"
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/clone="ID0ACC10DH01"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"
/notes="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

FEATURES
source
ORIGIN
Query Match      85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 232 CCAAAGCCCAAGGAGATCGAGCT 253

RESULT 27
CV829374
LOCUS
DEFINITION      332 bp mRNA linear EST 17-NOV-2004
ID0ACC12CC01RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC12CC01
5', mRNA sequence.
ACCESSION      CV829374
VERSION
KEYWORDS
SOURCE
ORGANISM
Acyrthosiphon pisum (pea aphid)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE      1 (bases 1 to 332)
AUTHORS
Sabater-Munoz,B., Leggai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rabbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
Annotated ESTs of the pea aphid
Unpublished (2004)
Contact: D. Tagu
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Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 12C row: C column: 1.
Location/Qualifiers
1. .332
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="P123"
/db_xref="taxon:7029"
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/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ID0ACC"
/notes="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

ORIGIN
Query Match      85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 232 CCAAAGCCCAAGGAGATCGAGCT 253

RESULT 28
CV830911
LOCUS
DEFINITION      332 bp mRNA linear EST 17-NOV-2004
ID0ACC16DD11RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC16DD11
5', mRNA sequence.
ACCESSION      CV830911
VERSION
KEYWORDS
SOURCE
ORGANISM
Acyrthosiphon pisum (pea aphid)

```

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

AUTHORS

1 (bases 1 to 332)
Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

TITLE

JOURNAL

COMMENT

Unpublished ESTs of the pea aphid

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 16D row: D column: 11.

FEATURES

source

1. .332

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="P123"

/db_xref="taxon:7029"

/clone="ID0ACC16DD11"

/tissue_type="head"

/dev_stage="larvae L3 (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ID0ACC"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0ACC; Plant growth place: INRA Rennes, UMR

BIO3P, 35327, 35653 Le Rheu Cedex France; Soil

conditions: Soil; Sowing date: 01/10/2003; Harvesting

date: 17/10/2003; Description: aphids inoculated on

one-week old Vicia faba germinations under non sterile

conditions experimental condition: long photoperiod (16-hr

light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 332;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 CCATCGCCCAAGGAGATCGAGCT 22

|||||

232 CCAAAGCCCAAGGAGATCGAGCT 253

RESULT 29

CV831091

LOCUS

DEFINITION ID0ACC17BE01RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC17BE01

5', mRNA sequence.

CV831091 332 bp mRNA linear EST 17-NOV-2004

CV831091 1 GI:55796774

EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Acyrthosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 332)

Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,

Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,

Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,

Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

Unpublished ESTs of the pea aphid

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

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Plate: 20D row: H column: 9.

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

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Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 20D row: H column: 9.

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Sample name: IDOACC ; Plant growth place: INRA Rennes, UMR Bio3P, 35327, 35653 Le Rheu Cedex France ; Soil conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting date: 17/10/2003 ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions experimental condition: long photoperiod (16-hr light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCAAGGAGATCGAGCT 22

Db 232 CCAAGCCAAAGGAGATCGAGCT 253

RESULT 31
CV838428
LOCUS
DEFINITION
CV838428 332 bp mRNA linear EST 17-NOV-2004
IDOACC7D09RM1 IDOACC Acyrthosiphon pisum cDNA clone IDOACC7D09
5', mRNA sequence.

ACCESSION
CV838428 1 GI:55804111

KEYWORDS
EST.

SOURCE
Acyrthosiphon pisum (pea aphid)

ORGANISM
Acyrthosiphon pisum

REFERENCE
CV838428 1 (bases 1 to 332)

AUTHORS
Sabater-Munoz, B., Legai, P., Bonhomme, J., Dang, P., Dossat, C.,

Duclert, A., Gauthier, J.P., Hunter, W., Martinez-Torres, D., Moya, A.,

Nakabachi, A., Prunier-Leterme, N., Rahbe, Y., Shigenobu, S.,

Simon, J.C., Stern, D., Wincker, P. and Tagu, D.

TITLE
Annotated ESTs of the pea aphid

JOURNAL
Unpublished (2004)

COMMENT
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Tel: +33.2.23.48.51.65

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PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 7D row: G column: 9.

FEATURES
source

1. .332

Location/Qualifiers

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

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/clone="IDOACC7D09"

/tissue_type="head"

/dev_stage="larvae L3 (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="IDOACC"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;

Sample name: IDOACC ; Plant growth place: INRA Rennes, UMR

Bio3P, 35327, 35653 Le Rheu Cedex France ; Soil

conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting

date: 17/10/2003 ; Description: aphids inoculated on

one-week old Vicia faba germinations under non sterile

conditions experimental condition: long photoperiod (16-hr

light/8-hr dark at 18 degC)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 8; Length 332;
Best Local Similarity 90.9%; Pred. No. 8.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCAAGGAGATCGAGCT 22

Db 232 CCAAGCCAAAGGAGATCGAGCT 253

Db

RESULT 32

CN764316

LOCUS

DEFINITION

CN764316 340 bp mRNA linear EST 20-MAY-2004

ID0AAA9CC12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA9CC12 5',

mRNA sequence.

ACCESSION

CN764316 1 GI:47538239

VERSION

EST.

KEYWORDS

Acyrthosiphon pisum (pea aphid)

SOURCE

Acyrthosiphon pisum

ORGANISM

Acyrthosiphon pisum

REFERENCE

CN764316 1 (bases 1 to 340)

AUTHORS

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

TITLE

An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

JOURNAL

Unpublished (2004)

COMMENT

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Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts. These sequences were

obtained in the frame of the International Consortium of Aphid

Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 9

Location/Qualifiers

1. .340

/organism="Acyrthosiphon pisum"

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/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA9CC12"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA ; Plant growth place: Department of

Ecology & Evolutionary Biology, Princeton University ;

Soil conditions: Soil ; Sowing date: 01/06/1999 ;

Harvesting date: 01/06/1999 ; Stress date: no stress ;

Description: Aphids inoculated on one-week old Vicia faba

under non-sterile conditions. All parthenogenetic stages

and both winged and wingless adults were collected for

library construction. ; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 340;

Best Local Similarity 90.9%; Pred. No. 8.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCAAGGAGATCGAGCT 22

Db 240 CCAAGCCAAAGGAGATCGAGCT 261

RESULT 33

CN750782

LOCUS

DEFINITION

CN750782 407 bp mRNA linear EST 19-MAY-2004

ApDT-XXVI-D10 ApDT Acyrthosiphon pisum cDNA clone ApDTXXVI-D10 5',

mRNA sequence.

ACCESSION

CN750782

VERSION

CN750782.1 GI:47515779

KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 407)
AUTHORS Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tegu, D. and Wincker, P.
TITLE An expressed sequence tags database for the pea aphid *Acyrthosiphon*

JOURNAL Unpublished (2004)
COMMENT Contact: D. Tegu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel.: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.
PCR Primers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: XXVI row: D column: 10.
FEATURES Location/Qualifiers
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1..407
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="inra-lyon-bf2i 1101"
/db_xref="taxon:7029"
/clone="ApDTXXVID10"
/tissue_type="digestive track"
/dev_stage="adults, parthenogenetic females"
/lab_host="TOP10"
/clone_lib="ApDT"
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;
Sample name: ApDT; Plant growth place: UMR INRA-INSA BP21
; Sowing date: 03/04/2003 ; Harvesting date: 12/06/2003 ;
Description: Long photoperiod 16-hr light/8-hr dark at 20
C; no overcrowding; grown on Vicia faba 3-wk old seedlings
sown under non sterile condition. ; experimental
condition: standard, see description"
ORIGIN
Query Match 85.5%; Score 18.8; DB 7; Length 407;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCATCGCCAGGAGATCGAGCT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 240 CCAAGCCAGGAGATCGAGCT 261
RESULT 34
CA999580
LOCUS CA999580 414 bp mRNA linear EST 10-JAN-2003
DEFINITION S345P G03 Rice cold stress germination cDNA library Oryza sativa
(japonica cultivar-group) cDNA 5', mRNA sequence.
ACCESSION CA999580
VERSION CA999580.1 GI:27576886
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoae; Oryza.
REFERENCE 1 (bases 1 to 414)
AUTHORS de los Reyes, B.G., Morsy, M., Gibbons, J., Varma, T.S.N., Antoine, W.,
Redus, M., McGrath, J.M. and Halgren, R.
Development of a chilling stress EST library of germinating rice
(Oryza sativa L. subsp. japonica) enriched with stress-related and
novel genes
JOURNAL Unpublished (2002)
COMMENT Contact: Benito G. de los Reyes
Plant Genomics Lab., Department of Crop, Soil and Environmental

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

```

Query Match      85.5%; Score 18.8; DB 6; Length 551;
Best Local Similarity 90.9%; Pred. No. 8.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
    |||||
Db 379 CCATCTCCAAAGGAGATCGAGTT 400
    |||||

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RESULT 44	CN583982	569 bp	linear	EST 04-MAY-2004
LOCUS	CN583982			
DEFINITION	USDA-PP_127048 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum cDNA clone WHAP053 C07, mRNA sequence.			

VERSION	CN583982.1	GI:45995705
KEYWORDS	Est.	
SOURCE	Acyrtosiphon pisum (pea aphid)	
ORGANISM	Acyrtosiphon pisum	
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiform	
	Aphidoidea; Aphididae; Macrosiphini; Acyrtosiphon.	
REFERENCE	1 (bases 1 to 569)	
AUTHORS	Hunter,W.B., Dang,P.M., Stern,D. and Lapointe,S.L.	
TITLE	Gene expression in Acyrtosiphon pisum (Hemiptera: Aphididae)	
JOURNAL	Unpublished (2004)	
COMMENT	Contact: Wayne Hunter; Phat Dang	

US. Horticultural Research Lab, Ft. Pierce, FL
USDA-ARS
2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@ushrl.ars.usda.gov.

FEATURES

```

1. .569
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP053_C07"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="XLI-Blue"
/clone_lib="Acyrtosiphon pisum, Pea Aphid"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; Acyrtosiphon pisum colonies. Library by Srini
Kambhampati; Peter dearden; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 258-0759. A high quality EST with at least 100
contiguous bases at Trace Tuner score of 20 or better.
Sequencing of clones by Dr. PM Dang, US. Horticultural
Research Lab, Ft. Pierce, FL. (772) 462- 5940."

```

ORIGIN

Query Match	85.5%	Score 18.8;	DB 7;	Length 569;
Best Local Similarity	90.9%;	Pred. No. 8.5e+02;		
Matches 20; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

1 CCATGCCCAAGGAGATCGAGCT 22 QY
224 CCAAAGCCCAAGGAGATCGAGCT 245 Db

RESULT 45	LOCUS	CF292207	570 bp	mRNA	linear	EST 14-AUG-2003
CF292207/c	DEFINITION	14ROOT--02-P05.g1	Rice root	plasmid cDNA	library (14ROOT)	Oryza
		sativa ([japonica cultivar-group])	cDNA clone	14ROOT--02-P05	mRNA	

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

sequence.
CF232207
CF232207.1 GI:33661240
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eurytota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE AUTHORS	TITLE JOURNAL COMMENT
1. J. H.
2. J. H.
3. J. H.
4. J. H.
5. J. H.
6. J. H.
7. J. H.
8. J. H.
9. J. H.
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93. J. H.
94. J. H.
95. J. H.
96. J. H.
97. J. H.
98. J. H.
99. J. H.
100. J. H.

Genomics and Genomics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@qbio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES

```
1. 370
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="14R00T-02-P05"
/tissue_type="root"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14R00T)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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ORIGIN

Query Match	85.5%	Score 18.8;	DB 6;	Length 570;
Best Local Similarity	90.9%	Pred. No. 8.5e+02;		
Matches 20; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
|||
Db 559 CCATCTCCAAGGAGATCGAGTT 538

RESULT 46

LOCUS	CN585977	572 bp	linear	EST 04-MAY-2004
DEFINITION	USDA-FP 129049 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum			
	CNDA clone WHAP079 F04. mRNA sequence.			

ACCESSION	CN385977	
VERSION	CN585977.1	GI:46997700
VERSIONS	PCF	

KEYWORDS
SOURCE
ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
-----------	---------	-------	---------	---------

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2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@usrl.ars.usda.gov.

FEATURES
source

/organism="Acyrtosiphon pisum"

```

/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP079_F04"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="XLI-Blue"
/clone_lib="Acyrtosiphon pisum, Pea Aphid"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Acyrthosiphon pisum colonies. Library by Srinil
Kambampati; Peter Dearden; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 259-0759. A high quality EST with at least 100
contiguous bases at Trace Tuner score of 20 or better.
Sequencing of clones by Dr. P.W. Dang, US. Horticultural
Research Lab, Ft. Pierce, FL. (772) 462- 5940."

ORIGIN
Query Match      85.5%; Score 18.8; DB 7; Length 572;
Best Local Similarity 90.9%; Pred. No. 8.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 80 CCAAGCCCAAGGAGATCGAGCT 101

RESULT 47
CB087986
LOCUS
DEFINITION
hkl0g08.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
centranthoides cDNA clone hkl0g08, mRNA sequence.
ACCESSION
CB087986
VERSION
1
KEYWORDS
EST.
SOURCE
Hedyotis centranthoides
ORGANISM
Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Gentianales; Rubiaceae; Rubioidae;
Spermacoceae; Hedyotis.
REFERENCE
1 (bases 1 to 581)
Levesque M.P., Twigg R.W., Motley T., Katari M.S., Dedhia N.N.,
O'Shaughnessy A.L., Balija V., Martienssen R.A., McCombie R.W.,
Benfey P. and Stevenson D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hkl0 row: g column: 08
Seq primer: -21M13Univrev
High quality sequence stop: 581.
Location/Qualifiers
1..581
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/clone="hkl0g08"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN
Query Match      85.5%; Score 18.8; DB 6; Length 599;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 229 CCAAGCCCAAGGAGATCGAGCT 250

RESULT 49
CN584119
LOCUS
DEFINITION
USDA-FP 127186 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum
cDNA clone WHAP055_A09, mRNA sequence.
ACCESSION
CN584119
VERSION
1
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)

```

```

ORIGIN
Query Match      85.5%; Score 18.8; DB 6; Length 581;
Best Local Similarity 90.9%; Pred. No. 8.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 234 CCAAGCCCAAGGAGATCGAGCT 255

RESULT 48
CD450119
LOCUS
DEFINITION
USDA-FP 102080 Adult Alate Brown Citrus Aphid Toxoptera citricida
cDNA clone WHWTC-28_H10 5', mRNA sequence.
ACCESSION
CD450119
VERSION
1
KEYWORDS
EST.
SOURCE
Toxoptera citricida (brown citrus aphid)
ORGANISM
Toxoptera citricida
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Aphidini; Toxoptera.
REFERENCE
1 (bases 1 to 599)
Hunter W.B., Dang P.M., Bausher M.G., Chaparro J.X., McKendree W.,
Shatters R.G. Jr., McKenzie C.L. and Sinisterza X.H.
Aphid biology: Expressed genes from alate Toxoptera citricida, the
brown citrus aphid
J. Insect Sci. 3 (23), 1-7 (2003)
Contact: Wayne B. Hunter
US Horticultural Research Laboratory
USDA - ARS
2001 South Rock Rd., Fort Pierce, FL 34945, USA
Tel: (772) 462-5898
Fax: (772) 462-5960
Email: whunter@uehrl.ars.usda.gov
Seq primer: T3 Primer.
Location/Qualifiers
1..599
/organism="Toxoptera citricida"
/mol_type="mRNA"
/db_xref="taxon:223852"
/clone="WHWTC-28_H10"
/sex="Mixed population"
/tissue_type="Entire insect"
/dev_stage="Adult Alate"
/lab_host="XLI-Blue"
/clone_lib="Adult Alate Brown Citrus Aphid"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Toxoptera citricida (Kirkaldy); A high quality EST
with at least 100 contiguous bases at Trace Tuner score of
20 or better."

ORIGIN
Query Match      85.5%; Score 18.8; DB 6; Length 599;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||| |||||||||
Db 229 CCAAGCCCAAGGAGATCGAGCT 250

RESULT 49
CN584119
LOCUS
DEFINITION
USDA-FP 127186 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum
cDNA clone WHAP055_A09, mRNA sequence.
ACCESSION
CN584119
VERSION
1
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)

```

```

ORGANISM
Acyrtosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE
1 (bases 1 to 612)
AUTHORS
Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.
JOURNAL
Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
COMMENT
Contact: Wayne Hunter; Phat Dang
US. Horticultural Research Lab, Ft. Pierce, FL
USDA-ARS
2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@ushrl.ars.usda.gov.

FEATURES
source
1..612
Location/Qualifiers
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP055_A09"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="Xhl-Blue"
/clone_lib="Acyrtosiphon pisum, Pea Aphid"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Acyrthosiphon pisum colonies. Library by Srin
Kambhampati; Peter Dearden; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 258-0759. A high quality EST with at least 100
contiguous bases at Trace Tuner score of 20 or better.
Sequencing of clones by Dr. PM Dang, US. Horticultural
Research Lab, Ft. Pierce, FL. (772) 462- 5940."

ORIGIN
Query Match 85.5%; Score 18.8; DB 7; Length 612;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 156 CCAGAGCCCAAGGAGATCGAGCT 177

RESULT 50
CL612592 629 bp DNA linear GSS 01-JUL-2004
LOCUS OR_BB0003013.r OR_BB0 Oryza nivara genomic clone OR_BB0003013 3',
DEFINITION genomic survey sequence.
ACCESSION CL612592
VERSION CL612592.1 GI:49101070
KEYWORDS GSS
SOURCE Oryza nivara
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 629)
AUTHORS Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161 Std Error: 0.00
Plate: 0003 row: O column: 13
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
1..629
Location/Qualifiers
/organism="Oryza nivara"
/mol_type="genomic DNA"
/db_xref="taxon:4536"
/clone="OR_BB0003013"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 629;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 314 CCATCTCCCAAGGAGATCGAGTT 335

RESULT 51
CB690026 640 bp mRNA linear EST 04-SEP-2003
LOCUS CEST-57-H-12 Mixed source, strain EP155 and EP155 infected with
DEFINITION hypovirus CHV1-EP713 Cryphonectria parasitica cDNA clone EP155,
EP155-CHV1-EP713 5-prime, mRNA sequence.
ACCESSION CB690026
VERSION CB690026.1 GI:34450895
KEYWORDS EST.
SOURCE Cryphonectria parasitica
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Diaporthales; Valsaceae; Cryphonectria-Endothia
complex; Cryphonectria.
REFERENCE
1 (bases 1 to 640)
AUTHORS Dawe, A.L., McMains, V.C., Panglao, M., Kasahara, S., Chen, B. and
Nuss, D.L.
TITLE An ordered collection of expressed sequences from Cryphonectria
parasitica and evidence of genomic microsynteny with Neurospora
crassa and Magnaporthe grisea
JOURNAL Microbiology 149 (9), 2373-2384 (2003)
PUBMED 12949163
COMMENT Contact: Dawe AL, Nuss DL
Center for Biosystems Research
University of Maryland Biotechnology Institute
5115 Plant Sciences Building, College Park, MD 20742, USA
Tel: 301-405-7661 or 5111
Fax: 301-314-9075
Email: dawe@umbi.umd.edu
Cryphonectria parasitica EST derived from mixed samples of cDNA
from wild-type (strain EP155) and hypovirus-infected cultures.
Seq primer: M13-reverse.

FEATURES
source
1..640
Location/Qualifiers
/organism="Cryphonectria parasitica"
/mol_type="mRNA"
/strain="EP155"
/db_xref="ATCC (inhost):38755 and 52571"
/db_xref="taxon:5116"
/clone="EP155, EP155-CHV1-EP713"
/clone_lib="Mixed source, strain EP155 and EP155 infected
with hypovirus CHV1-EP713"
/note="Cryphonectria parasitica EST derived from mixed
samples of cDNA from wild-type (strain EP155) and
hypovirus-infected cultures"

ORIGIN
Query Match 85.5%; Score 18.8; DB 6; Length 640;

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```

Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
Db 158 CCATCGCCAAAGGAGATCGAGCT 179

RESULT 52
CF587912
LOCUS
DEFINITION
USDA-FP 121300-059 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon
pisum cDNA clone WHAP-010_H06 5', mRNA sequence.
ACCESSION
CF587912
VERSION
CF587912.1 GI:35508012
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)
ORGANISM
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrolophini; Acyrthosiphon.
REFERENCE
1 (bases 1 to 646)
Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.
Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
Unpublished (2004)
CONTACT: Wayne Hunter; Phat Dang
US. Horticultural Research Lab, Ft. Pierce, FL
USDA-ARS
2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@ushrl.ars.usda.gov
Seq primer: T3 Primer.
FEATURES
source
1. 646
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP-010_H06"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="X11-Blue"
/clone_lib="Acyrthosiphon pisum, Pea Aphid"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Acyrthosiphon pisum colonies. Library by Srini
Kambhampati; Peter Dearaden; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 258-0759. A high quality EST with at least 100
contiguous bases at Trace Turner score of 20 or better.
Sequencing of clones by Dr. PW Dang, US. Horticultural
Research Lab, Ft. Pierce, FL. (772) 462- 5940."
ORIGIN
Query Match 85.5%; Score 18.8; DB 6; Length 646;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
Db 213 CCAAGGCCAAGGAGATCGAGCT 234

RESULT 53
AQ257000
LOCUS
DEFINITION
nxb0017E16f CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nxb0017E16f, genomic survey
sequence.
ACCESSION
AQ257000
VERSION
AQ257000.1 GI:3781482
KEYWORDS
GSS.
SOURCE
Oryza sativa (japonica cultivar-group)

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 656)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
CONTACT: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 397.
FEATURES
source
1. 656
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nxb0017E16f"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library"
/notes="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalent. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
ORIGIN
Query Match 85.5%; Score 18.8; DB 9; Length 656;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
Db 314 CCATCTCCAAAGGAGATCGAGTT 335

RESULT 54
CB000900/c
LOCUS
DEFINITION
S345K_B05 Rice cold stress germination cDNA library Oryza sativa
(japonica cultivar-group) cDNA 5', mRNA sequence.
ACCESSION
CB000900
VERSION
CB000900.1 GI:27578205
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 665)

```

AUTHORS
de los Reyes, B.G., Morsy, M., Gibbons, J., Varma, T.S.N., Antoine, W., Redus, M., McGrath, J.M. and Halgren, R.
TITLE
Development of a chilling stress EST library of germinating rice (Oryza sativa L. subsp. japonica) enriched with stress-related and novel genes
JOURNAL
Unpublished (2002)
COMMENT
Contact: Benito G. de los Reyes
Plant Genomics Lab., Department of Crop, Soil and Environmental Sciences
University of Arkansas
115 Plant Science Building, Fayetteville, AR 72701, USA
Tel: (479)-575-7465
Fax: (479)-575-8435
Email: breyes@uark.edu
Plate: S345K row: B column: 05
Seq primer: T3.

FEATURES

Source
Location/Qualifiers
1..665
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="PI560247"
/db_xref="taxon:39947"
/tissue_type="coleotile, radicle, prophyll, immature leaf"
/dev_stage="embryo at different stages of germination and shoots of germinated seeds under chilling stress (130C/100C)"
/lab_host="Solr"
/clone_lib="Rice cold stress germination cDNA library"
/note="Organ: seedlings; Vector: Lambda Uni-Zap XR excised as pluescript; Site_1: EcoRI; Site_2: XhoI; The cDNAs were derived from reverse transcription of mRNA samples from seeds at different stages of germination and seedlings at early phase of growth under chilling stress (130C/100C). The mRNA pool was used as template for double stranded cDNA synthesis using the Stratagene Uni-Zap XR cDNA synthesis and library kit. A total of 150,000 phages were excised from the primary library as pluescript phagenid clones. Enrichment of the primary excised library with chilling-induced transcripts was performed by hybridizing the primary excised library colony lifts with the PCR-select subtraction product, with cold germinated cDNA as tester and control temperature-germinated cDNA as driver."

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 665;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 481 CCATCTCCCAAGGAGATCGAGTT 460

RESULT 55
CN755289
LOCUS
ID0AAA15BG02RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA15BG02
5', mRNA sequence.
CN755289 671 bp mRNA linear EST 19-MAY-2004
CN755289.1 GI:47520325
EST.
ACCESSION
CN755289.1
VERSION
CN755289.1
KEYWORDS
Acyrthosiphon pisum (pea aphid)
SOURCE
Acyrthosiphon pisum
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE
1 (bases 1 to 671)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Winkler, P.
AUTHORS
An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
TITLE
Unpublished (2004)
JOURNAL

COMMENT

Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Plate: 15 row: G column: 2.
Location/Qualifiers
1..671
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA15BG02"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 C)"

FEATURES

source
Location/Qualifiers
1..671
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA15BG02"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 C)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 7; Length 671;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
DB 571 CCAAGCCCAAGGAGATCGAGCT 592

ORIGIN

RESULT 56
AQ576753
LOCUS
nbxb0089B04f CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0089B04f, genomic survey sequence.
AQ576753 671 bp DNA linear GSS 02-JUN-1999
AQ576753.1 GI:4977238
ACCESSION
AQ576753
VERSION
AQ576753.1
KEYWORDS
GSS.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 671)
Wing, R.A. and Dean, R.A.
AUTHORS
A BAC End Sequencing Framework to Sequence the Rice Genome
TITLE
Unpublished (1998)
JOURNAL
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
AUTHORS
Class: BAC ends
High quality sequence stop: 421.
Location/Qualifiers

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source
1. .671
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0089B04f"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CGI Rice BAC Library"
/note="Vector: pBelOBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN
Query Match 85.5%; Score 18.8; DB 9; Length 671;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
Db 314 CCATCTCCAAGGAGATCGAGTT 335

RESULT 57
CW775708 672 bp DNA linear GSS 15-NOV-2004
LOCUS OP_Ba0075J13.r OP_Ba Oryza punctata genomic clone OP_Ba0075J13
DEFINITION 3', genomic survey sequence.
VERSION CW775708.1 GI:55744089
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 672)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMAP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.19s.
Bases 163-840 of the raw sequence (length 1008) were retained after
clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0006 row: N column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

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source
1. .673
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0006N04"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/note="Vector: PAGIBAC1; Site 1: HindIII; Site 2: HindIII"

ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 673;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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FEATURES
source
1. .672
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0075J13"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/note="Vector: PAGIBAC1; Site 1: HindIII; Site 2: HindIII"

ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 672;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||||
Db 255 CCATCTCCAAGGAGATCGAGTT 276

RESULT 58
CW506965 673 bp DNA linear GSS 06-OCT-2004
LOCUS OP_Ba0006N04.r OP_Ba Oryza punctata genomic clone OP_Ba0006N04
DEFINITION 3', genomic survey sequence.
VERSION CW506965.1 GI:53836470
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 673)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMAP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.19s.
Bases 193-865 of the raw sequence (length 1400) were retained after
clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
Plate: 0006 row: N column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source
1. .673
/organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP_Ba0006N04"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/note="Vector: PAGIBAC1; Site 1: HindIII; Site 2: HindIII"

ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 673;
Best Local Similarity 90.9%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCATGCCAAGGAGATCGAGCT 22
 DB 235 CCATCTCCAAGGAGATCGAGTT 256

RESULT 59
 AQ287315

LOCUS

DEFINITION

AQ287315 684 bp DNA linear GSS 03-DEC-1998
 nbxb0029K22f CUGI Rice BAC Library Oryza sativa (japonica
 cultivar-group) genomic clone nbxb0029K22f, genomic survey
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 684)
 Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Rice Genome
 Unpublished (1998)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: TAATACGACTCATATAGGG
 Class: BAC ends
 High quality sequence stop: 460.

FEATURES

source

1..684
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="japonica"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="nbxb0029K22f"
 /tissue_type="Leaf"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice BAC Library"
 /note="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
 HindIII. Rice is one of two most popular grains in the
 world. Half of the world population especially those
 inhabiting highly populated areas of the humid tropics
 and subtropics, rely on rice as their primary source of
 carbohydrate. Monocotyledonous rice is a diploid plant
 (2n=24) with a haploid genome equivalent of 431 Mbp
 (Arumuganathan and Earle, 1991). The relatively small
 genome of rice, three times larger than that of
 Arabidopsis, makes it suitable for genomic studies. In
 order to facilitate positional cloning, physical mapping
 and genome sequencing of rice, we have constructed a BAC
 library from Oryza sativa, Nipponbare variety. The
 library contains 36,864 clones with an average insert size
 of 128.5 Kb providing 10.9 haploid genome equivalents. The
 deep coverage allows the isolation a particular sequence
 with a probability of 99.9 %. Two high density filters,
 each containing 18,432 clones (doubly spotted), represent
 the whole library for colony screening."

ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 684;
 Best Local Similarity 90.9%; Pred. No. 8.6e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22

DB

313 CCATCTCCAAGGAGATCGAGTT 334

RESULT 60

LOCUS

DEFINITION

CF588105 696 bp mRNA linear EST 25-SEP-2003
 USDA-FP_121000-060 Acyrthosiphon pisum, pea Aphid Acyrthosiphon
 pisum cDNA clone WHAP-007_B07 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Acyrthosiphon pisum (pea aphid)
 Acyrthosiphon pisum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 696)
 Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.
 Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
 Unpublished (2004)
 Contact: Wayne Hunter; Phat Dang
 US. Horticultural Research Lab, Ft. Pierce, FL
 USDA-ARS
 2001 South Rock Rd., Ft. Pierce, FL 34945, USA
 Tel: (772) 462-5898, (772) 462-5940
 Fax: (772) 462-5986
 Email: Whunter@ushrl.ars.usda.gov
 Seq primer: T3 Primer.

FEATURES

source

1..696
 Location/Qualifiers

/organism="Acyrthosiphon pisum"
 /mol_type="mRNA"
 /db_xref="taxon:7029"
 /clone="WHAP-007_B07"
 /sex="Mixed population"
 /tissue_type="whole body, nymphs and adults"
 /dev_stage="All"
 /lab_host="XLI-Blue"
 /clone_lib="Acyrthosiphon pisum, Pea Aphid"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI; Acyrthosiphon pisum colonies, Library by Srin
 Kambampati; Peter Dearden; David Stern, Department of
 Ecology and Evolutionary Biology, Princeton University,
 NJ. (609) 258-0759. A high quality EST with at least 100
 contiguous bases at Trace Tuner score of 20 or better.
 Sequencing of clones by Dr. PM Dang, US. Horticultural
 Research Lab, Ft. Pierce, FL. (772) 462-5940."

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 696;
 Best Local Similarity 90.9%; Pred. No. 8.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATGCCAAGGAGATCGAGCT 22

DB 283 CCAAAGCCAGGAGATCGAGCT 304

Search completed: April 2, 2006, 00:09:35
 Job time : 308.022 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:17:36 ; Search time 59.2198 Seconds
(without alignments)
3072.051 Million cell updates/sec

Title: US-10-824-527-1

Perfect score: 22
Sequence: 1 ccacgcgaagagatcgagct 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : Published Applications NA_Main:*
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	8	US-10-824-527-1
2	22	100.0	647	3	US-09-880-505-115
3	22	100.0	647	5	US-10-051-643-115
4	22	100.0	647	6	US-10-205-979-15
5	22	100.0	888	5	US-10-267-311-32
6	22	100.0	888	5	US-10-679-956-32
7	22	100.0	1569	3	US-09-880-505-113
8	22	100.0	1569	5	US-10-051-643-113
9	22	100.0	1620	7	US-10-282-122A-26142
10	22	100.0	1623	3	US-09-712-363-23
11	22	100.0	1623	5	US-10-267-311-3
12	22	100.0	1623	6	US-10-156-761-3915
13	22	100.0	1623	7	US-10-282-122A-25595
14	22	100.0	1623	7	US-10-282-122A-28196
15	22	100.0	1623	9	US-10-679-956-3
16	22	100.0	1626	3	US-09-880-505-159
17	22	100.0	1626	5	US-10-051-643-159
18	22	100.0	1626	6	US-10-205-979-14
19	22	100.0	1626	7	US-10-282-122A-27502
20	22	100.0	1626	9	US-10-491-300-1
21	22	100.0	1632	6	US-10-369-493-44560
22	22	100.0	1701	9	US-10-501-127A-21
23	22	100.0	1761	8	US-10-635-211-1

24	22	100.0	1920	5	US-10-267-311-16	Sequence 16, Appl
25	22	100.0	1920	5	US-10-679-956-16	Sequence 16, Appl
26	22	100.0	1947	5	US-10-267-311-28	Sequence 28, Appl
27	22	100.0	1947	5	US-10-679-956-28	Sequence 28, Appl
28	22	100.0	2073	5	US-10-068-059-9	Sequence 9, Appl
29	22	100.0	2073	9	US-10-941-049-9	Sequence 9, Appl
30	22	100.0	2130	5	US-10-068-059-7	Sequence 7, Appl
31	22	100.0	2130	5	US-10-941-049-7	Sequence 7, Appl
32	22	100.0	2175	5	US-10-068-059-11	Sequence 11, Appl
33	22	100.0	2175	5	US-10-941-049-11	Sequence 11, Appl
34	22	100.0	2241	5	US-10-068-059-5	Sequence 5, Appl
35	22	100.0	2241	5	US-10-941-049-5	Sequence 5, Appl
36	22	100.0	2847	5	US-10-267-311-20	Sequence 20, Appl
37	22	100.0	2847	9	US-10-679-956-20	Sequence 20, Appl
38	22	100.0	86114	6	US-10-080-170-648	Sequence 648, App
39	22	100.0	86114	7	US-10-080-170-648	Sequence 648, App
40	22	100.0	86114	8	US-10-468-356-648	Sequence 648, App
c 41	22	100.0	9025608	6	US-10-156-761-1	Sequence 1, Appl
c 42	20.4	92.7	1728	6	US-10-369-493-32009	Sequence 32009, A
c 43	20.4	92.7	99090	8	US-10-656-394A-13	Sequence 13, Appl
44	20	9.9	20	8	US-10-500-586-55	Sequence 55, Appl
45	19	86.4	4134	3	US-09-975-553-17	Sequence 17, Appl
46	19	86.4	4134	5	US-10-125-792-1	Sequence 1, Appl
47	19	86.4	4134	5	US-10-125-778-1	Sequence 1, Appl
48	19	86.4	4134	5	US-10-270-795-17	Sequence 17, Appl
49	19	86.4	4134	5	US-10-270-876-17	Sequence 17, Appl
50	19	86.4	4134	6	US-10-268-051-7	Sequence 7, Appl
51	19	86.4	4134	6	US-10-125-772-1	Sequence 1, Appl
52	19	86.4	4134	6	US-10-016-496-1	Sequence 1, Appl
53	19	86.4	4134	6	US-10-411-076-23	Sequence 23, Appl
54	19	86.4	4134	6	US-10-410-872-17	Sequence 17, Appl
55	19	86.4	4134	6	US-10-410-885-1	Sequence 1, Appl
56	19	86.4	4134	8	US-10-851-047-7	Sequence 7, Appl
57	19	86.4	4134	8	US-10-626-115-17	Sequence 17, Appl
58	19	86.4	4134	10	US-11-057-660-23	Sequence 23, Appl
59	19	86.4	4134	10	US-11-085-364-1	Sequence 1, Appl
60	19	86.4	4134	10	US-11-086-550-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-824-527-1
; Sequence 1, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-0000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer

US-10-824-527-1

Query Match 100.0%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 1 CCATGCCCAAGGAGATCGAGCT 22

RESULT 2

US-09-880-505-115
; Sequence 115, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.100762
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-115

Query Match 100.0%; Score 22; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 3

US-10-051-643-115
; Sequence 115, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-115

Query Match 100.0%; Score 22; DB 5; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 4

US-10-205-979-15
; Sequence 15, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-205-979-15

Query Match 100.0%; Score 22; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 5

US-10-267-311-32
; Sequence 32, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match 100.0%; Score 22; DB 5; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||

Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 6

US-10-679-956-32
; Sequence 32, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2006-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(885)
US-10-679-956-32

Query Match 100.0%; Score 22; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 7

US-09-880-505-113
; Sequence 113, Application US/09880505
; Publication No. US20030007876A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-113

Query Match 100.0%; Score 22; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 8

US-10-051-643-113
; Sequence 113, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-113

Query Match 100.0%; Score 22; DB 5; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
|||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 9

US-10-282-122A-26142
; Sequence 26142, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26142
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-282-122A-26142

Query Match      100.0%; Score 22; DB 7; Length 1620;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182
|||||

RESULT 10
US-09-712-363-23
; Sequence 23, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match      100.0%; Score 22; DB 3; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182
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RESULT 11
US-10-267-311-3
; Sequence 3, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match      100.0%; Score 22; DB 5; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182
|||||

RESULT 12
US-10-156-761-3915
; Sequence 3915, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3915
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
US-10-156-761-3915

Query Match      100.0%; Score 22; DB 6; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGCT 22
Db      161 CCATGCCCAAGGAGATCGAGCT 182
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RESULT 13
US-10-282-122A-25595
; Sequence 25595, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25595
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25595

Query Match      100.0%; Score 22; DB 7; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 14
US-10-282-122A-28196
; Sequence 28196, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25595
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25595

Query Match      100.0%; Score 22; DB 7; Length 1623;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATCGCCCAAGGAGATCGAGCT 182

RESULT 15
US-10-679-956-3
; Sequence 3, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
```

US-10-679-956-3

Query Match 100.0%; Score 22; DB 9; Length 1623;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 16

US-09-880-505-159
 ; Sequence 159, Application US/09880505
 ; Publication No. US2003000796A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L. J.
 ; APPLICANT: Prestidge, Ross
 ; TITLE OF INVENTION: Methods and Compounds for the Treatment
 ; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
 ; FILE REFERENCE: 11000.100762
 ; CURRENT APPLICATION NUMBER: US/09/880,505
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR FILING DATE: 1997-12-23
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 194
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 159
 ; LENGTH: 1626
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium vaccae
 US-09-880-505-159

Query Match 100.0%; Score 22; DB 3; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 17

US-10-051-643-159
 ; Sequence 159, Application US/10051643
 ; Publication No. US20020197265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L. J.
 ; TITLE OF INVENTION: Methods and Compounds for the Treatment
 ; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
 ; TITLE OF INVENTION: System using Mycobacterium Vaccae
 ; FILE REFERENCE: 11000.100862
 ; CURRENT APPLICATION NUMBER: US/10/051,643
 ; CURRENT FILING DATE: 2002-01-18
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 159
 ; LENGTH: 1626
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium vaccae
 US-10-051-643-159

Query Match 100.0%; Score 22; DB 5; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 18

US-10-205-979-14
 ; Sequence 14, Application US/10205979
 ; Publication No. US20030147861A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L. J.
 ; APPLICANT: Abernethy, Nevin
 ; TITLE OF INVENTION: Compounds and Methods for the Modulation
 ; TITLE OF INVENTION: of Immune Responses
 ; FILE REFERENCE: 11000.1063U
 ; CURRENT APPLICATION NUMBER: US/10/205,979
 ; CURRENT FILING DATE: 2002-07-25
 ; PRIOR FILING DATE: 2001-07-26
 ; PRIOR FILING DATE: 2001-07-26
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 1626
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium vaccae
 US-10-205-979-14

Query Match 100.0%; Score 22; DB 6; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
 |||||
 DB 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 19

US-10-282-122A-27502
 ; Sequence 27502, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR FILING DATE: 2000-11-27

Query Match 100.0%; Score 22; DB 6; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27502
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-282-122A-27502

Query Match      100.0%; Score 22; DB 7; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 20
US-10-491-300-1
; Sequence 1, Application US/10491300
; Publication No. US20050063984A1
; GENERAL INFORMATION:
; APPLICANT: MEDVET SCIENCE PTY LTD
; APPLICANT: RURAL INDUSTRIES RESEARCH AND DEVELOPMENT CORPORATION
; TITLE OF INVENTION: GroEL Chimeric Protein and Vaccine
; FILE REFERENCE: A20-061
; CURRENT APPLICATION NUMBER: US/10/491,300
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Rhodococcus equi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
; OTHER INFORMATION: groEL gene
US-10-491-300-1

Query Match      100.0%; Score 22; DB 9; Length 1626;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 21
US-10-369-493-44560
; Sequence 44560, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
```

```
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 44560
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: SYNECHOCOCCUS SP. WH 8102
US-10-369-493-44560

Query Match      100.0%; Score 22; DB 6; Length 1632;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 22
US-10-501-127A-21
; Sequence 21, Application US/10501127A
; Publication No. US20050232937A1
; GENERAL INFORMATION:
; APPLICANT: ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid.
; TITLE OF INVENTION: Paramycobacterial diagnostics and vaccines
; FILE REFERENCE: 2002-032-US
; CURRENT APPLICATION NUMBER: US/10/501,127A
; CURRENT FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: mycobacterium avium paratuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1701)
US-10-501-127A-21

Query Match      100.0%; Score 22; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 236 CCATGCCCAAGGAGATCGAGCT 257

RESULT 23
US-10-635-211-1
; Sequence 1, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant gene
; NAME/KEY: CDS
; LOCATION: (1)..(1761)
US-10-635-211-1

Query Match      100.0%; Score 22; DB 8; Length 1761;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 24
US-10-267-311-16
; Sequence 16, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-267-311-16

Query Match 100.0%; Score 22; DB 5; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 25
US-10-679-956-16
; Sequence 16, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-679-956-16

Query Match 100.0%; Score 22; DB 5; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 161 CCATGCCCAAGGAGATCGAGCT 182

RESULT 26
US-10-267-311-28
; Sequence 28, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-267-311-28

Query Match 100.0%; Score 22; DB 5; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
Db 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 27
US-10-679-956-28
; Sequence 28, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
```



```
; LOCATION: (1)...(1944)
US-10-679-956-28

Query Match      100.0%; Score 22; DB 9; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 28
US-10-068-059-9
; Sequence 9, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match      100.0%; Score 22; DB 5; Length 2073;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 611 CCATGCCCAAGGAGATCGAGCT 632

RESULT 29
US-10-941-049-9
; Sequence 9, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-9

; LOCATION: (1)...(1944)
US-10-679-956-28

Query Match      100.0%; Score 22; DB 9; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 28
US-10-068-059-9
; Sequence 9, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match      100.0%; Score 22; DB 5; Length 2073;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 611 CCATGCCCAAGGAGATCGAGCT 632

RESULT 29
US-10-941-049-9
; Sequence 9, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-9

; LOCATION: (1)...(1944)
US-10-679-956-28

Query Match      100.0%; Score 22; DB 9; Length 1947;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 485 CCATGCCCAAGGAGATCGAGCT 506

RESULT 28
US-10-068-059-7
; Sequence 7, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-7

Query Match      100.0%; Score 22; DB 5; Length 2130;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
DB 668 CCATGCCCAAGGAGATCGAGCT 689

RESULT 31
US-10-941-049-7
; Sequence 7, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-7
```

Query Match 100.0%; Score 22; DB 9; Length 2130;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 668 CCATGCCCAAGGAGATCGAGCT 689

RESULT 32
US-10-068-059-11
; Sequence 11, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 22; DB 5; Length 2175;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 713 CCATGCCCAAGGAGATCGAGCT 734

RESULT 33
US-10-941-049-11
; Sequence 11, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-11

Query Match 100.0%; Score 22; DB 9; Length 2175;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 713 CCATGCCCAAGGAGATCGAGCT 734

RESULT 34
US-10-068-059-5
; Sequence 5, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 22; DB 5; Length 2241;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
|||||
Db 779 CCATGCCCAAGGAGATCGAGCT 800

RESULT 35
US-10-941-049-5
; Sequence 5, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-5

Query Match 100.0%; Score 22; DB 9; Length 2241;

```
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 779 CCATCGCCCAAGGAGATCGAGCT 800

RESULT 36
US-10-267-311-20
; Sequence 20, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; .LOCATION: (1)...(2844)
US-10-267-311-20

Query Match 100.0%; Score 22; DB 5; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 221 CCATCGCCCAAGGAGATCGAGCT 242

RESULT 37
US-10-679-956-20
; Sequence 20, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/10/679,956
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; .LOCATION: (1)...(2844)

US-10-679-956-20

Query Match 100.0%; Score 22; DB 9; Length 2847;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 221 CCATCGCCCAAGGAGATCGAGCT 242

RESULT 38
US-10-080-170-648
; Sequence 648, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-648

Query Match 100.0%; Score 22; DB 6; Length 86114;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 15365 CCATCGCCCAAGGAGATCGAGCT 15386

RESULT 39
US-10-080-170-648
; Sequence 648, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-648

Query Match 100.0%; Score 22; DB 7; Length 86114;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGCT 22
    |||||
Db 15365 CCATCGCCCAAGGAGATCGAGCT 15386
```

RESULT 40
US-10-468-356-648
; Sequence 648, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468,356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-468-356-648

Query Match 100.0%; Score 22; DB 8; Length 86114;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
|||||
DB 15365 CCATCGCCAAAGGAGATCGAGCT 15386

RESULT 41
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 100.0%; Score 22; DB 6; Length 9025608;
Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
|||||
DB 4855659 CCATCGCCAAAGGAGATCGAGCT 4855638

RESULT 42
US-10-369-493-32009
; Sequence 32009, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32009
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Thermobifida fusca
US-10-369-493-32009

Query Match 92.7%; Score 20.4; DB 6; Length 1728;
Best Local Similarity 95.5%; Pred. No. 7.2; Indels 1; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
|||||
DB 269 CCATCGCTAAGGAGATCGAGCT 290

RESULT 43
US-10-656-394A-13/c
; Sequence 13, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 99090
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 23216
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-13

Query Match 92.7%; Score 20.4; DB 8; Length 99090;
Best Local Similarity 95.5%; Pred. No. 6.8; Indels 1; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAAGGAGATCGAGCT 22
|||||
DB 38860 CCATCGCCAAAGGAGATCGAGCT 38839

RESULT 44
US-10-500-586-55
; Sequence 55, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HS

; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIES
; TITLE OF INVENTION: WITH THE SAME

; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 55

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSPF3
US-10-500-586-55

Query Match 90.9%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATCGCCCAAGGAGATCGAGCT 22

Db 1 ATCGCCCAAGGAGATCGAGCT 20

RESULT 45

US-09-975-553-17
; Sequence 17, Application US/09975553
; Patent No. US20020152968A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies

; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish

; FILE REFERENCE: 2213.1004-001
; CURRENT APPLICATION NUMBER: US/09/975,553
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,477
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,476
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17

; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-975-553-17

Query Match 86.4%; Score 19; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20

Db 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 46

US-10-125-792-1
; Sequence 1, Application US/10125792
; Publication No. US20030051269A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.

; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-007
; CURRENT APPLICATION NUMBER: US/10/125,792
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-792-1

Query Match 86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20

Db 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 47

US-10-125-778-1
; Sequence 1, Application US/10125778
; Publication No. US20030082574A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.

; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-005

; CURRENT APPLICATION NUMBER: US/10/125,778
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-778-1

Query Match 86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20

Db 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 48

US-10-270-795-17
; Sequence 17, Application US/10270795
; Publication No. US20030084855A1
; GENERAL INFORMATION:

```
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/10/270,795
; CURRENT FILING DATE: 2002-10-11
; PRIOR FILING DATE: US/09/687,372
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17

Query Match      86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 49
US-10-270-876-17
; Sequence 17, Application US/10270876
; Publication No. US20030116096A1
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR FILING DATE: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17

Query Match      86.4%; Score 19; DB 5; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 50
US-10-268-051-7
; Sequence 7, Application US/10268051
; Publication No. US20030124090A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Species and Methods of Use Thereof

; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213.2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-268-051-7

Query Match      86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 51
US-10-125-772-1
; Sequence 1, Application US/10125772
; Publication No. US20030124657A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-006
; CURRENT APPLICATION NUMBER: US/10/125,772
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-772-1

Query Match      86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAG 20
Db      2256 CATGCCCAAGGAGATCGAG 2274

RESULT 52
US-10-016-496-1
; Sequence 1, Application US/10016496
; Publication No. US20030166908A1
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
```

; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/10/016,496
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: squalus acanthias
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (439)...(3522)
US-10-016-496-1

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 53
US-10-411-076-23
; Sequence 23, Application US/10411076
; Publication No. US20030226516A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Growing Marine Fish in Freshwater
; FILE REFERENCE: 2213.1003007
; CURRENT APPLICATION NUMBER: US/10/411,076
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US01/31625
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,373
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Mustelus canis
US-10-411-076-23

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 54
US-10-410-872-17
; Sequence 17, Application US/10410872
; Publication No. US20030230247A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous

; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-001
; CURRENT APPLICATION NUMBER: US/10/410,872
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/975,553
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,477
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,476
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-410-872-17

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 55
US-10-410-885-1
; Sequence 1, Application US/10410885
; Publication No. US20030232366A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Betka, Marlies
; APPLICANT: Nearing, Jacqueline A.
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-008
; CURRENT APPLICATION NUMBER: US/10/410,885
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 10/125,778
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/125,772
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/125,792
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-410-885-1

Query Match 86.4%; Score 19; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
|||||
DB 2256 CATGCCCAAGGAGATCGAG 2274

RESULT 56

RESULT 60
US-11-086-550-1
; Sequence 1, Application US/11086550
; Publication No. US20050181426A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-005
; CURRENT APPLICATION NUMBER: US/11/086,550
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: US/10/125,778
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-11-086-550-1

Query Match 86.4%; Score 19; DB 10; Length 4134;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGATCGAG 20
|||
Db 2256 CATGCCCAAGGATCGAG 2274

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Job time : 64.2198 secs

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Title: US-10-824-527-1

Perfect score: 22

Sequence: 1 ccattgcgaagatcgagct 22

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Searched: 9263891 seqs, 1996499642 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

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- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2.*
- 10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq3.*
- 11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
- 15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	45	14	US-11-099-683-70
2	17.8	80.9	997	10	US-10-301-480-592106
3	17.8	80.9	997	10	US-10-301-480-120515
4	17.8	80.9	1481	6	US-09-925-065A-673455
5	17.4	79.1	2430	14	US-11-024-959-133
6	17.2	78.2	25	9	US-10-932-182A-33211
7	17.2	78.2	25	9	US-10-932-182A-33211
8	17.2	78.2	486	9	US-10-932-182A-2466
9	17.2	78.2	486	9	US-10-932-182A-2466
10	17.2	78.2	2035	11	US-11-077-619-107
11	16.8	76.4	626	6	US-09-925-065A-913133
12	16.8	76.4	634	6	US-09-925-065A-909976
13	16.8	76.4	634	6	US-09-925-065A-911013
14	16.4	74.5	256	8	US-10-802-796-212
15	16.4	74.5	256	11	US-11-221-284-212
16	16.4	74.5	315	8	US-10-802-796-407
17	16.4	74.5	315	11	US-11-221-284-407
18	16.4	74.5	978	10	US-10-301-480-553257

19	16.4	74.5	978	10	US-10-301-480-1166666	Sequence 1166666,
20	16.4	74.5	6510	8	US-10-775-169-320	Sequence 320, App
21	16.2	73.6	25	14	US-11-136-527-262340	Sequence 262340,
22	16.2	73.6	415	9	US-10-504-389A-46	Sequence 46, Appl
23	16.2	73.6	478	6	US-09-925-065A-564483	Sequence 564483,
24	16.2	73.6	512	6	US-09-925-065A-804140	Sequence 804140,
25	16.2	73.6	512	6	US-09-925-065A-857058	Sequence 857058,
26	16.2	73.6	516	10	US-10-301-480-267847	Sequence 267847,
27	16.2	73.6	516	10	US-10-301-480-881256	Sequence 881256,
28	16.2	73.6	523	6	US-09-925-065A-176640	Sequence 176640,
29	16.2	73.6	544	11	US-11-096-568A-13286	Sequence 13286, A
30	16.2	73.6	557	6	US-09-925-065A-423193	Sequence 423193,
31	16.2	73.6	562	10	US-10-301-480-487545	Sequence 487545,
32	16.2	73.6	562	10	US-10-301-480-1100954	Sequence 1100954,
33	16.2	73.6	592	6	US-09-925-065A-497702	Sequence 497702,
34	16.2	73.6	606	6	US-09-925-065A-28876	Sequence 28876, A
35	16.2	73.6	606	9	US-10-301-480-130114	Sequence 130114,
36	16.2	73.6	606	10	US-10-301-480-743523	Sequence 743523,
37	16.2	73.6	607	6	US-09-925-065A-443435	Sequence 443435,
38	16.2	73.6	611	6	US-09-925-065A-193825	Sequence 193825,
39	16.2	73.6	617	10	US-10-301-480-896622	Sequence 896622,
40	16.2	73.6	617	10	US-10-301-480-71948	Sequence 71948, A
41	16.2	73.6	627	9	US-10-301-480-885357	Sequence 885357,
42	16.2	73.6	627	10	US-10-301-480-264567	Sequence 264567,
43	16.2	73.6	629	10	US-10-301-480-877976	Sequence 877976,
44	16.2	73.6	629	10	US-10-301-480-503870	Sequence 503870,
45	16.2	73.6	631	10	US-10-301-480-1117279	Sequence 1117279,
46	16.2	73.6	631	10	US-09-925-065A-172956	Sequence 172956,
47	16.2	73.6	633	6	US-09-925-065A-339781	Sequence 339781,
48	16.2	73.6	633	10	US-10-301-480-412794	Sequence 412794,
49	16.2	73.6	633	10	US-10-301-480-1026203	Sequence 1026203,
50	16.2	73.6	633	10	US-09-925-065A-942839	Sequence 942839,
51	16.2	73.6	674	6	US-09-925-065A-942840	Sequence 942840,
52	16.2	73.6	730	14	US-11-136-527-1439	Sequence 1439, Ap
53	16.2	73.6	730	14	US-11-136-527-5535	Sequence 5535, Ap
54	16.2	73.6	734	10	US-10-301-480-599819	Sequence 599819,
55	16.2	73.6	734	10	US-10-301-480-1213228	Sequence 1213228,
56	16.2	73.6	846	11	US-11-096-568A-8351	Sequence 8351, Ap
57	16.2	73.6	846	11	US-11-096-568A-8351	Sequence 8351, Ap
58	16.2	73.6	982	10	US-10-301-480-590859	Sequence 590859,
59	16.2	73.6	982	10	US-10-301-480-1204268	Sequence 1204268,
60	16.2	73.6	1989	14	US-11-183-136-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-11-099-683-70
; Sequence 70, Application US/11099683
; Publication No. US20060019916A1
; GENERAL INFORMATION:
; APPLICANT: Krueger, Arthur
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES
; FILE REFERENCE: C1037.70047US01
; CURRENT APPLICATION NUMBER: US/11/099,683
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/558,951
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-099-683-70

Query Match 100.0%; Score 22; DB 14; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
Db 2 CCATGCCCAAGGAGATCGAGCT 23

RESULT 2
US-10-301-480-592106
; Sequence 592106, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 592106
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-592106

Query Match 80.9%; Score 17.8; DB 10; Length 997;
Best Local Similarity 90.5%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
Db 805 CATGCCCAAGGAGATCGAGCT 825

RESULT 3
US-10-301-480-1205515
; Sequence 1205515, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1205515
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1205515

Query Match 80.9%; Score 17.8; DB 10; Length 997;
Best Local Similarity 90.5%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
Db 805 CATGCCCAAGGAGATCGAGCT 825

RESULT 4
US-09-925-065A-673455
; Sequence 673455, Application US/09925065A

Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 673455
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-673455

Query Match 80.9%; Score 17.8; DB 6; Length 1481;
Best Local Similarity 90.5%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
Db 683 CATGCCCAAGGAGATCGAGTT 703

RESULT 5
US-11-024-959-133
; Sequence 133, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 133
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Pinus radiata
US-11-024-959-133

Query Match 79.1%; Score 17.4; DB 14; Length 2430;
Best Local Similarity 94.7%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAG 20
Db 339 CATGCCCAAGGAGATCGAG 357

RESULT 6
US-10-932-182A-33211/c

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; Sequence 33211, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-33211

Query Match      78.2%; Score 17.2; DB 9; Length 25;
Best Local Similarity 86.4%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
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DB 22 CCATGCCCATCGAGATCGA 1

RESULT 7
US-10-932-182A-33211/c
; Sequence 33211, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-33211

Query Match      78.2%; Score 17.2; DB 9; Length 25;
Best Local Similarity 86.4%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
DB 22 CCATGCCCATCGAGATCGA 1

RESULT 8
US-10-932-182A-2466/c
; Sequence 2466, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
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; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2466
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2466

Query Match      78.2%; Score 17.2; DB 9; Length 486;
Best Local Similarity 86.4%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
DB 440 CCATGCCCATCGAGATCGA 419

RESULT 9
US-10-932-182A-2466/c
; Sequence 2466, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2466
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-2466

Query Match      78.2%; Score 17.2; DB 9; Length 486;
Best Local Similarity 86.4%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATGCCCAAGGAGATCGAGCT 22
    |||||
DB 440 CCATGCCCATCGAGATCGA 419

RESULT 10
US-11-077-619-107
; Sequence 107, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Feesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: DE 10242433.0
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107
; LENGTH: 2035
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; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2035)
; OTHER INFORMATION: groEL
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1835)
US-11-077-619-107

Query Match      78.2%; Score 17.2; DB 11; Length 2035;
Best Local Similarity 86.4%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCGCCCAAGGAGATCGAGCT 22
    ||||| ||||| ||||| |||||
Db 361 CCATCGCGAAAGAAATCGAGCT 382

RESULT 11
US-09-925-065A-913133
; Sequence 913133, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 913133
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-913133

Query Match      76.4%; Score 16.8; DB 6; Length 626;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCGCCCAAGGAGATCGAGCT 22
    ||||| ||||| ||||| |||||
Db 581 ATCGCCCAAGGAGATCGAGCT 600

RESULT 12
US-09-925-065A-909976/c
; Sequence 909976, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-911013

Query Match      76.4%; Score 16.8; DB 6; Length 634;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCGCCCAAGGAGATCGAGCT 22
    ||||| ||||| ||||| |||||
Db 581 ATCGCCCAAGGAGATCGAGCT 600

RESULT 14
US-10-802-796-212/c
; Sequence 212, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
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; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 212
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-212

Query Match          74.5%; Score 16.4; DB 8; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGA 19
      |||||
Db      67 CATGCCAAGGAGCTCGA 50

RESULT 15
US-11-221-284-212/c
; Sequence 212, Application US/11221284
; Publication No. US20060063182A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/11/221,284
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: US/09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-11-221-284-212

Query Match          74.5%; Score 16.4; DB 11; Length 256;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGA 19
      |||||
Db      67 CATGCCAAGGAGCTCGA 50

RESULT 16
US-10-802-796-407/c
; Sequence 407, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
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; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 407
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-407

Query Match          74.5%; Score 16.4; DB 8; Length 315;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGA 19
      |||||
Db      64 CATGCCAAGGAGCTCGA 47

RESULT 17
US-11-221-284-407/c
; Sequence 407, Application US/11221284
; Publication No. US20060063182A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/11/221,284
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: US/09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 407
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-11-221-284-407

Query Match          74.5%; Score 16.4; DB 11; Length 315;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCCAAGGAGATCGA 19
      |||||
Db      64 CATGCCAAGGAGCTCGA 47

RESULT 18
US-10-301-480-553257
; Sequence 553257, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
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; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553257
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-553257

Query Match 74.5%; Score 16.4; DB 10; Length 978;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCG 18
||||| |||||||
Db 51 CCATCGCCAAGGAGATCG 68

RESULT 19

US-10-301-480-1166666
; Sequence 1166666, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166666
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166666

Query Match 74.5%; Score 16.4; DB 10; Length 978;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCG 18
||||| |||||||
Db 51 CCATCGCCAAGGAGATCG 68

RESULT 20

US-10-775-169-320
; Sequence 320, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 320
; LENGTH: 6510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-320

Query Match 74.5%; Score 16.4; DB 8; Length 6510;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCGCCAAGGAGATCG 18
||||| |||||||
Db 2141 CCATCGCCAAGGAGATCG 2158

RESULT 21

US-11-136-527-262340
; Sequence 262340, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 262340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-262340

Query Match 73.6%; Score 16.2; DB 14; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCAAGGAGATCGAGCT 22
||||| |||||||
Db 5 CAACGCCCTGGAGATCGAGCT 25

RESULT 22

US-10-504-389A-46
; Sequence 46, Application US/10504389A
; Publication No. US20060045876A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Scott, Andrew
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: LUD 5821
; CURRENT APPLICATION NUMBER: US/10/504,389A
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US03/04243
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 46
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: nucleotide sequence for murine light chain variable region
US-10-504-389A-46

Query Match 73.6%; Score 16.2; DB 9; Length 415;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCAAGGAGATCGAGCT 22
||||| |||||||
Db 71 CAGCGCCATGGACATCGAGCT 91

RESULT 23
US-09-925-065A-564483
; Sequence 564483, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564483
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-564483

Query Match 73.6%; Score 16.2; DB 6; Length 478;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
DB 10 CATCCCAAGGAGATCGTCT 30

RESULT 24
US-09-925-065A-804140
; Sequence 804140, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 804140
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-804140

Query Match 73.6%; Score 16.2; DB 6; Length 512;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22

DB 38 CATCCCAAGGAGATCGTCT 58
RESULT 25
US-09-925-065A-857058
; Sequence 857058, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 857058
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-857058

Query Match 73.6%; Score 16.2; DB 6; Length 512;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
DB 38 CATCCCAAGGAGATCGTCT 58

RESULT 26
US-10-301-480-267847
; Sequence 267847, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267847
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-267847

Query Match 73.6%; Score 16.2; DB 10; Length 516;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCAAGGAGATCGAGCT 22
DB 4 CATCCCAAGGAGATCGTCT 24

```
RESULT 27
US-10-301-480-881256
; Sequence 881256, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 881256
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-881256

Query Match      73.6%; Score 16.2; DB 10; Length 516;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      4 CATCACCAAGGAGATGGTGCT 24

RESULT 28
US-09-925-065A-176640/c
; Sequence 176640, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176640
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-176640

Query Match      73.6%; Score 16.2; DB 6; Length 523;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      520 CATCACCAAGGAGATGGTGCT 500

RESULT 29
US-11-096-568A-13286
; Sequence 13286, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13286
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(544)
; OTHER INFORMATION: Ceres Seq. ID no. 15174132
US-11-096-568A-13286

Query Match      73.6%; Score 16.2; DB 11; Length 544;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      154 CGTCGTCACCAAGGAGATCGAGAT 174

RESULT 30
US-09-925-065A-423193/c
; Sequence 423193, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 423193
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-423193

Query Match      73.6%; Score 16.2; DB 6; Length 557;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      296 CATCACCAAGGAGATGGTGCT 276

RESULT 31
US-10-301-480-487545/c
; Sequence 487545, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487545
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-487545

Query Match          73.6%; Score 16.2; DB 10; Length 562;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      296 CATCACCACGAGATGCTGCT 276

RESULT 32
US-10-301-480-1100954/c
; Sequence 1100954, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1100954
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1100954

Query Match          73.6%; Score 16.2; DB 10; Length 562;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      296 CATCACCACGAGATGCTGCT 276

RESULT 33
US-09-925-065A-497702
; Sequence 497702, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
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; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 497702
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-497702

Query Match          73.6%; Score 16.2; DB 6; Length 592;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATGCCCAAGGAGATCGAGC 21
      ||||| ||||| ||||| ||||| |||||
Db      111 CCATCTCCAAAGAGGTGCGAGC 131

RESULT 34
US-09-925-065A-28876
; Sequence 28876, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28876
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-28876

Query Match          73.6%; Score 16.2; DB 6; Length 606;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCGCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      332 CATCACCACGAGATGCTGCT 352

RESULT 35
US-10-301-480-130114
; Sequence 130114, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
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; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130114
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-130114

Query Match      73.6%; Score 16.2; DB 9; Length 606;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      332 CATCACCACGAGGATCGTGCT 352

RESULT 36
US-10-301-480-743523
; Sequence 743523, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 743523
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-743523

Query Match      73.6%; Score 16.2; DB 10; Length 606;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      332 CATCACCACGAGGATCGTGCT 352

RESULT 37
US-09-925-065A-443435
; Sequence 443435, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
```

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; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 443435
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-443435

Query Match      73.6%; Score 16.2; DB 6; Length 607;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      119 CATCACCACGAGGATCGTGCT 139

RESULT 38
US-09-925-065A-193825/c
; Sequence 193825, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193825
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-193825

Query Match      73.6%; Score 16.2; DB 6; Length 611;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| |||||
Db      387 CATCACCACGAGGATCGAGCT 367

RESULT 39
US-10-301-480-283213/c
; Sequence 283213, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283213
```

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; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-283213

Query Match      73.6%; Score 16.2; DB 10; Length 617;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 387 CATCACCAGGAGATCGAGCT 367

RESULT 40
US-10-301-480-896622/c
; Sequence 896622, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896622
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-896622

Query Match      73.6%; Score 16.2; DB 10; Length 617;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 387 CATCACCAGGAGATCGAGCT 367

RESULT 41
US-10-301-480-71948
; Sequence 71948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71948
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-71948

Query Match      73.6%; Score 16.2; DB 9; Length 627;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 387 CATCACCAGGAGATCGAGCT 367

RESULT 42
US-10-301-480-685357
; Sequence 685357, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685357
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-685357

Query Match      73.6%; Score 16.2; DB 10; Length 627;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 347 CATCACCAGGAGATCGGTGCT 367

RESULT 43
US-10-301-480-264567
; Sequence 264567, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264567
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-264567

Query Match      73.6%; Score 16.2; DB 10; Length 629;
Best Local Similarity 85.7%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 492 CATCACCAGGAGATCGGTGCT 512

RESULT 44
US-10-301-480-877976
; Sequence 877976, Application US/10301480
; Publication No. US20060057564A1
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 877976
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-877976

Query Match      73.6%; Score 16.2; DB 10; Length 629;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      492 CATCACCAGGAGATGGTGCT 512

RESULT 45
US-10-301-480-503870/c
; Sequence 503870, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 503870
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-503870

Query Match      73.6%; Score 16.2; DB 10; Length 631;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      513 CATCACCAGGAGATGGTGCT 493

RESULT 46
US-10-301-480-1117279/c
; Sequence 1117279, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
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; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1117279
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1117279

Query Match      73.6%; Score 16.2; DB 10; Length 631;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      513 CATCACCAGGAGATGGTGCT 493

RESULT 47
US-09-925-065A-172956
; Sequence 172956, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 172956
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-172956

Query Match      73.6%; Score 16.2; DB 6; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
Db      496 CATCACCAGGAGATGGTGCT 516

RESULT 48
US-09-925-065A-339781/c
; Sequence 339781, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
```

```
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339781
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-339781

Query Match      73.6%; Score 16.2; DB 6; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      273 CATCACCAAGGAGATGCTGCT 253

RESULT 49
US-10-301-480-412794
; Sequence 412794, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412794
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-412794

Query Match      73.6%; Score 16.2; DB 10; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      361 CATCACCAAGGAGATGCTGCT 381

RESULT 50
US-10-301-480-1026203
; Sequence 1026203, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1026203
; LENGTH: 633
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-1026203

Query Match      73.6%; Score 16.2; DB 10; Length 633;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      361 CATCACCAAGGAGATGCTGCT 381

RESULT 51
US-09-925-065A-942839
; Sequence 942839, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 942839
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-942839

Query Match      73.6%; Score 16.2; DB 6; Length 674;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATGCCCAAGGAGATCGAGCT 22
      ||||| ||||| ||||| ||||| |||||
Db      368 CATCACCAAGGAGATGCTGCT 388

RESULT 52
US-09-925-065A-942840
; Sequence 942840, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 942840
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-942840

Query Match 73.6%; Score 16.2; DB 6; Length 674;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 368 CATCACCAAGGAGATCGTGTCT 388

RESULT 53

US-11-136-527-1439/c
; Sequence 1439, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1439
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1439

Query Match 73.6%; Score 16.2; DB 14; Length 730;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 704 CAACGCCCTGGAGATCGAGCT 684

RESULT 54

US-11-136-527-5535
; Sequence 5535, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5535
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5535

Query Match 73.6%; Score 16.2; DB 14; Length 730;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
|||||

Db 27 CAACGCCCTGGAGATCGAGCT 47

RESULT 55

US-10-301-480-599819/c
; Sequence 599819, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 599819
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-599819

Query Match 73.6%; Score 16.2; DB 10; Length 734;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 123 CATCACCAAGGAGATAGTGTCT 103

RESULT 56

US-10-301-480-1213228/c
; Sequence 1213228, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1213228
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1213228

Query Match 73.6%; Score 16.2; DB 10; Length 734;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATGCCCAAGGAGATCGAGCT 22
|||||
Db 123 CATCACCAAGGAGATAGTGTCT 103

RESULT 57

US-11-096-568A-8351
; Sequence 8351, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.


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; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8351
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(846)
; OTHER INFORMATION: Ceres Seq. ID no. 15225168
US-11-096-568A-8351

Query Match          73.6%; Score 16.2; DB 11; Length 846;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 436 CATCGCCCAAGGAGAAACGAGCT 456

RESULT 58
US-10-301-480-590859
; Sequence 590859, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590859
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-590859

Query Match          73.6%; Score 16.2; DB 10; Length 982;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 960 CATCACCACCAAGGAGATGGTGCT 980

RESULT 59
US-10-301-480-1204268
; Sequence 1204268, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1204268
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-1204268

Query Match          73.6%; Score 16.2; DB 10; Length 982;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCGCCCAAGGAGATCGAGCT 22
   ||||| ||||| ||||| |||||
Db 960 CATCACCACCAAGGAGATGGTGCT 980

RESULT 60
US-11-183-136-3
; Sequence 3, Application US/11183136
; Publication No. US20060019896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Dean
; APPLICANT: Park, Kye Won
; TITLE OF INVENTION: NETRIN-RELATED COMPOSITIONS AND USES
; FILE REFERENCE: UUTH-P01-011
; CURRENT APPLICATION NUMBER: US/11/183,136
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: US 60/587,796
; PRIOR FILING DATE: 2004-07-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-183-136-3

Query Match          73.6%; Score 16.2; DB 14; Length 1989;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCGCCCAAGGAGATCGAGC 21
   ||||| ||||| ||||| |||||
Db 684 CCATCACCACCAAGCAGAACGAGC 704

Search completed: April 1, 2006, 22:39:03
Job time : 57.3836 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:04:52 ; Search time 154.853 Seconds
(without alignments)
8075.738 Million cell updates/sec

Title: US-10-824-527-2
Perfect score: 21.6
Sequence: 1 tgaagtgccrccggtctgtt 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Capext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
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- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_av.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21.6	100.0	337	6	AR079996 Sequence
C 2	21.6	100.0	337	6	AR085922 Sequence
C 3	21.6	100.0	337	6	AR093308 Sequence
C 4	21.6	100.0	337	6	AR121888 Sequence
C 5	21.6	100.0	337	6	BD218097 Sequence
C 6	21.6	100.0	337	6	AR213734 Sequence
C 7	21.6	100.0	337	6	AR365966 Sequence
C 8	21.6	100.0	337	6	BD008519 Sequence
C 9	21.6	100.0	552	1	AF429652 Lactobaci
C 10	21.6	100.0	552	1	AY691245 Corynebact
C 11	21.6	100.0	552	1	AY691305 Streptomy
C 12	21.6	100.0	560	1	AY339132 Bifidobac
C 13	21.6	100.0	567	1	AY691243 Corynebact
C 14	21.6	100.0	590	1	AF240574 Bifidobac
C 15	21.6	100.0	590	1	AY004278 Bifidobac
C 16	21.6	100.0	590	1	AY004280 Bifidobac
C 17	21.6	100.0	590	1	AY166560 Bifidobac
C 18	21.6	100.0	590	1	AY166562 Bifidobac

C 19	21.6	100.0	591	1	AF240567
C 20	21.6	100.0	797	6	E10965
C 21	21.6	100.0	852	6	E41716
C 22	21.6	100.0	927	6	AR080019
C 23	21.6	100.0	927	6	AR085945
C 24	21.6	100.0	927	6	AR121711
C 25	21.6	100.0	927	6	BD218120
C 26	21.6	100.0	927	6	AR213757
C 27	21.6	100.0	927	6	AR365989
C 28	21.6	100.0	927	6	BD008542
C 29	21.6	100.0	985	6	AR080046
C 30	21.6	100.0	985	6	AR085972
C 31	21.6	100.0	985	6	AR121738
C 32	21.6	100.0	985	6	BD218147
C 33	21.6	100.0	985	6	AR213784
C 34	21.6	100.0	985	6	AR366016
C 35	21.6	100.0	1569	6	AR080017
C 36	21.6	100.0	1569	6	AR085943
C 37	21.6	100.0	1569	6	AR121709
C 38	21.6	100.0	1569	6	BD218118
C 39	21.6	100.0	1569	6	AR213755
C 40	21.6	100.0	1569	6	AR365987
C 41	21.6	100.0	1569	6	BD008540
C 42	21.6	100.0	1589	6	E41719
C 43	21.6	100.0	1620	1	TTU90204
C 44	21.6	100.0	1623	1	AF352578
C 45	21.6	100.0	1623	6	A46454
C 46	21.6	100.0	1623	6	CQ816174
C 47	21.6	100.0	1623	6	AR266836
C 48	21.6	100.0	1623	6	AR655543
C 49	21.6	100.0	1623	6	AX073911
C 50	21.6	100.0	1624	1	AF281650
C 51	21.6	100.0	1626	1	AF352577
C 52	21.6	100.0	1626	6	AR080045
C 53	21.6	100.0	1626	6	AR085971
C 54	21.6	100.0	1626	6	AR121737
C 55	21.6	100.0	1626	6	BD218146
C 56	21.6	100.0	1626	6	AR213783
C 57	21.6	100.0	1626	6	AR366015
C 58	21.6	100.0	1644	6	BD165187
C 59	21.6	100.0	1644	6	AX123070
C 60	21.6	100.0	1647	6	E10966

ALIGNMENTS

RESULT 1	AR079996/c	AR079996	Sequence 77 from patent US 5968524.	337 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	DEFINITION	AR079996	Sequence 77 from patent US 5968524.				
ACCESSION	AR079996						
VERSION	AR079996.1	GI:10006731					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 337)						
AUTHORS	Watson,J.D. and Tan,P.L.J.						
TITLE	Methods and compounds for the treatment of immunologically-mediated psoriasis						
JOURNAL	Patent: US 5968524-A 77 19-OCT-1999;						
FEATURES	Location/Qualifiers						
source	1..337						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
ORIGIN							

Query Match 100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGAAGTGCCRCGGATCTTGT 22

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Db      166 TGAAGTGCCGCGGATCTTGT 145
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RESULT 2
AR085922/c
LOCUS      AR085922      337 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 77 from patent US 5985287.
ACCESSION  AR085922
VERSION     AR085922.1 GI:10012688
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Tan, P., Skinner, M. and Prestidge, R.
TITLE      Compounds and methods for treatment and diagnosis of mycobacterial
           infections
JOURNAL    Patent: US 5985287-A 77 16-NOV-1999;
FEATURES    Location/Qualifiers
             source
             1..337
             /organism="unknown"
             /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db      166 TGAAGTGCCGCGGATCTTGT 145
|||||:|||||:|||||:|||||
RESULT 5
BD218097/c
LOCUS      BD218097      337 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for
           their use.
ACCESSION  BD218097
VERSION    BD218097.1 GI:33027867
KEYWORDS  JP 2002514385-A/22.
SOURCE    Mycobacterium vaccae
ORGANISM  Mycobacterium vaccae
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
TITLE      Compositions derived from mycobacterium vaccae and methods for
           their use
JOURNAL    Patent: JP 2002514385-A 22 21-MAY-2002;
           GENESIS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT    OS Mycobacterium vaccae
           PN JP 2002514385-A/22
           PD 21-MAY-2002
           PF 23-DEC-1998 JP 2000525553
           PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
           23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
           17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
           TAN,JAMES WATSON,ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
           PI L PRESTIDGE
           PC C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
           PC A61P17/00,
           PC A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
           PC C07K19/00,
           PC C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
           G01N33/68//
           PC C12N15/09,C12R1/32,C12N15/00,C12N5/00,(C12N15/00,C12R1/32)
           CC Compositions derived from mycobacterium
           vaccae and methods for
           their use
           CC Key Location/Qualifiers
           FH source
           FT 1..337
           /organism="Mycobacterium vaccae".
           /db_xref="taxon:1810"
           /organism="Mycobacterium vaccae"
           /mol_type="genomic DNA"
           /db_xref="taxon:1810"
FEATURES    source
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             /organism="Mycobacterium vaccae"
             /mol_type="genomic DNA"
             /db_xref="taxon:1810"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db      166 TGAAGTGCCGCGGATCTTGT 145
|||||:|||||:|||||:|||||
RESULT 3
AR093308/c
LOCUS      AR093308      337 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 77 from patent US 6001361.
ACCESSION  AR093308
VERSION    AR093308.1 GI:10020058
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 337)
AUTHORS    Tan, P., Hiyama, J., Visser, E., Skinner, M., Scott, L. and Prestidge, R.
TITLE      Mycobacterium vaccae antigens
JOURNAL    Patent: US 6001361-A 77 14-DEC-1999;
FEATURES    Location/Qualifiers
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             1..337
             /organism="unknown"
             /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
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Qy      1 TGAAGTGCCRCGGATCTTGT 22
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Db      166 TGAAGTGCCGCGGATCTTGT 145
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RESULT 4
AR121688/c
LOCUS      AR121688      337 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 77 from patent US 6160093.
ACCESSION  AR121688
VERSION    AR121688.1 GI:14105264
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
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Db 166 TGAAGTGCGCGGATCTTGTT 145

RESULT 6
LOCUS AR213734/c 337 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 77 from patent US 6406704.
ACCESSION AR213734
VERSION AR213734.1 GI:23311021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 337)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 77 18-JUN-2002;
Genensis Research and Development Corporation Limited;;
NZX;

FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGTT 22
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Db 166 TGAAGTGCGCGGATCTTGTT 145

RESULT 7
LOCUS AR365966/c 337 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 77 from patent US 6328978.
ACCESSION AR365966
VERSION AR365966.1 GI:34598219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 337)
AUTHORS Watson, J.D., Tan, P.L.J. and Prestidge, R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 77 11-DEC-2001;
Genensis Research & Development Corp. Ltd.; Parnell;
NZX;

FEATURES
source Location/Qualifiers
1..337
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/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGTT 22
|||||:|||||
Db 166 TGAAGTGCGCGGATCTTGTT 145

RESULT 8
LOCUS BD008519/c 337 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial infections.
ACCESSION BD008519

BD008519.1 GI:18636892
JP 2001503969-A/22.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 337)
AUTHORS Tan, P., Hiyaama, J., Visser, E.S., Skinner, M.A., Scott, L.M. and Prestidge, R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial infections
JOURNAL Patent: JP 2001503969-A 22 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT OS Unidentified
PN JP 2001503969-A/22
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI PAUL TAN, JUN HIYAMA, ELIZABETH S VISSER, MARGOT A SKINNER, PI LINDA M SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..337
/organism="Unidentified".

FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 337;
Best Local Similarity 95.5%; Pred. No. 7.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCGCGGATCTTGTT 22
|||||:|||||
Db 166 TGAAGTGCGCGGATCTTGTT 145

RESULT 9
AF429652/c 552 bp DNA linear BCT 23-NOV-2004
LOCUS Lactobacillus rhamnosus strain ATCC 21052 60 kDa heat shock protein (HSP60) gene, partial cds.
DEFINITION
ACCESSION AF429652
VERSION AF429652.1 GI:33312999
KEYWORDS
SOURCE Lactobacillus rhamnosus
ORGANISM Lactobacillus rhamnosus
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
REFERENCE 1 (bases 1 to 552)
AUTHORS Dobson, C.M., Chaban, B., Deneer, H. and Ziola, B.
TITLE Lactobacillus casei, Lactobacillus rhamnosus, and Lactobacillus zeae isolates identified by sequence signature and immunoblot phenotype
JOURNAL Can. J. Microbiol. 50 (7), 482-488 (2004)
PUBMED 15381972
REFERENCE 2 (bases 1 to 552)
AUTHORS Dobson, M.C., Deneer, H., Lee, S., Hemmingsen, S., Hill, J. and Ziola, B.R.
TITLE Redefining speciation of Lactobacillus and Pediococcus based on phylogenetic analysis of the partial 16S rRNA gene, 16S-23S rRNA region and 60 kDa heat shock protein sequences
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 552)
AUTHORS Dobson, M.C. and Ziola, B.R.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2001) Microbiology and Immunology, University of Saskatchewan, 107 Wiggins Road, Saskatoon, Saskatchewan S7N 5E5,

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                Query Match 100.0%; Score 21.6; DB 1; Length 552;
                Best Local Similarity 95.5%; Pred. No. 7.5;
                Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

                QY 1 TGAAGTGCCRCGGATCTTGT 22
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                Db 538 TGAAGTGCCCGGATCTTGT 517

            RESULT 10
            AY691245/c
            LOCUS 552 bp DNA linear BCT 17-AUG-2004
            DEFINITION Streptomyces thermoviolaceus subsp. thermoviolaceus
            chaperonin (cpn60) gene, partial cds.
            ACCESSION AY691305
            VERSION AY691305.1 GI:51103898
            KEYWORDS
            SOURCE
            ORGANISM
                Streptomyces thermoviolaceus subsp. thermoviolaceus
                Streptomyces thermoviolaceus subsp. thermoviolaceus
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Streptomycineae; Streptomycetaceae; Streptomyces.
            REFERENCE
            AUTHORS Hill,J.E., Penny,S.L., Crowell,K.G., Goh,S.H. and Hemmingsen,S.M.
            TITLE cpnDB: a chaperonin sequence database
            JOURNAL Genome Res. 14 (8), 1669-1675 (2004)
            PUBMED 15289485
            REFERENCE
            AUTHORS Hill,J.E., Van Kessel,A.G., Dumonceaux,T.J. and Hemmingsen,S.M.
            TITLE cpnDB - a chaperonin sequence database
            JOURNAL Submitted (20-JUL-2004) NRC Plant Biotechnology Institute, 110
            Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada
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                    Query Match 100.0%; Score 21.6; DB 1; Length 552;
                    Best Local Similarity 95.5%; Pred. No. 7.5;
                    Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

                    QY 1 TGAAGTGCCRCGGATCTTGT 22
                    |||||:|||||
                    Db 538 TGAAGTGCCCGGATCTTGT 517

            RESULT 10
            AY691245/c
            LOCUS 552 bp DNA linear BCT 17-AUG-2004
            DEFINITION Corynebacterium amycolatum 60 kDa chaperonin (cpn60) gene, partial
            cds.
            ACCESSION AY691245
            VERSION AY691245.1 GI:51103778
            KEYWORDS
            SOURCE
            ORGANISM
                Corynebacterium amycolatum
                Corynebacterium amycolatum
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Corynebacteriaceae; Corynebacterium.
            REFERENCE
            AUTHORS Hill,J.E., Penny,S.L., Crowell,K.G., Goh,S.H. and Hemmingsen,S.M.
            TITLE cpnDB: a chaperonin sequence database
            JOURNAL Genome Res. 14 (8), 1669-1675 (2004)
            PUBMED 15289485
            REFERENCE
            AUTHORS Hill,J.E., Van Kessel,A.G., Dumonceaux,T.J. and Hemmingsen,S.M.
            TITLE cpnDB - a chaperonin sequence database
            JOURNAL Submitted (20-JUL-2004) NRC Plant Biotechnology Institute, 110
            Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada
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                    Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

                    QY 1 TGAAGTGCCRCGGATCTTGT 22
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                    Db 538 TGAAGTGCCCGGATCTTGT 517

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Db 538 TGAAGGTGCGCGGATCTTGTT 517

RESULT 12
AY339132/c
LOCUS
DEFINITION
Bifidobacterium psychraerophilum heat shock protein 60 gene,
partial cds.
ACCESSION
AY339132
VERSION
AY339132.1 GI:33439355
KEYWORDS
Bifidobacterium psychraerophilum
SOURCE
Bifidobacterium psychraerophilum
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 560)
AUTHORS
Simpson,P.J., Ross,R.P., Fitzgerald,G.F. and Stanton,C.
TITLE
Bifidobacterium psychraerophilum sp. nov. and Aeriscardovia
aeriphila gen. nov., sp. nov., isolated from a porcine caecum
JOURNAL
Int. J. Syst. Evol. Microbiol. 54 (2), 401-406 (2004)
PUBMED
15023951
REFERENCE
2 (bases 1 to 560)
AUTHORS
Simpson,P.J., Ross,R.P., Fitzgerald,G.F. and Stanton,C.
TITLE
Direct Submission
JOURNAL
Submitted (08-JUL-2003) Food Quality, Dairy Products Research
Centre, Moorepark, Fermoy, Cork, Ireland
LOCATION/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:218140"
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ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 560;
Best Local Similarity 95.5%; Pred. No. 7.5;
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Qy 1 TGAAGTGCRCGGATCTTGTT 22
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Db 541 TGAAGTGCACGGATCTTGTT 520

RESULT 13
AY691243/c
LOCUS
DEFINITION
Corynebacterium callunae 567 bp DNA linear BCT 17-AUG-2004
cds.
ACCESSION
AY691243
VERSION
AY691243.1 GI:51103774
KEYWORDS
Corynebacterium callunae
SOURCE
Corynebacterium callunae
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
1 (bases 1 to 567)
AUTHORS
Hill,J.E., Penny,S.L., Crowell,K.G., Goh,S.H. and Hemmingsen,S.M.
TITLE
cpnDB: a chaperonin sequence database
JOURNAL
Genome Res. 14 (8), 1669-1675 (2004)
PUBMED
15289485
REFERENCE
2 (bases 1 to 567)

Db 538 TGAAGTGCRCGGATCTTGTT 517

RESULT 12
AY339132/c
LOCUS
DEFINITION
Bifidobacterium psychraerophilum heat shock protein 60 gene,
partial cds.
ACCESSION
AY339132
VERSION
AY339132.1 GI:33439355
KEYWORDS
Bifidobacterium psychraerophilum
SOURCE
Bifidobacterium psychraerophilum
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 560)
AUTHORS
Simpson,P.J., Ross,R.P., Fitzgerald,G.F. and Stanton,C.
TITLE
Bifidobacterium psychraerophilum sp. nov. and Aeriscardovia
aeriphila gen. nov., sp. nov., isolated from a porcine caecum
JOURNAL
Int. J. Syst. Evol. Microbiol. 54 (2), 401-406 (2004)
PUBMED
15023951
REFERENCE
2 (bases 1 to 560)
AUTHORS
Simpson,P.J., Ross,R.P., Fitzgerald,G.F. and Stanton,C.
TITLE
Direct Submission
JOURNAL
Submitted (08-JUL-2003) Food Quality, Dairy Products Research
Centre, Moorepark, Fermoy, Cork, Ireland
LOCATION/Qualifiers
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Query Match 100.0%; Score 21.6; DB 1; Length 560;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCRCGGATCTTGTT 22
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Db 541 TGAAGTGCACGGATCTTGTT 520

RESULT 13
AY691243/c
LOCUS
DEFINITION
Corynebacterium callunae 567 bp DNA linear BCT 17-AUG-2004
cds.
ACCESSION
AY691243
VERSION
AY691243.1 GI:51103774
KEYWORDS
Corynebacterium callunae
SOURCE
Corynebacterium callunae
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
1 (bases 1 to 567)
AUTHORS
Hill,J.E., Penny,S.L., Crowell,K.G., Goh,S.H. and Hemmingsen,S.M.
TITLE
cpnDB: a chaperonin sequence database
JOURNAL
Genome Res. 14 (8), 1669-1675 (2004)
PUBMED
15289485
REFERENCE
2 (bases 1 to 567)

AUTHORS
Hill,J.E., Van Kessel,A.G., Dumonceaux,T.J. and Hemmingsen,S.M.
CONSRTM
cpnDB - a chaperonin sequence database
TITLE
Direct Submission
JOURNAL
Submitted (20-JUL-2004) NRC Plant Biotechnology Institute, 110
Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada
FEATURES
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ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 567;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCRCGGATCTTGTT 22
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Db 553 TGAAGTGCACGGATCTTGTT 532

RESULT 14
AF240574/c
LOCUS
DEFINITION
Bifidobacterium indicum heat shock protein 60 (hsp60) gene, partial
cds.
ACCESSION
AF240574
VERSION
AF240574.1 GI:7243802
KEYWORDS
Bifidobacterium indicum
SOURCE
Bifidobacterium indicum
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 590)
AUTHORS
Jian,W., Zhu,L. and Dong,X.
TITLE
New approach to phylogenetic analysis of the genus Bifidobacterium
based on partial Hsp60 gene sequences
JOURNAL
Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1633-1638 (2001)
PUBMED
11594590
REFERENCE
2 (bases 1 to 590)
AUTHORS
Jian,W. and Dong,X.
TITLE
Direct Submission
JOURNAL
Submitted (02-MAR-2000) China General Microorganisms Culture
Collection Centre, Institute of Microbiology, Chinese Academy of
Sciences, P.O.Box 2714, Beijing 100080, P.R.China
3 (bases 1 to 590)
AUTHORS
Jian,W. and Dong,X.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUN-2000) China General Microorganisms Culture
Collection Centre, Institute of Microbiology, Chinese Academy of
Sciences, Zhongguancun, Beiyitiao 13, Beijing 100080, P.R.China
REMARK
Sequence update by submitter
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ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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Db 556 TGAAGGTGCGCGGATCTTGT 535

RESULT 16
AY004280/c
LOCUS
DEFINITION
Bifidobacterium bifidum heat shock protein 60 (hsp60) gene, partial
cda.
ACCESSION AY004280
VERSION AY004280.1 GI:11999206
KEYWORDS
SOURCE
ORGANISM
Bifidobacterium bifidum
Bacteria: Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 590)
Jian, W., Zhu, L. and Dong, X.
New approach to phylogenetic analysis of the genus Bifidobacterium
based on partial Hsp60 gene sequences
Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1633-1638 (2001)
JOURNAL PUBMED 11594590
REFERENCE
2 (bases 1 to 590)
Jian, W., Zhu, L. and Dong, X.
Direct Submission
Submitted (06-JUL-2000) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
JOURNAL
REFERENCE
3 (bases 1 to 590)
Jian, W., Zhu, L. and Dong, X.
Direct Submission
Submitted (16-MAR-2001) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
JOURNAL
REMARK
FEATURES
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ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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ELIAQSKVETKQIAATAATISAADPEIGAEIAEALDKVQDGVVTVENNRFGDLLE
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LLIIAEDVDGEALPTLILNKIRGTFTNSCAVKAQPGF"

ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 557 TGAAGGTGCGCGGATCTTGT 536

RESULT 15
AY004278/c
LOCUS
DEFINITION
Bifidobacterium pullorum heat shock protein 60 (hsp60) gene,
partial cda.
ACCESSION AY004278
VERSION AY004278.1 GI:11999202
KEYWORDS
SOURCE
ORGANISM
Bifidobacterium pullorum
Bacteria: Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 590)
Jian, W., Zhu, L. and Dong, X.
New approach to phylogenetic analysis of the genus Bifidobacterium
based on partial Hsp60 gene sequences
Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1633-1638 (2001)
JOURNAL PUBMED 11594590
REFERENCE
2 (bases 1 to 590)
Jian, W., Zhu, L. and Dong, X.
Direct Submission
Submitted (06-JUL-2000) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
JOURNAL
REFERENCE
3 (bases 1 to 590)
Jian, W., Zhu, L. and Dong, X.
Direct Submission
Submitted (16-MAR-2001) China General Microorganisms Culture
Collection Center, Institute of Microbiology, Chinese Academy of
Sciences, P.O. Box 2714, Beijing 100080, P.R. China
JOURNAL
REMARK
FEATURES
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1..590
/organism="Bifidobacterium pullorum"
/mol_type="genomic DNA"
/strain="JCM1214"
/db_xref="taxon:78448"
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/gene="hsp60"
<1..>590
/gene="hsp60"
/notes="HSP60"
/codon_start=1
/transl_table=11
/product="heat shock protein 60"
/protein_id="AAF89503.1"
/db_xref="GI:11999203"

ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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Db      556  TGAAGGTGCGCGGATCTTGT 535
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RESULT 17
AY166560/c      590 bp  DNA  linear  BCT 10-NOV-2002
LOCUS
DEFINITION
Bifidobacterium thermacidophilum subsp. suis strain P3-11 heat
shock protein 60 (hsp60) gene, partial cds.
ACCESSION
AY166560
VERSION
AY166560.1 GI:24850358
KEYWORDS
SOURCE
ORGANISM
Bifidobacterium thermacidophilum subsp. porcinum
Bifidobacterium thermacidophilum subsp. porcinum
Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 590)
AUTHORS
Xiuzhu,D., Lin,Z. and Wei,L.
TITLE
Species Identification of Genus Bifidobacterium Based on Partial
thermacidophilum subsp. suis subsp. nov.
JOURNAL
2 (bases 1 to 590)
REFERENCE
Xiuzhu,D., Lin,Z. and Wei,L.
AUTHORS
Direct Submission
TITLE
Submitted (18-OCT-2002) State Key Laboratory of Microbial
Resources, Institute of Microbiology, Chinese Academy of Sciences,
No. 13 North 1st Street, Zhongguancun, Beijing 100080, P. R. China
JOURNAL
Unpublished
FEATURES
source
1..590
/organism="Bifidobacterium boum"
/mol_type="genomic DNA"
/strain="P3-11"
/sub_species="suis"
/db_xref="taxon:212365"
<1..>590
/gene="hsp60"
<1..>590
/gene="hsp60"
/codon_start=1
/transl_table=11
/product="heat shock protein 60"
/protein_id="AA62544.1"
/db_xref="GI:24850359"
/translation="GDGTTTATVLAQSLVHGLKNVAGSNPIALRRGIEKATDRIVK
ELVAKDQVETKDOIATATISAADPEVGEKIAELDKVGQGVVTVEDNRRPGLDLE
FTGHRFQKGYIAPFTVNADDTAVLENPYILLTSGKVSQQDDIVHLADLVKMSGRP
LLIIVAEVDVGEALPTLIILNKIRGTNTCAVKAPGFG"

gene
1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||:|||||:|||||:|||||
Db      556  TGAAGGTGCGCGGATCTTGT 535

RESULT 19
AF240567/c      591 bp  DNA  linear  BCT 16-NOV-2001
LOCUS
DEFINITION
Bifidobacterium thermophilum heat shock protein 60 (hsp60) gene,
partial cds.
ACCESSION
AF240567
VERSION
AF240567.1 GI:7243788
KEYWORDS
SOURCE
Bifidobacterium thermophilum
ORGANISM
Bifidobacterium thermophilum
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 591)
AUTHORS
Jian,W., Zhu,L. and Dong,X.
TITLE
New approach to phylogenetic analysis of the genus Bifidobacterium
based on partial HSP60 gene sequences
JOURNAL
Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1633-1638 (2001)
PUBMED
11594590
REFERENCE
2 (bases 1 to 591)
AUTHORS
Jian,W. and Dong,X.
TITLE
Direct Submission
JOURNAL
Submitted (02-MAR-2000) China General Microorganisms Culture
Collection Centre, Institute of Microbiology, Chinese Academy of
Sciences, P.O.Box 2714, Beijing 100080, P.R.China
REFERENCE
3 (bases 1 to 591)
AUTHORS
Jian,W. and Dong,X.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUN-2000) China General Microorganisms Culture
Collection Centre, Institute of Microbiology, Chinese Academy of
Sciences, Zhongguancun, Beiyitiao 13, Beijing 100080, P.R.China
REMARK
Sequence update by submitter
FEATURES
Location/Qualifiers

Query Match      100.0%; Score 21.6; DB 1; Length 590;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TGAAGGTGCGCGGATCTTGT 22
|||||:|||||:|||||:|||||:|||||
Db      556  TGAAGGTGCGCGGATCTTGT 535

RESULT 18
AY166562/c      590 bp  DNA  linear  BCT 10-NOV-2002
LOCUS
DEFINITION
Bifidobacterium boum strain 03-4-8 heat shock protein 60 (hsp60)
gene, partial cds.
ACCESSION
AY166562
VERSION
AY166562.1 GI:24850362
KEYWORDS
SOURCE
Bifidobacterium boum
ORGANISM
Bifidobacterium boum
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 (bases 1 to 590)

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source
1. .591
/organism="Bifidobacterium thermophilum"
/mol_type="genomic DNA"
/strain="JCM1207"
/db_xref="taxon:33905"
<1. .>591
/gene="hsp60"
<1. .>591
/gene="hsp60"
/codon_start=2
/transl_table=11
/product="heat shock protein 60"
/protein_id="AAP43452.1"
/db_xref="GI:7243789"
/translation="GGGTTATVLAQSLVHGLKXNVVAGSNPIALRGGIEKAADEIVK
ELVASAKDVEKQIAATATISAADPEVGEKIAEDKVGQGVVTVENNRPLGLE
FTGMRFDKGYIAPYFVTNADQTAVENTPYILLTSGRVSSQDVIHLADLVKMSGR
LLVAEDVDGEALPTLILNKIRGTFTNTCAVKAPFG"

ORIGIN
Query Match 100.0%; Score 21.6; DB 1; Length 591;
Best Local Similarity 95.5%; Pred. No. 7.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
|||||:|||||:|||||:|||||:|||||:
Db 557 TGAAGGTGCCCGCATCTTGT 536

RESULT 20
E10965/c
LOCUS E10965 797 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA fragment encoding a part of GroEL protein.
ACCESSION E10965
VERSION E10965.1 GI:22028829
KEYWORDS JP 1996070873-A/1.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 797)
Imai, R., Inui, M., Asai, Y., Kobayashi, M. and Yugawa, H.
NEW DNA FRAGMENT
Patent: JP 1996070873-A 1 19-MAR-1996;
MITSUBISHI CHEM CORP
OS Brevibacterium flavum
PN JP 1996070873-A/1
PD 19-MAR-1996
PF 07-SEP-1994 JP 1994213483
PI IMAI RITSUKO, INUI MASAYUKI, ASAI YOKO, KOBAYASHI MIKI, PI
YUGAWA HIDEAKI
PC C12N15/09, (C12N15/09, C12R1:13);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1. .797
FT /strain="MJ-233".
FT Location/Qualifiers
FEATURES
source
1. .797
/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/db_xref="taxon:1718"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 797;
Best Local Similarity 95.5%; Pred. No. 7.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
|||||:|||||:|||||:|||||:|||||:
Db 748 TGAAGGTGCCCGCATCTTGT 727

RESULT 21
E41716/c
LOCUS E41716 852 bp DNA linear PAT 31-JAN-2002
DEFINITION Process for producing L-glutamic acid by fermentation.
ACCESSION E41716
VERSION E41716.1 GI:18633387
KEYWORDS JP 2001069979-A/33.
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 852)
Fuji, M. and Imanaka, T.
Process for producing L-glutamic acid by fermentation
Patent: JP 2001069979-A 33 21-MAR-2001;
JAPAN TOBACCO INC, TAKAYUKI IMANAKA
OS Corynebacterium glutamicum
PN JP 2001069979-A/33
PD 21-MAR-2001
PF 31-AUG-1999 JP 1999245121
PR MIKIO FUJII, TAKAYUKI IMANAKA
PC C12N15/09, C12N1/21, C12P13/14// (C12N1/21, C12R1:15), (C12P13/14,
C12R1:15),
PC C12N15/00
CC Key Location/Qualifiers
FH source 1. .852
FT /organism="Corynebacterium glutamicum".
FT Location/Qualifiers
FEATURES
source
1. .852
/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/db_xref="taxon:1718"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 852;
Best Local Similarity 95.5%; Pred. No. 7.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
|||||:|||||:|||||:|||||:|||||:
Db 802 TGAAGGTGCCCGCATCTTGT 781

RESULT 22
AR080019/c
LOCUS AR080019 927 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 116 from patent US 5968524.
ACCESSION AR080019
VERSION AR080019.1 GI:10006754
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 927)
AUTHORS Watson, J.D. and Tan, P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated psoriasis
JOURNAL Patent: US 5968524-A 116 19-OCT-1999;
FEATURES
source
1. .927
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 927;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGCATCTTGT 22
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[illegible][illegible]


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RESULT 31
LOCUS AR121738/c 985 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 161 from patent US 6160093.
ACCESSION AR121738
VERSION AR121738.1 GI:14105314
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Visser,E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6160093-A 161 12-DEC-2000;
FEATURES
source Location/Qualifiers
1..985
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
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Db 167 TGAAGTGCCRCGGATCTTGT 146
|||||:|||||
RESULT 32
LOCUS BD218147/c 985 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for
their use.
ACCESSION BD218147
VERSION BD218147.1 GI:33027917
KEYWORDS JP 2002514385-A/72.
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
REFERENCE 1 (bases 1 to 985)
AUTHORS Tan,P., Watson,J., Visser,E.S., Skinner,M.A. and Prestid,R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for
their use
JOURNAL Patent: JP 2002514385-A 72 21-MAY-2002;
COMMENT OS Mycobacterium vaccae
PN JP 2002514385-A/72
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
TAN,JAMES WATSON,ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
PI L PRESTIDGE
PC C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
A61P17/00,
PC A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
G01N33/68//
PC (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
CC Compositions derived from mycobacterium
vaccae and methods for
their use
FH Key Location/Qualifiers
FT source 1..985
/mol_type="Mycobacterium vaccae"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 167 TGAAGTGCCRCGGATCTTGT 146
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RESULT 33
LOCUS AR213784/c 985 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 161 from patent US 6406704.
ACCESSION AR213784
VERSION AR213784.1 GI:23311071
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6406704-A 161 18-JUN-2002;
COMMENT NZX;
GENESIS Research and Development Corporation Limited;;
FEATURES
source Location/Qualifiers
1..985
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 167 TGAAGTGCCRCGGATCTTGT 146
|||||:|||||
RESULT 34
LOCUS AR366016/c 985 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 161 from patent US 6328978.
ACCESSION AR366016
VERSION AR366016.1 GI:34598269
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 985)
AUTHORS Watson,J.D., Tan,P.L.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin
disorders
JOURNAL Patent: US 6328978-A 161 11-DEC-2001;
COMMENT NZX;
GENESIS Research & Development Corp. Ltd.; Parnell;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 7.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
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Db      167 TGAAGGTGCGCGGATCTTGTT 146
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RESULT 35
LOCUS   AR080017/c
DEFINITION Sequence 113 from patent US 5968524.
ACCESSION AR080017
VERSION  AR080017.1 GI:10006752
KEYWORDS
SOURCE  Unknown.
ORGANISM
REFERENCE
AUTHORS  Watson,J.D. and Tan,P.L.J.
TITLE    Methods and compounds for the treatment of immunologically-mediated psoriasis
JOURNAL  Patent: US 5968524-A 113 19-OCT-1999;
FEATURES
source   Location/Qualifiers
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/mol_type="unknown"
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||:|||||:|||||
Db      808 TGAAGGTGCGCGGATCTTGTT 787

RESULT 36
LOCUS   AR085943/c
DEFINITION Sequence 113 from patent US 5985287.
ACCESSION AR085943
VERSION  AR085943.1 GI:10012709
KEYWORDS
SOURCE  Unknown.
ORGANISM
REFERENCE
AUTHORS  Tan,P., Skinner,M. and Prestidge,R.
TITLE    Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL  Patent: US 5985287-A 113 16-NOV-1999;
FEATURES
source   Location/Qualifiers
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/mol_type="unknown"
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||:|||||:|||||
Db      808 TGAAGGTGCGCGGATCTTGTT 787

RESULT 37
LOCUS   AR121709/c
DEFINITION Sequence 113 from patent US 6160093.
ACCESSION AR121709
VERSION  AR121709.1 GI:14105285
KEYWORDS
SOURCE  Unknown.
ORGANISM
REFERENCE
AUTHORS  Tan,P., Visser,J., Visser,E.S., Skinner,M.A. and Preslid,R.L.
TITLE    Compositions derived from mycobacterium vaccae and methods for their use.
JOURNAL  Patent: JP 2002514385-A 43 21-MAY-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Mycobacterium vaccae
PN JP 2002514385-A/43
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
TAN,JAMES WATSON ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
PI L PRESTIDGE
PC C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
PC A61P17/00,
PC A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
G01N33/68//
PC C12N15/09,C12R1:32,C12N15/00,C12N5/00, (C12N15/00,C12R1:32)
CC Compositions derived from mycobacterium
vaccae and methods for
their use
FH Key Location/Qualifiers
FT source 1..1569
/organism="Mycobacterium vaccae".
/organism="Mycobacterium vaccae"
/mol_type="genomic DNA"
/db_xref="taxon:1810"

FEATURES
source   Location/Qualifiers
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/organism="Mycobacterium vaccae"
/mol_type="genomic DNA"
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ORIGIN
Query Match      100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGAAGGTGCGCGGATCTTGTT 22
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source 1. .1589
/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/db_xref="taxon:1718"

ORIGIN

Query Match 100.0%; Score 21.6; DB 6; Length 1589;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
DB 1533 TGAAGGTGCGCGGATCTTGT 1512

RESULT 43

TTU92024/c

LOCUS

DEFINITION Tsukamurella tyrosinosolvens heat shock protein 60 (hsp60) gene, BCT 21-MAR-1997

complete cds.

ACCESSION U90204

VERSION U90204.1 GI:1899189

SOURCE Tsukamurella tyrosinosolvens

ORGANISM Tsukamurella tyrosinosolvens

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.

REFERENCE 1 (bases 1 to 1620)

Zimmermann, O., Pinkenburg, O. and Koechel, H.G.

Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock

protein 60

Unpublished

2 (bases 1 to 1620)

Zimmermann, O., Pinkenburg, O. and Koechel, H.G.

Direct Submission

Submitted (20-FEB-1997) Med. Microbiology, University,

Kreuzberg 57, Goettingen D-37075, Germany

Location/Qualifiers

1. .1620

/organism="Tsukamurella tyrosinosolvens"

/mol_type="genomic DNA"

/strain="IMMIB D-1411"

/db_xref="taxon:57704"

/note="aerobic, gram positive, slightly acid-alcohol fast bacilli; genus is closely related to the genera

Mycobacterium, Nocardia, Rhodococcus, Gordonia, and

Corynebacterium"

1. .1620

/gene="hsp60"

1. .1620

/gene="hsp60"

/note="GroEL protein"

/codon_start=1

/transl_table=11

/product="heat shock protein 60"

/protein_id="AA849990.1"

/db_xref="GI:1899190"

/translation="MAKTIAPDEARRGLERGLNALADAVKVTLPKGRNVLEKKG
APTITNDGVSIAKEIELEDPEYKIGAEVLKVEAKTDDVAGDGTATTATVLAQALVREG
LRNVAAGNPLGKRGIEKAVEAVTEHLLKEAVEVTEKEQIATAGISAGDPAIGELI
AEAMDVKVGEVITVEESNTFGLQLELTGEMFDFKGFISGYPATDAERQEAVIDAYI
LVSQKISTVKDILLPLEKVIQSGKPLAIIAEDVGEALSTLIVNKIRGTFSKVAIKA
PGGDRRKLQMDAILTGQGVISEHIGLSLDTAGLEVGLQARQVVTQKDETVVUGA
GSKEQIAGRVQIRAEIESDSDYDREKLERLAKGAVAVIKAGATDELKERRH
IEDAVRNAAKAAVEEIVAGGGAALQSGKVFETLNLEGEATGANIVKVALDAPVKQI
AVNAGLEPGVVAEKVRNSPAGTGLNATGVYEDLLAAGINDPVKVTLSALQNAASIAA
LFLTTEAVVADKPEKAGAPVPTGCGMGDMF"

ORIGIN

Query Match 100.0%; Score 21.6; DB 1; Length 1620;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 44

AF352578/c

LOCUS

DEFINITION Tsukamurella paurometabola heat shock protein 60 (hsp60) gene, BCT 13-MAR-2001

complete cds.

ACCESSION AF352578

VERSION AF352578.1 GI:13310800

KEYWORDS

SOURCE Tsukamurella paurometabola

ORGANISM Tsukamurella paurometabola

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.

REFERENCE 1 (bases 1 to 1623)

Zimmermann, O.S. and Koechel, H.G.

Tsukamurella paurometabola heat shock protein 60 (hsp60) gene

Unpublished

2 (bases 1 to 1623)

Zimmermann, O.S. and Koechel, H.G.

Direct Submission

Submitted (23-FEB-2001) Virology, Univ. Goettingen, Kreuzberg 57, Goettingen D-37075, Germany

Location/Qualifiers

1. .1623

/organism="Tsukamurella paurometabola"

/mol_type="genomic DNA"

/db_xref="taxon:2061"

1. .1623

/gene="hsp60"

1. .1623

/gene="hsp60"

/codon_start=1

/transl_table=11

/product="heat shock protein 60"

/protein_id="AAK18614.1"

/db_xref="GI:13310801"

/translation="MAKTIAPDEARRGLERGLNALADAVKVTLPKGRNVLEKKG
APTITNDGVSIAKEIELEDPEYKIGAEVLKVEAKTDDVAGDGTATTATVLAQALVREG
LRNVAAGNPLGKRGIEKAVEAVTEHLLKEAVEVTEKEQIATAGISAGDPAIGELI
AEAMDVKVGEVITVEESNTFGLQLELTGEMFDFKGFISGYPATDAERQEAVIDAYI
LVSQKISTVKDILLPLEKVIQSGKPLAIIAEDVGEALSTLIVNKIRGTFSKVAIKA
PGGDRRKLQMDAILTGQGVISEHIGLSLDTAGLEVGLQARQVVTQKDETVVUGA
GSKEQIAGRVQIRAEIESDSDYDREKLERLAKGAVAVIKAGATDELKERRH
IEDAVRNAAKAAVEEIVAGGGAALQSGKVFETLNLEGEATGANIVKVALDAPVKQI
AVNAGLEPGVVAEKVRNSPAGTGLNATGVYEDLLAAGINDPVKVTLSALQNAASIAA
LFLTTEAVVADKPEKAGAPVPTGCGMGDMF"

ORIGIN

Query Match 100.0%; Score 21.6; DB 1; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 45

A46454/c

LOCUS

DEFINITION Sequence 1 from Patent WO9525744.

ACCESSION A46454

VERSION A46454.1 GI:2300634

KEYWORDS

SOURCE Mycobacterium bovis

ORGANISM Mycobacterium bovis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 1623)
AUTHORS Anderson, S.M., Van, D.Z. and Van, E.W.
TITLE PEPTIDE FRAGMENTS OF MICROBIAL STRESS PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES
JOURNAL Patent: WO 9525744-A 1 28-SEP-1995;
UNIV UTRECHT (NL)
COMMENT Other publication AU 1962895 951009.
FEATURES
source Location/Qualifiers
1..1623
/organism="Mycobacterium bovis"
/mol_type="unassigned DNA"
/db_xref="taxon:1765"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
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Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 46
LOCUS CQ816174 1623 bp DNA linear PAT 03-JUN-2004
DEFINITION Sequence 3 from Patent WO2004041304.
ACCESSION CQ816174
VERSION CQ816174.1 GI:48144533
KEYWORDS Mycobacterium tuberculosis
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1
AUTHORS Coates, A.R.
TITLE Pain relief agents
JOURNAL Patent: WO 2004041304-A 3 21-MAY-2004;
HELPERBY Therapeutics Limited (GB)
FEATURES
source Location/Qualifiers
1..1623
/organism="Mycobacterium tuberculosis"
/mol_type="unassigned DNA"
/db_xref="taxon:1773"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
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Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 47
LOCUS AR266836 1623 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6495347.
ACCESSION AR266836
VERSION AR266836.1 GI:29696202
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1623)
AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: US 6495347-A 3 17-DEC-2002;
Stressgen Biotechnologies Corporation; Victoria, CA;

REFERENCE 1 (bases 1 to 1623)
AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: WO 0104344-A 3 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
FEATURES
source Location/Qualifiers
1..1623
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion sequence"
1..1623
/note="unnamed protein product"
/codon_start=1
/transl_table=1
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/db_xref="GI:12710172"

FEATURES
source Location/Qualifiers
1..1623
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 48
LOCUS AR655543 1623 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 23 from patent US 6892139.
ACCESSION AR655543
VERSION AR655543.1 GI:67587586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1623)
AUTHORS Eisenberg, D., Rotstein, S.H. and Marcotte, E.M.
TITLE Determining the functions and interactions of proteins by comparative analysis
JOURNAL Patent: US 6892139-A 23 10-MAY-2005;
The Regents of the University of California; Alameda, CA
FEATURES
source Location/Qualifiers
1..1623
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 49
LOCUS AX073911 1623 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 3 from Patent WO0104344.
ACCESSION AX073911
VERSION AX073911.1 GI:12710171
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: WO 0104344-A 3 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
FEATURES
source Location/Qualifiers
1..1623
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion sequence"
1..1623
/note="unnamed protein product"
/codon_start=1
/transl_table=1
/protein_id="CAC28419.1"
/db_xref="GI:12710172"

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 LEAMDKVNGEVIITVEESNTFGLQLETEGMRFDKGYISGYFVTDPERQEAILEDPI
 LVSSTVTKDILLPLEKVIQAGKPLLIIAEDVEGEALSTLVNKRIGTFKSVAKA
 PGFGRKRAQLQMAILTGQVISEVGLTLENADISLLGKARKVVTVDKETTIVEGA
 GDTDAIGRAVQAOIRIENSDDYDEKLOERLAKLAGGVAVIKAGAAVEVLEKERRK
 RIEDAVRNAKAAVEGIVAGGVVTLQAAPTLDLKLGEDEATGANIVKVALEAPLKQ
 IAFNGLGPGVVAEKVRLNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRESALQNAASIA
 GLFLITTEAVVADKPEKAAAPAGDPTGGMGMDP"

ORIGIN

Query Match 100.0%; Score 21.6; DB 6; Length 1623;
 Best Local Similarity 95.5%; Pred. No. 8.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGTT 22

Db 808 TGAAGGTGCCCGGATCTTGTT 787

RESULT 50

AF281650/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

11564153

2 (bases 1 to 1624)

Nagabhushanam,V., Praszkier,J. and Cheers,C.

Molecular and immunological characterization of Mycobacterium avium

65 kDa heat shock protein (Hsp65)

Immunol. Cell Biol. 79 (5), 454-461 (2001)

Location/Qualifiers

1..1624

/organism="Mycobacterium avium"

/mol_type="genomic DNA"

/db_xref="taxon:1764"

1..1624

/note="GroEL-like protein; 65 kilodalton protein"

/codon_start=1

/transl_table=11

/product="heat shock protein Hsp65"

/protein_id="AAF91444.1"

/db_xref="GI:9652216"

/translation="MAKTIAYDEARRGLERGLNALADAVKVTGLGKRNVLKKGW

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LEAMDKVNGEVIITVEESNTFGLQLETEGMRFDKGYISGYFVTDPERQEAILEDPI

LVSSTVTKDILLPLEKVIQAGKPLLIIAEDVEGEALSTLVNKRIGTFKSVAKA

PGFGRKRAQLQMAILTGQVISEVGLTLENADISLLGKARKVVTVDKETTIVEGA

GSDATAGRAVQAOIRIENSDDYDEKLOERLAKLAGGVAVIKAGAAVEVLEKERRK

RIEDAVRNAKAAVEGIVAGGVVTLQAAPTLDLKLGEDEATGANIVKVALEAPLKQ

IAFNGLGPGVVAEKVRLNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRESALQNAASIA

GLFLITTEAVVADKPEKAAAPAGDPTGGMGMDP"

ORIGIN

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 Best Local Similarity 95.5%; Pred. No. 8.2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGTT 22

Db 808 TGAAGGTGCCCGGATCTTGTT 787

RESULT 51

AF352577/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

2 (bases 1 to 1626)

Zimmermann,O.S. and Koechel,H.G.

Nocardia farcinica heat shock protein 60 (hsp60) gene

Unpublished

Location/Qualifiers

1..1626

/organism="Nocardia farcinica"

/mol_type="genomic DNA"

/db_xref="taxon:37329"

1..1626

/gene="hsp60"

1..1626

/codon_start=1

/transl_table=11

/product="heat shock protein 60"

/protein_id="AAK18613.1"

/db_xref="GI:13310799"

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LEAMDKVNGEVIITVEESNTFGLQLETEGMRFDKGYISGYFVTDPERQEAILEDPI

LVSSTVTKDILLPLEKVIQAGKPLLIIAEDVEGEALSTLVNKRIGTFKSVAKA

PGFGRKRAQLQMAILTGQVISEVGLTLENADISLLGKARKVVTVDKETTIVEGA

GSDATAGRAVQAOIRIENSDDYDEKLOERLAKLAGGVAVIKAGAAVEVLEKERRK

RIEDAVRNAKAAVEGIVAGGVVTLQAAPTLDLKLGEDEATGANIVKVALEAPLKQ

IAFNAGLEPGVVAEKVRLNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRESALQNAASIA

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ORIGIN

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 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGGTGCCCGGATCTTGTT 22

Db 808 TGAAGGTGCCCGGATCTTGTT 787

RESULT 52

AR080045/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Sequence 159 from patent US 5968524.

AR080045

AR080045.1

GI:10006780

Unknown.

Unclassified.

1 (bases 1 to 1626)

Watson,J.D. and Tan,P.L.J.

Methods and compounds for the treatment of immunologically-mediated

PAT 31-AUG-2000

```
psoriasis
JOURNAL Patent: US 5968524-A 159 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..1626
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 95.5%; Pred. No. 8.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 53
AR085971/c
LOCUS 1626 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 159 from patent US 5985287.
ACCESSION AR085971
VERSION AR085971.1 GI:10012737
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Tan, P., Skinner, M. and Prestidge, R.
TAN, P., SKINNER, M. and PRESTIDGE, R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 159 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..1626
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/mol_type="unassigned DNA"

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Qy 1 TGAAGTGCCCGGATCTTGT 22
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Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 54
AR121737/c
LOCUS 1626 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 159 from patent US 6160093.
ACCESSION AR121737
VERSION AR121737.1 GI:14105313
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Visser, E.
VISSE, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 159 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..1626
/organism="unknown"
/mol_type="unassigned DNA"

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Db 808 TGAAGTGCCCGGATCTTGT 22

RESULT 55
BD218146/c
LOCUS 1626 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION BD218146
VERSION BD218146.1 GI:33027916
KEYWORDS Mycobacterium vaccae
SOURCE Mycobacterium vaccae
ORGANISM Mycobacteriaceae; Actinobacteridae; Actinomycetales; Bacteria; Actinobacteria; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestidge, R.L.
TAN, P., WATSON, J., VISSER, E.S., SKINNER, M.A. and PRESTIDGE, R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for their use
JOURNAL Patent: JP 2002514385-A 71 21-MAY-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT OS Mycobacterium vaccae
PN JP 2002514385-A/71
PF 21-MAY-2002
PR 23-DEC-1997 US 08/997362,23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624,11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
PC A61P17/00,
PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
PC C07K19/00,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC C12N15/09, C12R1/32, C12N15/00, C12N5/00, (C12N15/00, C12R1:32)
CC Compositions derived from mycobacterium
vaccae and methods for
their use
CC Key Location/Qualifiers
FH source 1..1626
FT /organism="Mycobacterium vaccae".
FEATURES Location/Qualifiers
source 1..1626
/organism="Mycobacterium vaccae"
/mol_type="genomic DNA"
/db_xref="taxon:1810"

ORIGIN
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Qy 1 TGAAGTGCCCGGATCTTGT 22
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Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 56
AR213783/c
LOCUS 1626 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 159 from patent US 6406704.
ACCESSION AR213783
VERSION AR213783.1 GI:23311070
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TAN, P., VISSER, E., PRESTIDGE, R. and WATSON, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
```


ORGANISM Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE 1 (bases 1 to 1647)
 AUTHORS Imai, R., Inui, M., Asai, Y., Kobayashi, M. and Yugawa, H.
 TITLE NEW DNA FRAGMENT.
 JOURNAL Patent: JP 1996070873-A 2 19-MAR-1996;
 MITSUBISHI CHEM CORP
 OS Brevibacterium flavum
 PN JP 1996070873-A/2
 PD 19-MAR-1996
 PP 07-SEP-1994 JP 1994213483
 PI IMAI RITSUKO, INUI MASAYUKI, ASAI YOKO, KOBAYASHI MIKI, PI
 YUGAWA HIDEAKI
 PC C12N15/09, (C12N15/09, C12R1:13);
 CC strandedness: Double;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FH source 1..1647
 FT /strain='MJ-233',
 FT /organism='Brevibacterium flavum' FT
 FT CDS 1..1647
 FT /product='GroEL protein'.
 FT Location/Qualifiers
 1..1647
 /organism='Corynebacterium glutamicum'
 /mol_type='genomic DNA'
 /db_xref='taxon:1718'

FEATURES
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 ORIGIN

Query Match 100.0%; Score 21.6; DB 6; Length 1647;
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 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 Db 823 TGAGGTGCCCGGATCTTGT 802

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 16:58:33 ; Search time 12.7069 Seconds
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Perfect score: 21.6

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Maximum Match 100%

Listing first 60 summaries

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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	21.6	100.0	337	2	US-08-997-080-77
C 2	21.6	100.0	337	2	US-08-997-362-77
C 3	21.6	100.0	337	3	US-08-873-970-77
C 4	21.6	100.0	337	3	US-09-095-855-77
C 5	21.6	100.0	337	3	US-09-324-542-77
C 6	21.6	100.0	337	3	US-09-205-426-77
C 7	21.6	100.0	927	2	US-08-997-080-116
C 8	21.6	100.0	927	2	US-08-997-362-116
C 9	21.6	100.0	927	3	US-09-095-855-116
C 10	21.6	100.0	927	3	US-09-324-542-116
C 11	21.6	100.0	927	3	US-09-205-426-116
C 12	21.6	100.0	985	2	US-08-997-080-161
C 13	21.6	100.0	985	2	US-08-997-362-161
C 14	21.6	100.0	985	3	US-09-095-855-161
C 15	21.6	100.0	985	3	US-09-324-542-161
C 16	21.6	100.0	985	3	US-09-205-426-161
C 17	21.6	100.0	1569	2	US-08-997-080-113
C 18	21.6	100.0	1569	2	US-08-997-362-113
C 19	21.6	100.0	1569	3	US-09-095-855-113
C 20	21.6	100.0	1569	3	US-09-324-542-113
C 21	21.6	100.0	1569	3	US-09-205-426-113
C 22	21.6	100.0	1623	3	US-09-613-303-3
C 23	21.6	100.0	1623	3	US-10-267-311-3
C 24	21.6	100.0	1623	3	US-09-712-363-23

C 25	21.6	100.0	1626	2	US-08-997-080-159	Sequence 159, App
C 26	21.6	100.0	1626	2	US-08-997-362-159	Sequence 159, App
C 27	21.6	100.0	1626	3	US-09-095-855-159	Sequence 159, App
C 28	21.6	100.0	1626	3	US-09-324-542-159	Sequence 159, App
C 29	21.6	100.0	1626	3	US-09-205-426-159	Sequence 159, App
C 30	21.6	100.0	1920	3	US-09-613-303-16	Sequence 16, Appl
C 31	21.6	100.0	1920	3	US-10-267-311-16	Sequence 16, Appl
C 32	21.6	100.0	1947	3	US-09-613-303-28	Sequence 28, Appl
C 33	21.6	100.0	1947	3	US-10-267-311-28	Sequence 28, Appl
C 34	21.6	100.0	2073	3	US-10-068-059-9	Sequence 9, Appl
C 35	21.6	100.0	2130	3	US-10-068-059-7	Sequence 7, Appl
C 36	21.6	100.0	2175	3	US-10-068-059-11	Sequence 11, Appl
C 37	21.6	100.0	2241	3	US-10-068-059-5	Sequence 5, Appl
C 38	21.6	100.0	2847	3	US-09-613-303-20	Sequence 20, Appl
C 39	21.6	100.0	2847	3	US-10-267-311-20	Sequence 20, Appl
C 40	21.6	100.0	4380	3	US-08-955-565A-3	Sequence 3, Appl
C 41	21.6	100.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 42	21.6	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 43	20	92.6	732	3	US-09-634-238-67	Sequence 67, Appl
C 44	20	92.6	1320	2	US-08-461-775-8	Sequence 8, Appl
C 45	20	92.6	1320	3	US-09-031-606-8	Sequence 8, Appl
C 46	20	92.6	1620	2	US-08-461-775-10	Sequence 10, Appl
C 47	20	92.6	1620	3	US-09-031-606-10	Sequence 10, Appl
C 48	20	92.6	2167	2	US-08-461-775-9	Sequence 9, Appl
C 49	20	92.6	2167	3	US-09-031-606-9	Sequence 9, Appl
C 50	20	92.6	2668	2	US-08-461-775-11	Sequence 11, Appl
C 51	20	92.6	2668	3	US-09-031-606-11	Sequence 11, Appl
C 52	19.6	90.7	706	3	US-09-470-191-60	Sequence 60, Appl
C 53	18.4	85.2	1623	3	US-09-583-110-1024	Sequence 1024, Ap
C 54	18.4	85.2	1926	3	US-09-613-303-50	Sequence 50, Appl
C 55	18.4	85.2	1926	3	US-10-267-311-50	Sequence 50, Appl
C 56	18.4	85.2	5365	3	US-08-961-527-77	Sequence 77, Appl
C 57	17.4	80.6	1844	3	US-10-105-729-7	Sequence 7, Appl
C 58	17.4	80.6	2003	3	US-10-105-729-1	Sequence 1, Appl
C 59	17	78.7	4352	3	US-09-620-312D-383	Sequence 383, App
C 60	16.8	77.8	966	3	US-09-107-433-1679	Sequence 1679, Ap

ALIGNMENTS

RESULT 1

US-08-997-080-77/c

; Sequence 77, Application US/08997080

; Patent No. 5968524

; GENERAL INFORMATION:

; APPLICANT: WATSON, JAMES D.

; APPLICANT: TAN, PAUL L.J.

; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-

; CORRESPONDENCE ADDRESS: 194

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/997,080

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1007

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
;
; INFORMATION FOR SEQ ID NO: 77:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-080-77

Query Match 100.0%; Score 21.6; DB 2; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
   |||||||:|||||||
Db 166 TGAAGGTGCCRCGGATCTTGTT 145

RESULT 2
US-08-997-362-77/c
; Sequence 77, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-362-77

Query Match 100.0%; Score 21.6; DB 2; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
   |||||||:|||||||
Db 166 TGAAGGTGCCRCGGATCTTGTT 145

RESULT 3
US-08-873-970-77/c
; Sequence 77, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-873-970-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
   |||||||:|||||||
Db 166 TGAAGGTGCCRCGGATCTTGTT 145

RESULT 4
US-09-095-855-77/c
; Sequence 77, Application US/09095855
; Patent No. 6160093
```



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; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-09-095-855-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 5
US-09-324-542-77/c
; Sequence 77, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; EARLIER FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 6
US-09-205-426-77/c
; Sequence 77, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-205-426-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.71;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 166 TGAAGTGCCCGGATCTTGT 145

RESULT 7
US-08-997-080-116/c
; Sequence 116, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; MEDIATED SKIN DISORDERS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/997,080
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1007
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 927 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-08-997-080-116

Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
    |||||:|||||
Db 166 TGAAGGTGCCCGGATCTTGT 145

RESULT 8
US-08-997-362-116/c
/ Sequence 116, Application US/08997362
/ Patent No. 5985287
/ GENERAL INFORMATION:
/ APPLICANT: Tan, Paul
/ APPLICANT: Hiyama, Jun
/ APPLICANT: Visser, Elizabeth
/ APPLICANT: Skinner, Margot
/ APPLICANT: Scott, Linda
/ APPLICANT: Prestidge, Ross
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
/ TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
/ NUMBER OF SEQUENCES: 194
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Ann W. Speckman
/ STREET: 2601 Elliott Avenue, Suite 4185
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/997,362
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/705,347
/ FILING DATE: 29-AUG-1996
/ APPLICATION NUMBER: 08/873,970
/ FILING DATE: 12-JUN-1997
/ APPLICATION NUMBER: 08/997,362
/ FILING DATE: 23-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1002c3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 927 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-09-095-855-116

Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
    |||||:|||||
Db 166 TGAAGGTGCCCGGATCTTGT 145

RESULT 9
US-09-095-855-116/c
/ Sequence 116, Application US/09095855
/ Patent No. 6160093
/ GENERAL INFORMATION:
/ APPLICANT: Tan, Paul
/ APPLICANT: Visser, Elizabeth
/ APPLICANT: Skinner, Margot
/ APPLICANT: Prestidge, Ross
/ TITLE OF INVENTION: Compounds and Methods for
/ TREATMENT AND DIAGNOSIS OF Mycobacterial Infections
/ NUMBER OF SEQUENCES: 208
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Ann W. Speckman
/ STREET: 2601 Elliott Avenue, Suite 4185
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/095,855
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/705,347
/ FILING DATE: 29-AUG-1996
/ APPLICATION NUMBER: 08/873,970
/ FILING DATE: 12-JUN-1997
/ APPLICATION NUMBER: 08/997,362
/ FILING DATE: 23-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1002c3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 927 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-09-095-855-116
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Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCCCGGATCTTGT 145

RESULT 10

US-09-324-542-116/c
; Sequence 116, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; EARLIER FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-324-542-116.

Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCCCGGATCTTGT 145

RESULT 11

US-09-205-426-116/c
; Sequence 116, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-116

Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.79;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCCCGGATCTTGT 145

RESULT 12

US-08-997-080-161/c
; Sequence 161, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-997-080-161

Query Match 100.0%; Score 21.6; DB 2; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 167 TGAAGGTGCCCGGATCTTGT 146

RESULT 13

US-08-997-362-161/c
; Sequence 161, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194

```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-161

Query Match 100.0%; Score 21.6; DB 2; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
Db 167 TGAAGGTGCCRCGGATCTTGTT 146

RESULT 14
US-09-855-855-161/c
; Sequence 161, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TREATMENT OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:

;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-161

Query Match 100.0%; Score 21.6; DB 2; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
Db 167 TGAAGGTGCCRCGGATCTTGTT 146

RESULT 15
US-09-324-542-161/c
; Sequence 161, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; OF IMMUNOLOGICALLY-MEDIATED SKIN DISORDERS
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-161

Query Match 100.0%; Score 21.6; DB 3; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGTT 22
Db 167 TGAAGGTGCCRCGGATCTTGTT 146

RESULT 16
US-09-205-426-161/c
; Sequence 161, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
```

; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; TYPE: DNA
; LENGTH: 985
; ORGANISM: Mycobacterium vaccae
US-09-205-426-161

Query Match 100.0%; Score 21.6; DB 3; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
DB 167 TGAAGTGCCRCGGATCTTGT 146

RESULT 17

US-08-997-080-113/c
; Sequence 113, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; CORRESPONDENCE ADDRESS: 194
; STREET: Law Offices of Ann W. Speckman
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 37,007
; FILING DATE: 1997
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-080-113

Query Match 100.0%; Score 21.6; DB 2; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 18

US-08-997-362-113/c
; Sequence 113, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; STREET: Law Offices of Ann W. Speckman
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-997-362-113

Query Match 100.0%; Score 21.6; DB 2; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 19

US-09-095-855-113/c

; Sequence 113, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-095-855-113

Query Match 100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 808 TGAAGTGCCCGGATCTTGT 787

RESULT 20
US-09-324-542-113/c
; Sequence 113, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080

; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-324-542-113

Query Match 100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 808 TGAAGTGCCCGGATCTTGT 787

RESULT 21
US-09-205-426-113/c
; Sequence 113, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-113

Query Match 100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
DB 808 TGAAGTGCCCGGATCTTGT 787

RESULT 22
US-09-613-303-3/c
; Sequence 3, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623

;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: fusion sequence
;; NAME/KEY: CDS
;; LOCATION: (1)...(1620)
US-09-613-303-3

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGTT 22
|||||||:|||||||
DB 808 TGAAGTGCCCGGATCTTGTT 787

RESULT 23

US-10-267-311-3/c
; Sequence 3, Application US/10267311
; Patent No. 6657055

;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Marvin

;; APPLICANT: Chu, N. Randall

;; APPLICANT: Mizzen, Lee A.

;; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
;; FILE REFERENCE: 12071/002001

;; CURRENT APPLICATION NUMBER: US/10/267,311
;; CURRENT FILING DATE: 2002-10-09

;; PRIOR APPLICATION NUMBER: US/09/613,303

;; PRIOR FILING DATE: 2000-07-10

;; PRIOR APPLICATION NUMBER: US 60/143,757

;; PRIOR FILING DATE: 1999-07-08

;; NUMBER OF SEQ ID NOS: 55

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3

;; LENGTH: 1623

;; TYPE: DNA

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: fusion sequence

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (1)...(1620)

US-10-267-311-3

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGTT 22
|||||||:|||||||
DB 808 TGAAGTGCCCGGATCTTGTT 787

RESULT 24

US-09-712-363-23/c
; Sequence 23, Application US/09712363
; Patent No. 6892139

;; GENERAL INFORMATION:

;; APPLICANT: Eisenberg, David

;; APPLICANT: Rotstein, Sergio H.

;; APPLICANT: Marcotte, Edward M.

;; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

;; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

;; FILE REFERENCE: 07419-032001

;; CURRENT APPLICATION NUMBER: US/09/712,363

;; CURRENT FILING DATE: 2000-11-13

;; PRIOR APPLICATION NUMBER: PCT/US00/02246

;; PRIOR FILING DATE: 2000-01-28

;; PRIOR APPLICATION NUMBER: 60/179,531

;; PRIOR FILING DATE: 2000-02-01

;; PRIOR APPLICATION NUMBER: 60/117,844

;;

;;

;;

;;

;;

;;

;; PRIOR FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: 60/118,206,
;; PRIOR FILING DATE: 1999-02-01
;; PRIOR APPLICATION NUMBER: 60/126,593
;; PRIOR FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: 60/134,093
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/134,092
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/165,124
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/165,086
;; PRIOR FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 292
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 23

;; LENGTH: 1623

;; TYPE: DNA

;; ORGANISM: Mycobacterium tuberculosis

US-09-712-363-23

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGTT 22
|||||||:|||||||
DB 808 TGAAGTGCCCGGATCTTGTT 787

RESULT 25

US-08-997-080-159/c

;; Sequence 159, Application US/08997080

;; Patent No. 5968524

;; GENERAL INFORMATION:

;; APPLICANT: WATSON, JAMES D.

;; APPLICANT: TAN, PAUL L.J.

;; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-

;; NUMBER OF SEQUENCES: 194

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Law Offices of Ann W. Speckman

;; STREET: 2601 Elliott Avenue, Suite 4185

;; CITY: Seattle

;; STATE: WA

;; COUNTRY: USA

;; ZIP: 98121

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq for Windows Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/997,080

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Sleath, Janet

;; REGISTRATION NUMBER: 37,007

;; REFERENCE/DOCKET NUMBER: 11000.1007

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 206-269-0565

;; TELEFAX: 206-269-0563

;; TELEX:

;; INFORMATION FOR SEQ ID NO: 159:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 1626 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

US-08-997-080-159

Query Match 100.0%; Score 21.6; DB 2; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 26
US-08-997-362-159/c
; Sequence 159, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Marget
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 23-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-997-362-159

Query Match 100.0%; Score 21.6; DB 2; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 27
US-09-095-855-159/c
; Sequence 159, Application US/09095855

; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Marget
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITL OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 23-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-095-855-159

Query Match 100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 28
US-09-324-542-159/c
; Sequence 159, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITL OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-324-542-159

Query Match 100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 29

US-09-205-426-159/c
; Sequence 159, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002e4
; CURRENT APPLICATION NUMBER: US/09/205,426
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-159.

Query Match 100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.84;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 30

US-09-613-303-16/c
; Sequence 16, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-09-613-303-16

Query Match 100.0%; Score 21.6; DB 3; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 31

US-10-267-311-16/c
; Sequence 16, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Chu, N. Randall
; APPLICANT: Siegel, Marvin
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-267-311-16

Query Match 100.0%; Score 21.6; DB 3; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 32

US-09-613-303-28/c
; Sequence 28, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
;
US-09-613-303-28
Query Match 100.0%; Score 21.6; DB 3; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1132 TGAAGTGCCRCGGATCTTGT 1111

RESULT 33
US-10-267-311-28/c
; Sequence 28, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
; OTHER INFORMATION: fusion sequence
;
US-10-267-311-28
Query Match 100.0%; Score 21.6; DB 3; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.86;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1132 TGAAGTGCCRCGGATCTTGT 1111

RESULT 34
US-10-068-059-9/c
; Sequence 9, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Siegel, Marvin
; APPLICANT: Hongwei, Liu
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
;
US-10-068-059-9
Query Match 100.0%; Score 21.6; DB 3; Length 2073;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1258 TGAAGTGCCRCGGATCTTGT 1237

RESULT 35
US-10-068-059-7/c
; Sequence 7, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
;
US-10-068-059-7
Query Match 100.0%; Score 21.6; DB 3; Length 2130;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 1315 TGAAGTGCCRCGGATCTTGT 1294

RESULT 36
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: fusion protein
;
US-10-068-059-11
```

; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 21.6; DB 3; Length 2175;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 1360 TGAAGTGCCCGGATCTTGT 1339

RESULT 37

US-10-068-059-5/c
; Sequence 5, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 21.6; DB 3; Length 2241;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 1426 TGAAGTGCCCGGATCTTGT 1405

RESULT 38

US-09-613-303-20/c
; Sequence 20, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-09-613-303-20

Query Match 100.0%; Score 21.6; DB 3; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.9;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 868 TGAAGTGCCCGGATCTTGT 847

RESULT 39

US-10-267-311-20/c
; Sequence 20, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match 100.0%; Score 21.6; DB 3; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.9;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 868 TGAAGTGCCCGGATCTTGT 847

RESULT 40

US-08-955-565A-3/c
; Sequence 3, Application US/08955565A
; Patent No. 6331388
; GENERAL INFORMATION:
; APPLICANT: Malkovsky, Miroslav
; APPLICANT: Wells, Andrew
; TITLE OF INVENTION: Immune Response Enhancer Therapy
; FILE REFERENCE: WARF-02625
; CURRENT APPLICATION NUMBER: US/08/955,565A
; CURRENT FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4380
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-08-955-565A-3

Query Match 100.0%; Score 21.6; DB 3; Length 4380;
Best Local Similarity 95.5%; Pred. No. 0.94;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22
|||||:|||||:|||||:|||||
Db 1059 TGAAGTGCCCGGATCTTGT 1038

```
RESULT 41
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 100.0%; Score 21.6; DB 3; Length 4403765;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGATCTTGT 22
Db 530855 TGAAGTGCCGCGATCTTGT 530834

RESULT 42
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 100.0%; Score 21.6; DB 3; Length 4411529;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGATCTTGT 22
Db 529413 TGAAGTGCCGCGATCTTGT 529392

RESULT 43
US-09-634-238-67/c
; Sequence 67, Application US/09634238
; Patent No. 6544772
```

```
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; US-09-634-238-67

Query Match 92.6%; Score 20; DB 3; Length 732;
Best Local Similarity 90.9%; Pred. No. 4.5;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGATCTTGT 22
Db 229 TGAAGTGCCGCGATCTTGT 208

RESULT 44
US-08-461-775-8/c
; Sequence 8, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
```

;
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1320
US-08-461-775-8

Query Match 92.6%; Score 20; DB 2; Length 1320;
Best Local Similarity 90.9%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
||| |||||:|||||
DB 814 TGAACGTGCGCGGATCTTGT 793

RESULT 45
US-09-031-606-8/c
; Sequence 8, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1320
US-09-031-606-8

Query Match 92.6%; Score 20; DB 3; Length 1320;
Best Local Similarity 90.9%; Pred. No. 4.8;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
||| |||||:|||||
DB 814 TGAACGTGCGCGGATCTTGT 793

RESULT 46
US-08-461-775-10/c
; Sequence 10, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1620
US-08-461-775-10

Query Match 92.6%; Score 20; DB 2; Length 1620;
Best Local Similarity 90.9%; Pred. No. 4.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCGCGGATCTTGT 22
||| |||||:|||||
DB 814 TGAACGTGCGCGGATCTTGT 793

RESULT 47
US-09-031-606-10/c
; Sequence 10, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-09-031-606-10

Query Match 92.6%; Score 20; DB 3; Length 1620;
Best Local Similarity 90.9%; Pred. No. 4.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 814 TGAACGTGCGCGGATCTTGT 793

RESULT 48
US-08-461-775-9/c
Sequence 9, Application US/08461775
Patent No. 5858773
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,775
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-461-775-9

Query Match 92.6%; Score 20; DB 2; Length 2167;
Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 1662 TGAACGTGCGCGGATCTTGT 1641

RESULT 49
US-09-031-606-9/c
Sequence 9, Application US/09031606
Patent No. 6153404
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 2167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-031-606-9

Query Match 92.6%; Score 20; DB 3; Length 2167;
Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 1662 TGAACGTGCCGGATCTTGT 1641

RESULT 50

US-08-461-775-11/c
; Sequence 11, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-461-775-11

Query Match 92.6%; Score 20; DB 2; Length 2668;
Best Local Similarity 90.9%; Pred. No. 5.2;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 1662 TGAACGTGCCGGATCTTGT 1641

RESULT 51

US-09-031-606-11/c
; Sequence 11, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-031-606-11

Query Match 92.6%; Score 20; DB 3; Length 2668;
Best Local Similarity 90.9%; Pred. No. 5.2;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 1662 TGAACGTGCCGGATCTTGT 1641

RESULT 52

US-09-470-191-60
; Sequence 60, Application US/09470191
; Patent No. 6465833
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods of Their Use in
; TITLE OF INVENTION: the Treatment, Prevention and Diagnosis of Tuberculosis
; FILE REFERENCE: 014058-00891005
; CURRENT APPLICATION NUMBER: US/09/470,191
; PRIOR FILING DATE: 1999-12-23
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113,952
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 706

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 1662 TGAACGTGCCGGATCTTGT 1641

```
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)...(706)
; OTHER INFORMATION: n = any nucleotide
US-09-470-191-60

Query Match          90.7%; Score 19.6; DB 3; Length 706;
Best Local Similarity 95.0%; Pred. No. 7;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGGATCTTGT 22
Db 608 AAGTGCCRCGGATCTTGT 627

RESULT 53
US-09-583-110-1024/c
; Sequence 1024, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1024
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1024

Query Match          85.2%; Score 18.4; DB 3; Length 1623;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 54
US-09-613-303-50/c
; Sequence 50, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
US-09-613-303-50/c

Query Match          85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 55
US-10-267-311-50/c
; Sequence 50, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
US-10-267-311-50

Query Match          85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 56
US-08-961-527-77/c
; Sequence 77, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
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```
; LOCATION: (1)...(1923)
US-09-613-303-50

Query Match          85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 55
US-10-267-311-50/c
; Sequence 50, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
US-10-267-311-50

Query Match          85.2%; Score 18.4; DB 3; Length 1926;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 808 TGAAGGTTCCACGAATCTTGT 787

RESULT 56
US-08-961-527-77/c
; Sequence 77, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
```


; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5365 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-77

Query Match 85.2%; Score 18.4; DB 3; Length 5365;
Best Local Similarity 86.4%; Pred. No. 33;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
Db 1085 TGAAGTTCACGATCTTGT 1064

RESULT 57
US-10-729-7/c
; Sequence 7, Application US/10105729
; Patent No. 6911331
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Lightner, Johathan E.
; TITLE OF INVENTION: CHORISMATE BIOSYNTHESIS ENZYMES
; FILE REFERENCE: BB1159 US CIP
; CURRENT APPLICATION NUMBER: US/10/105,729
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/743,210
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Glycine max
US-10-105-729-7

Query Match 80.6%; Score 17.4; DB 3; Length 1844;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
Db 513 GAAGGTGTACGGATGTGT 493

RESULT 58
US-10-729-1/c
; Sequence 1, Application US/10105729
; Patent No. 6911331
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Lightner, Johathan E.
; TITLE OF INVENTION: CHORISMATE BIOSYNTHESIS ENZYMES
; FILE REFERENCE: BB1159 US CIP
; CURRENT APPLICATION NUMBER: US/10/105,729
; CURRENT FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: 09/743,210
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Zea mays
US-10-105-729-1

Query Match 80.6%; Score 17.4; DB 3; Length 2003;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
Db 562 GAAGGTGTACGGATGTGT 542

RESULT 59
US-09-620-312D-383/c
; Sequence 383, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 383
; LENGTH: 4352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3675)
US-09-620-312D-383

Query Match 78.7%; Score 17; DB 3; Length 4352;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTG 20
Db 2943 GAAGTCCCATGGATCTTG 2925

RESULT 60

US-09-107-433-1679/c
; Sequence 1679, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1679:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...966
; SEQUENCE DESCRIPTION: SEQ ID NO: 1679:
US-09-107-433-1679

Query Match 77.8%; Score 16.8; DB 3; Length 966;
Best Local Similarity 81.8%; Pred. No. 1.6e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
|||||
DB 151 TGAAGGTTCACGAATATTGT 130
|||||

Search completed: April 1, 2006, 17:06:39
Job time : 24.7069 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 21:55:10 ; Search time 44.7112 Seconds
(without alignments)
3279.340 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaagtgccrcggatcttgg 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1980s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	100.0	22	14	ADV99122
2	21.6	100.0	337	2	AAV34588
3	21.6	100.0	337	2	AAZ11322
4	21.6	100.0	337	6	ABL36228
5	21.6	100.0	852	4	AAH21760
6	21.6	100.0	927	2	AAV34610
7	21.6	100.0	927	2	AAZ11345
8	21.6	100.0	927	6	ABL36251
9	21.6	100.0	985	2	AAZ11372
10	21.6	100.0	985	6	ABL36278
11	21.6	100.0	985	8	ACC42533
12	21.6	100.0	1496	13	ADW23618
13	21.6	100.0	1569	2	AAV34608
14	21.6	100.0	1569	2	AAZ11343
15	21.6	100.0	1569	6	ABL36249
16	21.6	100.0	1589	4	AAH21763
17	21.6	100.0	1620	8	ACA38272
18	21.6	100.0	1620	13	ADR12623
19	21.6	100.0	1623	4	AAH51969

C 20	21.6	100.0	1623	5	AAF25002
C 21	21.6	100.0	1623	8	ACA40326
C 22	21.6	100.0	1623	8	ACA37725
C 23	21.6	100.0	1623	12	ADN11336
C 24	21.6	100.0	1626	2	AAZ11371
C 25	21.6	100.0	1626	6	ABL36277
C 26	21.6	100.0	1626	8	ACC42531
C 27	21.6	100.0	1626	9	ACC70275
C 28	21.6	100.0	1626	12	ADO51196
C 29	21.6	100.0	1626	12	ADO50828
C 30	21.6	100.0	1626	13	ADS64696
C 31	21.6	100.0	1638	8	ACA29800
C 32	21.6	100.0	1644	5	AAH67951
C 33	21.6	100.0	1647	2	AAAT14265
C 34	21.6	100.0	1701	9	AAAD57198
C 35	21.6	100.0	1752	8	ACC49833
C 36	21.6	100.0	1761	14	ADX05272
C 37	21.6	100.0	1800	10	ADK68629
C 38	21.6	100.0	1914	8	ACC49834
C 39	21.6	100.0	1920	5	AAF25012
C 40	21.6	100.0	1947	5	AAF25019
C 41	21.6	100.0	1965	13	ADM23606
C 42	21.6	100.0	1980	12	ADN00588
C 43	21.6	100.0	2016	12	ADK72374
C 44	21.6	100.0	2073	6	ABS54448
C 45	21.6	100.0	2130	6	ABS54447
C 46	21.6	100.0	2175	6	ABS54449
C 47	21.6	100.0	2241	6	ABS54446
C 48	21.6	100.0	2847	5	AAF25014
C 49	21.6	100.0	4260	1	AAH81768
C 50	21.6	100.0	4380	1	AAH80222
C 51	21.6	100.0	4380	2	AAV05708
C 52	21.6	100.0	4380	6	ABA99141
C 53	21.6	100.0	86114	6	ABX09143
C 54	21.6	100.0	110000	4	AAI99682_05
C 55	21.6	100.0	110000	4	AAI99683_05
C 56	21.6	100.0	349980	5	AAH68533
C 57	20	92.6	732	12	ADI67068
C 58	20	92.6	1320	2	AAQ22481
C 59	20	92.6	1620	2	AAQ22482
C 60	20	92.6	1626	8	ACA39632

ALIGNMENTS

RESULT 1

ADV99122
ID ADV99122 standard; DNA; 22 BP.

XX AC ADV99122;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene forward primer, STGROR2, SEQ ID 2.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; PCR; primer; ss.
XX OS Streptomyces sp.
XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

```

XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
XX or purifying natural products using such microorganisms.
XX
XX Claim 2; SEQ ID NO 2; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
XX STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX Potato scab is a pathogenic disease caused by certain Streptomyces
XX species. Primers ADV99121 and ADV99122 are useful in a method for
XX identifying Streptomyces species, comprising amplifying groEL2 gene
XX fragment of target strain, analyzing the nucleotide sequence of groEL2
XX gene fragment amplified, and comparing the nucleotide sequence obtained
XX with that of groEL2 gene fragment of a reference strain.
XX
XX Sequence 22 BP; 3 A; 4 C; 7 G; 7 T; 0 U; 1 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 14; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 1.3;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TGAAGTGCCRCGGATCTTGTT 22
DB 1 TGAAGTGCCRCGGATCTTGTT 22
XX
RESULT 2
AAV34588/c
ID AAV34588 standard; DNA; 337 BP.
XX
XX AAV34588;
XX
XX 25-AUG-1998 (first entry)
XX
XX M. vaccae GroEL-homologue clone GV-27 partial DNA sequence.
XX
XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
XX M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
XX mycobacteria infection; vaccine; cancer; ss.
XX
XX Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
XX CDS 1..336
XX /*tag= a
XX /product= "M. vaccae antigen GV-27 partial sequence"
XX /note= "the start and stop codons are not indicated"
XX
XX WO9808542-A2.
XX
XX 05-MAR-1998.
XX
XX 28-AUG-1997; 97WO-NZ000105.
XX
XX 29-AUG-1996; 96US-00705347.
XX 12-JUN-1997; 97US-00873970.
XX
XX (GENE-) GENESIS RES & DEV CORP.
XX
XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
XX P-PSDB; AAW60130.
XX
XX Mycobacterium vaccae polypeptides - used to develop products for use in
XX detection, therapy and prevention of mycobacteria infections or as immune
XX response enhancers.
XX
XX
XX Example 6; Page 97; 153pp; English.
XX
XX This is the partial DNA sequence of a Mycobacterium vaccae GroEL-
XX homologue clone GV-27. The invention provides M. vaccae polypeptides that
XX comprise an immunogenic portion of a soluble M. vaccae antigen, or a
XX variant, where the antigen induces an immune response in patients
XX previously exposed to a mycobacterium. Such M. vaccae polypeptides can be
XX used in methods for enhancing non-specific immune response. The methods
XX and products can be used for the detection, treatment and prevention of
XX infectious diseases caused by mycobacteria such as M. vaccae, M. avium or
XX M. tuberculosis. The products also have the ability to induce cell
XX proliferation and cytokine production (e.g. interferon-gamma and
XX interleukin-12 production) in T cells, NK cells, B cells, or macrophages.
XX They can be used for enhancing immune responses for use in vaccines or
XX immunotherapy of infectious diseases and cancers
XX
XX Sequence 337 BP; 60 A; 112 C; 108 G; 57 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 2; Length 337;
XX Best Local Similarity 95.5%; Pred. No. 1.8;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TGAAGTGCCRCGGATCTTGTT 22
DB 166 TGAAGTGCCRCGGATCTTGTT 145
XX
RESULT 3
AAZ11322/c
ID AAZ11322 standard; DNA; 337 BP.
XX
XX AAZ11322;
XX
XX 25-OCT-1999 (first entry)
XX
XX M. vaccae GroEL-homologue clone GV-27 DNA sequence.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
XX dendritic cell maturation; infectious disease; immune disorder; cancer;
XX respiratory system; mycobacterial infection; allergy; tuberculosis;
XX leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
XX dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
XX squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
XX
XX WO932634-A2.
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
XX 23-DEC-1997; 97US-00997080.
XX 23-DEC-1997; 97US-00997362.
XX 11-JUN-1998; 98US-00095855.
XX 17-SEP-1998; 98US-00156181.
XX 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI; 1999-430163/36.
XX P-PSDB; AAY14876.
XX
XX Enhancing immune response to an antigen.
XX
XX Example 14; Page 175; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
XX M. vaccae proteins. The M. vaccae proteins may be employed to activate T
XX cells and natural killer cells, to stimulate the production of cytokines,
XX

```

CC to enhance the expression of co-stimulatory molecules on dendritic cells
 CC and monocytes, and to enhance dendritic cell maturation and function. The
 CC proteins can be expressed by standard recombinant methodology.
 CC Pharmaceutical compositions comprising the proteins or nucleic acid
 CC sequences encoding the proteins can be used for the treatment,
 CC prevention, and detection of disorders including infectious diseases,
 CC immune disorders and cancer. In particular, the compounds and methods are
 CC used for treatment of diseases of the respiratory system, such as
 CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
 CC sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma

SQ Sequence 337 BP; 60 A; 112 C; 108 G; 57 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 2; Length 337;
 Best Local Similarity 95.5%; Pred. No. 1.8;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
 |||||:|||||
 DB 166 TGAAGTGCRCGGATCTTGT 145

RESULT 4
 ABL36228/c
 ID ABL36228 standard; DNA; 337 BP.

XX ABL36228;

XX 08-APR-2002 (first entry)

XX M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 77.

XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
 KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
 KW Th2 immune response; immunomodulatory; gene; ds.

XX Mycobacterium vaccae.

XX US6328978-B1.

XX 11-DEC-2001.

XX 02-JUN-1999; 99US-00324542.

XX 23-DEC-1997; 97US-00997080.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Tan PLJ, Prestidge R;

XX WPI; 2002-138361/18.

DR P-PSDB; ABB73482.

XX Inhibiting skin inflammation associated with skin disorder e.g.
 PT psoriasis, by administering composition comprising delipidated and
 PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
 PT culture filtrate.

XX Example 4; Col 95-98; 116pp; English.

XX The present invention relates to a method of inhibiting skin inflammation
 CC associated with a skin disorder selected from psoriasis, atopic
 CC dermatitis and allergic contact dermatitis, which involves administering
 CC a composition containing delipidated and deglycolipidated Mycobacterium
 CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
 CC treated may also include alopecia areata, and skin cancers such as basal
 CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
 CC acts by inhibiting the Th2 immune response. The present sequence is a
 CC coding sequence described in the exemplification of the invention

XX SQ Sequence 337 BP; 60 A; 112 C; 108 G; 57 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 6; Length 337;
 Best Local Similarity 95.5%; Pred. No. 1.8;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
 |||||:|||||
 DB 166 TGAAGTGCRCGGATCTTGT 145

RESULT 5

AAH21760/c

ID AAH21760 standard; DNA; 852 BP.

XX AC AAH21760;

XX 14-AUG-2001 (first entry)

XX Corynebacterium glutamicum chaperonin groEL nucleotide sequence SEQ:34.

XX Corynebacterium glutamicum; chaperone; chaperonin; CpxB; groEL;
 KW fermentation; L-glutamic acid; thermophilic microbe; ds.

XX Corynebacterium glutamicum.

XX JP2001069979-A.

XX 21-MAR-2001.

XX 31-AUG-1999; 99JP-00245121.

XX 31-AUG-1999; 99JP-00245121.

XX (NISB) JAPAN TOBACCO INC.

PA (BEAB-) BE ABLE KK.

XX WPI; 2001-321175/34.

XX Preparation of L-glutamic acid by fermentation.

XX Example 1; Page 14; 18pp; Japanese.

XX The present invention describes an L-glutamic acid-producing microbe (I)
 CC or its mutant which expresses the molecular chaperone derived from a
 CC thermophilic microbe and produces stably L-glutamic acid at a temperature
 CC near the upper limit of optimum growth or higher. (I) or its mutant
 CC transformed by a recombinant DNA containing a gene encoding the molecular
 CC chaperone derived from a thermophilic microbe and a promoter operably
 CC associated with a gene (II) comprising: (a) a fully defined 1661 base
 CC pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a
 CC protein comprising: (i) a base sequence in which 1-20 bases are deleted,
 CC replaced or added in AAH21757; or (ii) at least one base is deleted,
 CC replaced or added in a fully defined 519 base sequence (AAH21768), and
 CC having molecular chaperone activity in (I). Also described is a method
 CC for the preparation of L-glutamic acid by fermentation in which the
 CC transformed (I) is used and cultured at a high temperature limiting the
 CC production of L-glutamic acid with the untransformed (I). The microbe can
 CC be used for the preparation of L-glutamic acid. The present sequence
 CC represents a nucleotide sequence of the Corynebacterium glutamicum
 CC chaperonin groEL, which is used in an example from the present invention

XX SQ Sequence 852 BP; 196 A; 217 C; 258 G; 181 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 4; Length 852;

Best Local Similarity 95.5%; Pred. No. 2;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22

|||||:|||||

DB 802 TGAAGTGCRCGGATCTTGT 781

```
RESULT 6
AAV34610/C
ID AAV34610 standard; DNA; 927 BP.
XX
AC AAV34610;
XX
XX 25-AUG-1998 (first entry)
XX
DE M. vaccae antigen GV-27B encoding DNA.
XX
XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW mycobacteria infection; vaccine; cancer; ss.
XX
OS Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
FH 1. .927
FT CDS
FT /*tag= a
FT /product= "GV-27B antigen"
FT /note= "The start and stop codons are not indicated"
XX
XX WO9808542-A2.
XX
XX 05-MAR-1998.
XX
XX 28-AUG-1997; 97WO-NZ000105.
XX
XX 29-AUG-1996; 96US-00705347.
XX 12-JUN-1997; 97US-00873970.
XX
XX (GENE-) GENESIS RES & DEV CORP.
XX
XX Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
XX P-PSDB; AAW60146.
XX
XX Mycobacterium vaccae polypeptides - used to develop products for use in
PT detection, therapy and prevention of mycobacteria infections or as immune
PT response enhancers.
XX
XX Example 6; Page 117; 153pp; English.
XX
XX This DNA encodes a Mycobacterium vaccae antigen GV-27B. The invention
CC provides M. vaccae polypeptides that comprise an immunogenic portion of a
CC soluble M. vaccae antigen, or a variant, where the antigen induces an
CC immune response in patients previously exposed to a mycobacterium. Such
CC M. vaccae polypeptides can be used in methods for enhancing non-specific
CC immune response. The methods and products can be used for the detection,
CC treatment and prevention of infectious diseases caused by mycobacteria
CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC the ability to induce cell proliferation and cytokine production (e.g.
CC interferon-gamma and interleukin-12 production) in T cells, NK cells, B
CC cells, or macrophages. They can be used for enhancing immune responses
CC for use in vaccines or immunotherapy of infectious diseases and cancers
XX
XX Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
DB 166 TGAAGGTGCCCGGATCTTGT 145
XX
RESULT 7
AAZ11345/C
ID AAZ11345 standard; DNA; 927 BP.
XX
XX
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AC AAZ11345;
XX
XX 25-OCT-1999 (first entry)
XX
DE Nucleotide sequence of M. vaccae antigen GV-27B.
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
XX
XX WO9932634-A2.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
XX 23-DEC-1997; 97US-00997080.
XX 23-DEC-1997; 97US-00997362.
XX 11-JUN-1998; 98US-00095855.
XX 17-SEP-1998; 98US-00156181.
XX 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI; 1999-430163/36.
XX P-PSDB; AAY14893.
XX
XX Enhancing immune response to an antigen.
XX
XX Example 14; Page 191; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC to enhance the expression of co-stimulatory molecules on dendritic cells
CC and monocytes, and to enhance dendritic cell maturation and function. The
CC proteins can be expressed by standard recombinant methodology.
CC Pharmaceutical compositions comprising the proteins or nucleic acid
CC sequences encoding the proteins can be used for the treatment,
CC prevention, and detection of disorders including infectious diseases,
CC immune disorders and cancer. In particular, the compounds and methods are
CC used for treatment of diseases of the respiratory system, such as
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma
XX
XX Query Match 100.0%; Score 21.6; DB 2; Length 927;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
DB 166 TGAAGGTGCCCGGATCTTGT 145
XX
RESULT 8
ABL36251/C
ID ABL36251 standard; DNA; 927 BP.
XX
XX ABL36251;
XX
```

DT 08-APR-2002 (first entry)
 DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 116.
 XX
 KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
 KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
 KW Th2 immune response; immunomodulatory; gene; ds.
 OS Mycobacterium vaccae.
 XX US6328978-B1.
 XX
 XX 11-DEC-2001.
 XX
 XX 02-JUN-1999; 99US-00324542.
 XX
 XX 23-DEC-1997; 97US-00997080.
 XX
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 XX Watson JD, Tan PLJ, Prestidge R;
 XX WPI: 2002-138361/18.
 XX P-PSDB; ABB73499.
 XX
 XX Inhibiting skin inflammation associated with skin disorder e.g.
 PT psoriasis, by administering composition comprising delipidated and
 PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
 PT culture filtrate.
 XX
 XX Example 4; Col 125-128; 116pp; English.
 XX
 CC The present invention relates to a method of inhibiting skin inflammation
 CC associated with a skin disorder selected from psoriasis, atopic
 CC dermatitis and allergic contact dermatitis, which involves administering
 CC a composition containing delipidated and deglycolipidated Mycobacterium
 CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
 CC treated may also include alopecia areata, and skin cancers such as basal
 CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
 CC acts by inhibiting the Th2 immune response. The present sequence is a
 CC coding sequence described in the exemplification of the invention
 XX
 SQ Sequence 927 BP; 157 A; 317 C; 317 G; 136 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 6; Length 927;
 Best Local Similarity 95.5%; Pred. No. 2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAAGTGCCGCGGATCTTGT 22
 Db 166 TGAAGTGCCGCGGATCTTGT 145
 RESULT 9
 AAZ11372/c
 ID AAZ11372 standard; DNA; 985 BP.
 XX
 XX AAZ11372;
 XX
 XX 25-OCT-1999 (first entry)
 DE Nucleotide sequence of M. vaccae antigen GV-27B.
 XX
 KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 KW squamous cell carcinoma; melanoma; ss.
 XX
 XX Mycobacterium vaccae.
 OS

PN WO9932634-A2.
 XX
 PD 01-JUL-1999.
 XX
 XX 23-DEC-1998; 98WO-NZ000189.
 PF
 XX 23-DEC-1997; 97US-00996624.
 PR 23-DEC-1997; 97US-00997080.
 PR 23-DEC-1997; 97US-00997362.
 PR 11-JUN-1998; 98US-00095855.
 PR 17-SEP-1998; 98US-00156181.
 PR 04-DEC-1998; 98US-00205426.
 XX
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
 XX WPI: 1999-430163/36.
 DR P-PSDB; AAY14910.
 DR
 XX
 XX Enhancing immune response to an antigen.
 PT
 XX
 XX Claim 3; Page 215; 243pp; English.
 PS
 XX
 CC The invention provides heat-killed Mycobacterium vaccae, or recombinant
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
 CC cells and natural killer cells, to stimulate the production of cytokines,
 CC to enhance the expression of co-stimulatory molecules on dendritic cells
 CC and monocytes, and to enhance dendritic cell maturation and function. The
 CC proteins can be expressed by standard recombinant methodology.
 CC Pharmaceutical compositions comprising the proteins or nucleic acid
 CC sequences encoding the proteins can be used for the treatment,
 CC prevention, and detection of disorders including infectious diseases,
 CC immune disorders and cancer. In particular, the compounds and methods are
 CC used for treatment of diseases of the respiratory system, such as
 CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
 CC sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma
 XX
 XX Sequence 985 BP; 167 A; 335 C; 339 G; 144 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 21.6; DB 2; Length 985;
 Best Local Similarity 95.5%; Pred. No. 2;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAAGTGCCGCGGATCTTGT 22
 Db 167 TGAAGTGCCGCGGATCTTGT 146
 RESULT 10
 ABL36278/c
 ID ABL36278 standard; DNA; 985 BP.
 XX
 XX ABL36278;
 XX
 XX 08-APR-2002 (first entry)
 DT
 XX
 DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 161.
 XX
 KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
 KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
 KW Th2 immune response; immunomodulatory; gene; ds.
 XX
 OS Mycobacterium vaccae.
 XX
 XX US6328978-B1.
 XX
 XX 11-DEC-2001.
 XX

```

PF 02-JUN-1999; 99US-00324542.
XX
PR 23-DEC-1997; 97US-00997080.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Prestidge R;
XX
DR WPI; 2002-138361/18.
XX
DR P-PSDB; ABB73516.
XX
XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
XX Example 4; Col 171-174; 116pp; English.
XX
XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC coding sequence described in the exemplification of the invention
XX
SQ Sequence 985 BP; 167 A; 335 C; 339 G; 144 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 167 TGAAGGTGCGCGGATCTTGT 146

RESULT 11
ID ACC42533/c
AC ACC42533;
XX
XX 26-AUG-2003 (first entry)
XX
XX Mycobacterium vaccae antigen GV-27B coding sequence, SEQ ID 16.
XX
XX Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
XX antidiabetic; antipruritic; dermatological; anti-inflammatory;
XX immune response; Notch signalling pathway; autoimmune disorder;
XX Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
XX apoptotic cell death; cell proliferation; gens; ds.
XX
XX Mycobacterium vaccae.
XX
XX Key Location/Qualifiers
XX CDS 2..985
XX /*tag= a
XX /partial
XX /product= "Antigen GV-27B"
XX /note= "No start codon given"
XX
XX WO2003013595-A1.
XX
XX 20-FEB-2003.
XX
XX 26-JUL-2002; 2002WO-NZ000135.
XX
XX 26-JUL-2001; 2001US-0308446P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Tan PLJ, Abernethy N;
XX
XX WPI; 2003-239567/23.
XX
XX P-PSDB; ABP70893.
XX
XX Methods for modulating immune responses by modulating the Notch signaling
PT and Toll-like receptor signaling pathways, and treating e.g. autoimmune
PT disorders.
XX
XX Claim 7; Page 109; 136pp; English.
XX
XX The present invention relates to methods for modulating immune responses
CC by modulating the Notch signalling and Toll-like receptor signalling
CC pathways using compositions comprising mycobacteria antigens (ACC42518-
CC ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
CC immune responses and treating e.g. autoimmune disorders (such as multiple
CC sclerosis, rheumatoid arthritis, Type 1 diabetes mellitus, psoriasis,
CC systemic lupus erythematosus, scleroderma), allergic disease and graft
CC rejection and also disorders characterised by undesired apoptotic cell
CC death or undesired cell proliferation
XX
SQ Sequence 985 BP; 167 A; 335 C; 339 G; 144 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 8; Length 985;
Best Local Similarity 95.5%; Pred. No. 2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
Db 167 TGAAGGTGCGCGGATCTTGT 146

RESULT 12
ID ADW23618/c
XX ADW23618 standard; DNA; 1496 BP.
XX
XX AC ADW23618;
XX
XX DT 10-MAR-2005 (first entry)
XX
XX DE HSP65 DNA.
XX
XX KW recombinant protein; vaccine; fusion protein; HSP65; ds.
XX
XX OS Unidentified.
XX
XX PN CN1462636-A.
XX
XX PD 24-DEC-2003.
XX
XX PF 30-MAY-2002; 2002CN-00122116.
XX
XX PR 30-MAY-2002; 2002CN-00122116.
XX
XX PA (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX
XX PI Wang L, Sun M, Yu Y;
XX
XX DR WPI; 2004-239553/23.
XX
XX PT Vaccine of recombinated albumen for preventing and treating infection of
XX human hepatitis C virus.
XX
XX PS Example 1; Page 14; 54pp; Chinese.
XX
XX The invention relates to a recombinant protein vaccine which is a fusion
CC protein of BCG vaccine's heat shock protein 65 and the core antigen of
CC multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
CC and nucleotide sequence for coding it, the expression carrier containing
CC a nucleotide sequence, the host cell containing expression carrier, the
CC preparing process of recombinant protein vaccine, the vaccine containing
CC recombinant protein for preventing and treating hepatitis C and a method

```


CC for detecting the activity of specifically killing T-lymphocytes by the
CC hepatitis C induced by vaccine and its cell model are disclosed. The
CC present sequence represents a HSP65 DNA.

XX Sequence 1496 BP; 300 A; 456 C; 523 G; 217 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 21.6; DB 13; Length 1496;
Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22

Db 666 TGAAGGTGCGCGGATCTTGT 645

RESULT 13

AAV34608/c

ID AAV34608 standard; DNA; 1569 BP.

XX

AC AAV34608;

XX

DT 25-AUG-1998 (first entry)

XX M. vaccae antigen GV-27 encoding DNA.

XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;

KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;

KW mycobacteria infection; vaccine; cancer; ss.

XX Mycobacterium vaccae.

XX

PH Key Location/Qualifiers

FT CDS 1..1569

FT /*tag= a

FT /product= "GV-27 antigen"

FT /note= "the stop codon is not indicated"

XX

XX

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XX

Query Match 100.0%; Score 21.6; DB 2; Length 1569;
Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22

Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 14

AAZ11343/c

ID AAZ11343 standard; DNA; 1569 BP.

XX

AC AAZ11343;

XX

DT 25-OCT-1999 (first entry)

XX

DE Nucleotide sequence of M. vaccae antigen GV-27.

XX

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;

KW dendritic cell maturation; infectious disease; immune disorder; cancer;

KW respiratory system; mycobacterial infection; allergy; tuberculosis;

KW leprosy; sarcoidosis; lung cancer; skin disorder; psoriasis;

KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;

KW squamous cell carcinoma; melanoma; ss.

XX

OS Mycobacterium vaccae.

XX

FN WO9932634-A2.

XX

PD 01-JUL-1999.

XX

PF 23-DEC-1998; 98WO-NZ000189.

XX

PR 23-DEC-1997; 97US-00996624.

PR 23-DEC-1997; 97US-00997080.

PR 23-DEC-1997; 97US-00997362.

PR 11-JUN-1998; 98US-00095855.

PR 17-SEP-1998; 98US-00156181.

PR 04-DEC-1998; 98US-00205426.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX

PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;

XX

DR WPI; 1999-430163/36.

XX

DR P-PSDB; AAY14891.

XX

PT Enhancing immune response to an antigen.

XX

PS Example 14; Page 188-189; 243pp; English.

XX

CC The invention provides heat-killed Mycobacterium vaccae, or recombinant

CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T

CC cells and natural killer cells, to stimulate the production of cytokines,

CC to enhance the expression of co-stimulatory molecules on dendritic cells

CC and monocytes, and to enhance dendritic cell maturation and function. The

CC proteins can be expressed by standard recombinant methodology.

CC Pharmaceutical compositions comprising the proteins or nucleic acid

CC sequences encoding the proteins can be used for the treatment,

CC prevention, and detection of disorders including infectious diseases,

CC immune disorders and cancer. In particular, the compounds and methods are

CC used for treatment of diseases of the respiratory system, such as

CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,

CC sarcoidosis and lung cancers, and disorders of the skin such as

CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,

CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell

CC carcinoma and melanoma

XX

SQ Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;

XX

XX

XX

XX

CC for detecting the activity of specifically killing T-lymphocytes by the
CC hepatitis C induced by vaccine and its cell model are disclosed. The
CC present sequence represents a HSP65 DNA.

XX Sequence 1496 BP; 300 A; 456 C; 523 G; 217 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 21.6; DB 13; Length 1496;
Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22

Db 666 TGAAGGTGCGCGGATCTTGT 645

RESULT 13

AAV34608/c

ID AAV34608 standard; DNA; 1569 BP.

XX

AC AAV34608;

XX

DT 25-AUG-1998 (first entry)

XX M. vaccae antigen GV-27 encoding DNA.

XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;

KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;

KW mycobacteria infection; vaccine; cancer; ss.

XX Mycobacterium vaccae.

XX

PH Key Location/Qualifiers

FT CDS 1..1569

FT /*tag= a

FT /product= "GV-27 antigen"

FT /note= "the stop codon is not indicated"

XX

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XX

Query Match 100.0%; Score 21.6; DB 2; Length 1569;
Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22

Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 14

AAZ11343/c

ID AAZ11343 standard; DNA; 1569 BP.

XX

AC AAZ11343;

XX

DT 25-OCT-1999 (first entry)

XX

DE Nucleotide sequence of M. vaccae antigen GV-27.

XX

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;

KW dendritic cell maturation; infectious disease; immune disorder; cancer;

KW respiratory system; mycobacterial infection; allergy; tuberculosis;

KW leprosy; sarcoidosis; lung cancer; skin disorder; psoriasis;

KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;

KW squamous cell carcinoma; melanoma; ss.

XX

OS Mycobacterium vaccae.

XX

FN WO9932634-A2.

XX

PD 01-JUL-1999.

XX

PF 23-DEC-1998; 98WO-NZ000189.

XX

PR 23-DEC-1997; 97US-00996624.

PR 23-DEC-1997; 97US-00997080.

PR 23-DEC-1997; 97US-00997362.

PR 11-JUN-1998; 98US-00095855.

PR 17-SEP-1998; 98US-00156181.

PR 04-DEC-1998; 98US-00205426.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

XX

PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;

XX

DR WPI; 1999-430163/36.

XX

DR P-PSDB; AAY14891.

XX

PT Enhancing immune response to an antigen.

XX

PS Example 14; Page 188-189; 243pp; English.

XX

CC The invention provides heat-killed Mycobacterium vaccae, or recombinant

CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T

CC cells and natural killer cells, to stimulate the production of cytokines,

CC to enhance the expression of co-stimulatory molecules on dendritic cells

CC and monocytes, and to enhance dendritic cell maturation and function. The

CC proteins can be expressed by standard recombinant methodology.

CC Pharmaceutical compositions comprising the proteins or nucleic acid

CC sequences encoding the proteins can be used for the treatment,

CC prevention, and detection of disorders including infectious diseases,

CC immune disorders and cancer. In particular, the compounds and methods are

CC used for treatment of diseases of the respiratory system, such as

CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,

CC sarcoidosis and lung cancers, and disorders of the skin such as

CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,

CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell

CC carcinoma and melanoma

XX

SQ Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;

XX

XX

XX

XX

Query Match 100.0%; Score 21.6; DB 2; Length 1569;
Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22

Db 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 14

AAZ11343/c

ID AAZ11343 standard; DNA; 1569 BP.

XX

AC AAZ11343;

XX

DT 25-OCT-1999 (first entry)

XX

DE Nucleotide sequence of M. vaccae antigen GV-27.

XX

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;

KW dendritic cell

```

Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 15
ABL36249/c
ID ABL36249 standard; DNA; 1569 BP.
XX
AC ABL36249;
XX
DT 08-APR-2002 (first entry)
XX
DE M vaccae GroEL homologue GV-27 partial coding sequence SEQ ID NO: 113.
XX
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipeptidic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; gene; ds.
XX
OS Mycobacterium vaccae.
XX
PN US6328978-B1.
XX
PD 11-DEC-2001.
XX
PF 02-JUN-1999; 99US-00324542.
XX
PR 23-DEC-1997; 97US-00997080.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Prestidge R;
XX
DR WPI; 2002-138361/18.
XX
P-PSDB; ABB73497.
XX
Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
Example 4; Col 121-124; 116pp; English.
XX
The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present invention is a
CC coding sequence described in the exemplification of the invention
XX
SQ Sequence 1569 BP; 292 A; 519 C; 531 G; 227 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 6; Length 1569;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 16
AAH21763/c
ID AAH21763 standard; DNA; 1589 BP.
XX
AC AAH21763;
XX

```

```

XX
DT 14-AUG-2001 (first entry)
XX
DE Corynebacterium glutamicum chaperonin groEL nucleotide sequence SEQ.34.
XX
KW Corynebacterium glutamicum; chaperone; chaperonin; CpxB; groEL;
KW fermentation; L-glutamic acid; thermophilic microbe; ds.
XX
OS Corynebacterium glutamicum.
XX
PN JP2001069979-A.
XX
PD 21-MAR-2001.
XX
PF 31-AUG-1999; 99JP-00245121.
XX
PR 31-AUG-1999; 99JP-00245121.
XX
PA (NIBS ) JAPAN TOBACCO INC.
PA (BEAB-) BE ABLE KK.
XX
DR WPI; 2001-321175/34.
XX
Preparation of L-glutamic acid by fermentation.
XX
Example 1; Page 15; 18pp; Japanese.
XX
The present invention describes an L-glutamic acid-producing microbe (I)
CC or its mutant which expresses the molecular chaperone derived from a
CC thermophilic microbe and produces stably L-glutamic acid at a temperature
CC near the upper limit of optimum growth or higher. (I) or its mutant
CC transformed by a recombinant DNA containing a gene encoding the molecular
CC chaperone derived from a thermophilic microbe and a promoter operably
CC associated with a gene (II) comprising: (a) a fully defined 1661 base
CC pair (bp) sequence (AAH21757); (b) a nucleic acid sequence encoding a
CC protein comprising: (i) a base sequence in which 1-20 bases are deleted,
CC replaced or added in AAH21757; or (ii) at least one base is deleted,
CC replaced or added in a fully defined 519 base sequence (AAH21768), and
CC having molecular chaperone activity in (I). Also described is a method
CC for the preparation of L-glutamic acid by fermentation in which the
CC transformed (I) is used and cultured at a high temperature limiting the
CC production of L-glutamic acid with the untransformed (I). The microbe can
CC be used for the preparation of L-glutamic acid. The present sequence
CC represents a nucleotide sequence of the Corynebacterium glutamicum
CC chaperonin groEL, which is used in an example from the present invention
XX
SQ Sequence 1589 BP; 363 A; 396 C; 469 G; 361 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 4; Length 1589;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 1533 TGAAGGTGCCCGGATCTTGT 1512

RESULT 17
ACA38272/c
ID ACA38272 standard; DNA; 1620 BP.
XX
AC ACA38272;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #19929.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Mycobacterium bovis.
XX
PN WO200277183-A2.

```

XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haeelbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU34402.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 26142; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 8; Length 1620;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787
RESULT 18
ADRI2623/c
ID ADRI2623 standard; DNA; 1620 BP.
XX
AC ADRI2623;

XX DT 04-NOV-2004 (first entry)
XX DE Gene vaccine nucleic acid #41.
XX XX
KW ds; gene; antimalarial; antitubercular; tuberculostatic; anti-HIV;
KW antibacterial; haemostatic; protozoicide; antiinflammatory;
KW neuroprotective; virucide; gene vaccine; ubiquitin; antigen;
KW intracellular parasite; protozoan parasite infection; malaria;
KW tuberculosis; toxoplasmosis; trypanosomiasis; AIDS;
KW cytomegalovirus infection; achlamydia disease; Rickettsia; leishmaniasis;
KW Ebola hemorrhagic fever; trypanosoma; Chagas disease;
KW Japanese encephalitis; influenza; rubella; dengue virus; poliomyelitis;
KW Herpes virus; severe acute respiratory syndrome.
XX
OS Unidentified.
XX
XX WO2004067040-A1.
XX
XX 12-AUG-2004.
XX PD
XX PF 30-JAN-2004; 2004WO-JP000975.
XX
XX 31-JAN-2003; 2003JP-00023507.
XX
XX (KYUS-) KYUSHU TLO CO LTD.
XX
XX Himeno K, Ishii K;
XX
XX WPI; 2004-594036/57.
XX P-PSDB; ADRI2624.
XX
XX Gene vaccine having nucleic acids encoding ubiquitin and antigen protein
PT of intracellular parasite, useful for treating parasite infections such
PT as malaria, tuberculosis, toxoplasmosis.
XX
XX Disclosure; SEQ ID NO 90; 266pp; Japanese.
XX
CC A gene vaccine (I) comprises nucleic acid sequence encoding ubiquitin,
CC and a nucleic acid sequence encoding the antigen protein of an
CC intracellular parasite containing T-cell target sequence. (I) is useful
CC for preventing or treating the disease resulting from intracellular
CC protozoan parasite infection such as malaria, tuberculosis,
CC toxoplasmosis, trypanosomiasis, AIDS, cytomegalovirus infection,
CC achlamydia disease, infections caused by Rickettsia, leishmaniasis,
CC Ebola hemorrhagic fever, Trypanosoma infections, Chagas disease, Japanese
CC encephalitis, influenza, rubella and dengue viral infections,
CC poliomyelitis, Herpes virus (alpha) infections, or severe acute
CC respiratory syndrome. This sequence represent a nucleic acid used in the
CC method of the invention.
XX
SQ Sequence 1620 BP; 321 A; 489 C; 571 G; 239 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 13; Length 1620;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787
RESULT 19
AAH51969/c
ID AAH51969 standard; DNA; 1623 BP.
XX
XX AAH51969;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 23.
XX
KW Drug target; growth; organism viability; characterisation; ds.

```
XX OS Mycobacterium tuberculosis.
XX PN WO200135317-A1.
XX PD 17-MAY-2001.
XX PF 13-NOV-2000; 2000WO-US031152.
XX PR 12-NOV-1999; 99US-0165086P.
XX PR 12-NOV-1999; 99US-0165124P.
XX PR 01-FEB-2000; 2000US-0179531P.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Eisenberg D, Rotstein SH, Marcotte EM;
XX DR WPI; 2001-329193/34.
XX DR P-PSDB; AAG81118.
XX PT Identifying nucleotide or polypeptide sequence for use as drug target,
XX PT involves providing algorithm that analyzes a functional relationship
XX PT between nucleotide or polypeptide sequences, and comparing the sequences.
XX PS Disclosure; Page 63-64; 207pp; English.
XX CC This invention relates to a method for identifying a nucleotide or
XX CC polypeptide sequence that may be a drug target, or essential for growth
XX CC or viability of an organism. Polynucleotide sequences AAG81947 - AAG82092
XX CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX CC tuberculosis proteins which are potential drug targets. The DNA and
XX CC protein sequences are used to illustrate the method of the invention. The
XX CC method involves providing an unknown nucleotide or polypeptide sequences,
XX CC and comparing it to a number of sequences along with at least one
XX CC algorithm capable of analysing a functional relationship between
XX CC nucleotide and polypeptide sequences. The method is useful for
XX CC characterising the function of nucleic acids and polypeptides that may be
XX CC useful as a target for a drug or essential for the growth or viability of
XX CC an organism
XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 4; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 20
AAF25002/c
ID AAF25002 standard; DNA; 1623 BP.
XX AC AAF25002;
XX DT 30-APR-2001 (first entry)
XX DE Nucleotide sequence of M. bovis BCG heat shock protein 65 (Hsp65).
XX KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
XX KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen; ss.
XX OS Mycobacterium bovis.
XX PH Key Location/Qualifiers
XX CDS 1..1623
XX FT /*tag= a
XX FT /product= "Hsp65"
XX PN WO200104344-A2.

18-JAN-2001.
XX 10-JUL-2000; 2000WO-US018828.
XX 08-JUL-1999; 99US-0143757P.
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX PI Siegel M, Chu NR, Mizzen LA;
XX DR WPI; 2001-138361/14.
XX DR P-PSDB; AAB31606.
XX PT Screening for compounds that stimulate Th1-like responses in CD4+ T
XX PT lymphocyte cells.
XX PS Example 2; Fig 1A-B; 88pp; English.
XX CC The present sequence encodes the Mycobacterium bovis BCG heat shock
XX CC protein (Hsp) 65. Hsp65 is used in the course of the invention. The
XX CC specification describes a method of determining whether a compound
XX CC stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
XX CC lymphocyte cells. The method comprises contacting naive lymphocytes in
XX CC vitro with a fusion protein comprising at least a fragment of Hsp, and
XX CC then detecting the Th1-like response exhibited by the cell sample. The
XX CC proteins which may be used in the method of the invention are Hsp65,
XX CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
XX CC compounds that stimulate Th1-like responses in response to microbial
XX CC pathogens
XX SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 5; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787

RESULT 21
ACA40326/c
ID ACA40326 standard; DNA; 1623 BP.
XX AC ACA40326;
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #21983.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW drug design; gene.
XX OS Mycobacterium tuberculosis.
XX PN WO200277183-A2.
XX DT 03-OCT-2002.
XX DE 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
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DR WPI; 2003-029926/02.
DR P-PSDB; ABU36456.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX
PS Claim 14; SEQ ID NO 28196; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 8; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCCGGATCTTGT 22
DB 808 TGAAGTGCCCGGATCTTGT 787
RESULT 22
ACA37725/c
ID ACA37725 standard; DNA; 1623 BP.
XX
AC ACA37725;
XX
XX 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #19382.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Mycobacterium avium.
XX
PN WO200277183-A2.
XX
XX 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US0009107.
XX
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PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU33855.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX
PS Claim 14; SEQ ID NO 25595; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1623 BP; 304 A; 545 C; 566 G; 208 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 8; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCCGGATCTTGT 22
DB 808 TGAAGTGCCCGGATCTTGT 787
RESULT 23
ADN11336/c
ID ADN11336 standard; DNA; 1623 BP.
XX
AC ADN11336;
XX
XX 17-JUN-2004 (first entry)
XX
DE Chaperonin 60.2 coding sequence.
XX
```

KW Analgesic; heat shock protein; pain relief; chaperonin 60.2; gene; ds.
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
FH 1. .1623
FT /*tag= a
FT /product= "Chaperonin 60.2"
XX
XX GB2391477-A.
XX
XX 11-FEB-2004.
XX
XX 05-NOV-2003; 2003GB-00025782.
XX
XX 08-NOV-2002; 2002GB-00026105.
XX
XX (HELP-) HELPERBY THERAPEUTICS LTD.
XX
XX Coates ARM;
XX
XX WPI; 2004-159054/16.
XX P-PSDB; ADN11337.
XX
XX Use of heat shock polypeptide and/or encoding nucleic acid sequence, in
XX manufacture of medicament for use in relief of pain such as backache,
XX headache, or earache.
XX
XX Claim 6; Fig 2; 39pp; English.
XX
XX The present invention relates to heat shock proteins (I) and their coding
XX sequences (II), which are useful in the manufacture of a medicament for
XX use in pain relief. (I) is a chaperonin derived from Mycobacterium
XX tuberculosis (ADN11335, ADN11337 or ADN11339). (I) and (II) are useful in
XX the manufacture of a medicament used as a pain relief, where the pain is
XX at least one chosen from backache, headache, toothache, earache,
XX arthritis, gout, soft tissue trauma, ligament/tendon traumatic damage,
XX broken bones, cancer, post operative pain, menstrual pain, obstetric
XX pain, renal tract pain, visceral pain, burns, abscesses and other
XX infections. The present sequence is a coding sequence for one such
XX chaperonin.
XX
XX Sequence 1623 BP; 322 A; 489 C; 572 G; 240 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 21.6; DB 12; Length 1623;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787
RESULT 24
AAZ11371/c
ID AAZ11371 standard; DNA; 1626 BP.
XX
XX AAZ11371;
XX
XX 25-OCT-1999 (first entry)
XX
XX Nucleotide sequence of M. vaccae antigen GV-27.
DE
XX
XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
XX dendritic cell maturation; infectious disease; immune disorder; cancer;
XX respiratory system; mycobacterial infection; allergy; tuberculosis;
XX leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
XX dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
XX squamous cell carcinoma; melanoma; ss.
XX
XX Mycobacterium vaccae.
OS
XX
XX W09932634-A2.
PN

XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-NZ000189.
XX
XX 23-DEC-1997; 97US-00996624.
PR 23-DEC-1997; 97US-00997080.
PR 23-DEC-1997; 97US-00997362.
PR 11-JUN-1998; 98US-00095855.
PR 17-SEP-1998; 98US-00156181.
PR 04-DEC-1998; 98US-00205426.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX WPI; 1999-430163/36.
DR P-PSDB; AAY14909.
XX
XX Enhancing immune response to an antigen.
XX
XX Claim 3; Page 212-213; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
XX M. vaccae proteins. The M. vaccae proteins may be employed to activate T
XX cells and natural killer cells, to stimulate the production of cytokines,
XX to enhance the expression of co-stimulatory molecules on dendritic cells
XX and monocytes, and to enhance dendritic cell maturation and function. The
XX proteins can be expressed by standard recombinant methodology.
XX Pharmaceutical compositions comprising the proteins or nucleic acid
XX sequences encoding the proteins can be used for the treatment,
XX prevention, and detection of disorders including infectious diseases,
XX immune disorders and cancer. In particular, the compounds and methods are
XX used for treatment of diseases of the respiratory system, such as
XX mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
XX sarcoidosis and lung cancer, and disorders of the skin such as
XX psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
XX alopecia areata, and skin cancers such as basal carcinoma, squamous cell
XX carcinoma and melanoma
XX
XX Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 21.6; DB 2; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCCGGATCTTGT 22
Db 808 TGAAGGTGCCCGGATCTTGT 787
RESULT 25
ABL36277/c
ID ABL36277 standard; DNA; 1626 BP.
XX
XX ABL36277;
XX
XX 08-APR-2002 (first entry)
XX
XX M vaccae GroEL homologue GV-27 coding sequence SEQ ID NO: 159.
DE
XX
XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
XX alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
XX antipsoriatic; dermatological; antinflammatory; antiallergic;
XX Th2 immune response; immunomodulatory; gene; ds.
XX
XX Mycobacterium vaccae.
XX
XX US6328978-B1.
PN
XX
XX 11-DEC-2001.
PD
XX
XX 02-JUN-1999; 99US-00324542.
PF

XX 23-DEC-1997; 97US-00997080.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX Watson JD, Tan PLJ, Prestidge R;
 XX WPI; 2002-138361/18.
 XX P-PSDB; ABB73515.
 XX Inhibiting skin inflammation associated with skin disorder e.g.
 XX psoriasis, by administering composition comprising delipidated and
 XX deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
 XX culture filtrate.
 XX Example 4; Col 167-170; 116pp; English.
 XX The present invention relates to a method of inhibiting skin inflammation
 XX associated with a skin disorder selected from psoriasis, atopic
 XX dermatitis and allergic contact dermatitis, which involves administering
 XX a composition containing delipidated and deglycolipidated Mycobacterium
 XX vaccae cells or M. vaccae culture filtrate. The skin disorder to be
 XX treated may also include alopecia areata, and skin cancers such as basal
 XX cell carcinoma, squamous cell carcinoma and melanoma. The composition
 XX acts by inhibiting the Th2 immune response. The present sequence is a
 XX coding sequence described in the exemplification of the invention
 XX
 XX Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 6; Length 1626;
 Best Local Similarity 95.5%; Pred. No. 2.1;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TGAAGTGCCTCCGCGGATCTTGT 22
 |||||
 DB 808 TGAAGTGCCTCCGCGGATCTTGT 787
 |||||
 RESULT 26
 ACC42531/c
 ID ACC42531 standard; DNA; 1626 BP.
 XX ACC42531;
 XX 26-AUG-2003 (first entry)
 XX Mycobacterium vaccae antigen GV-27 coding sequence, SEQ ID 14.
 XX Immunosuppressive; neuroprotective; antirheumatic; antiarthritic;
 XX antidiabetic; antipsoriatic; dermatological; anti-inflammatory;
 XX immune response; Notch signalling pathway; autoimmune disorder;
 XX Toll-like receptor signalling pathway; antigen; allergy; graft rejection;
 XX apoptotic cell death; cell proliferation; gene; ds.
 XX Mycobacterium vaccae.
 XX Key Location/Qualifiers
 XX CDS 1..1626
 XX /*tag= a
 XX /product= "Antigen GV-27"
 XX WO2003013595-A1.
 XX 20-FEB-2003.
 XX 26-JUL-2002; 2002WO-NZ000135.
 XX 26-JUL-2001; 2001US-0308446P.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX Watson JD, Tan PLJ, Abernethy N;
 XX

DR WPI; 2003-239567/23.
 DR P-PSDB; ABP70891.
 XX Methods for modulating immune responses by modulating the Notch signaling
 XX and Toll-like receptor signaling pathways, and treating e.g. autoimmune
 XX disorders.
 XX Claim 7; Page 108-109; 136pp; English.
 XX The present invention relates to methods for modulating immune responses
 XX by modulating the Notch signalling and Toll-like receptor signalling
 XX pathways using compositions comprising mycobacteria antigens (ACC42518-
 XX ACC42543 and ABP70878-ABP70903). The methods are useful for modulating
 XX immune responses and treating e.g. autoimmune disorders (such as multiple
 XX sclerosis, rheumatoid arthritis, Type I diabetes mellitus, psoriasis,
 XX systemic lupus erythematosus, scleroderma), allergic disease and graft
 XX rejection and also disorders characterised by undesired apoptotic cell
 XX death or undesired cell proliferation
 XX
 XX Sequence 1626 BP; 302 A; 537 C; 552 G; 235 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 8; Length 1626;
 Best Local Similarity 95.5%; Pred. No. 2.1;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TGAAGTGCCTCCGCGGATCTTGT 22
 |||||
 DB 808 TGAAGTGCCTCCGCGGATCTTGT 787
 |||||
 RESULT 27
 ACC70275/c
 ID ACC70275 standard; DNA; 1626 BP.
 XX ACC70275;
 XX 11-AUG-2003 (first entry)
 XX Nucleotide sequence of the Rhodococcus equi GroEL2 protein.
 XX GroEL protein; protein aggregation; protein folding; immune response;
 XX antigen; pathogenic infection; gene; ss.
 XX Rhodococcus equi.
 XX Key Location/Qualifiers
 XX CDS 1
 XX /*tag= a
 XX /product= "GroEL2"
 XX WO2003035676-A1.
 XX 01-MAY-2003.
 XX 25-OCT-2002; 2002WO-AU001460.
 XX 26-OCT-2001; 2001AU-00008523.
 XX (UYSA-) UNIV SOUTH AUSTRALIA.
 XX (MEDV-) MEDVET SCI PTY LTD.
 XX (RURA-) RURAL IND RES & DEV CORP.
 XX Vanniasinkam T, Barton M, Heuzenroeder MW;
 XX WPI; 2003-482030/45.
 XX P-PSDB; ABR55530.
 XX New GroEL protein, useful for preparing a composition for preventing or
 XX treating pathogenic infections.
 XX Disclosure; Fig 1; 77pp; English.
 XX The present sequence encodes a GroEL protein. The groEL2 gene is highly

CC conserved between species, and the protein facilitates the correct
CC folding of various bacterial proteins as well as prevent the aggregation
CC of denatured proteins by an ATP-dependent mechanism. The specification
CC describes a chimeric protein, consisting of a GroEL protein which has a
CC modification or analogue comprising a surface exposed exogenous amino
CC acid sequence inserted to it. The exogenous amino acid sequence is
CC configured to elicit an immune response specifically reactive to the
CC antigenic determinant. The chimeric protein is useful for preparing a
CC composition for preventing or treating pathogenic infections
XX

CC SQ Sequence 1626 BP; 300 A; 544 C; 549 G; 233 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 9; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGTT 22
Db 808 TGAAGGTGCCCGGATCTTGTT 787

RESULT 28
AD051196/c
ID AD051196 standard; DNA; 1626 BP.
AC AD051196;
XX
XX DT 12-AUG-2004 (first entry)
XX DE Staphylococcus coelicolor cpn60 gene.
XX KW Chaperonin 60; cpn60; microbe detection; gene; ds.
XX OS Staphylococcus coelicolor.
XX FH Key Location/Qualifiers
XX FT primer_bind /tag= a (244..269)
XX FT primer_bind /note= "Universal cpn60 primer binds at this location"
XX FT primer_bind 829..854
XX FT primer_bind /tag= b
XX FT primer_bind /note= "Universal cpn60 primer binds at this location"
XX PN US2004101826-A1.
XX PD 27-MAY-2004.
XX PF 18-MAR-2003; 2003US-00392041.
XX PR 27-NOV-2002; 2002US-00306113.
XX PA (JONE/) JONES A M.
XX PA (ROBE/) ROBEY W W.
XX PI Jones AM, Robey WW;
XX WPI; 2004-399671/37.
XX GENBANK; AL39121.
XX PT Monitoring high-risk environments for presence or absence of microbes, by
XX providing a sample and detecting presence or absence of cpn60 markers in
XX the sample, which indicates the presence of microbes.
XX PS Disclosure; SEQ ID NO 3; 30pp; English.
XX CC The invention relates to methods for monitoring high-risk environments
XX for the presence or absence of microbes by detecting the presence or
XX absence of chaperonin 60 (cpn60) marker in the sample. The method is
XX useful for monitoring the presence of one or more microbes such as
XX bacteria, protozoan microbe, fungi and rickettsiae microbe in high-risk
XX environment such as butcher shop, grocery store, restaurant, cafeteria,
XX convenience store, entertainment facility, school and medical
XX environment. The present sequence is Staphylococcus coelicolor cpn60

CC gene. This sequence is used to illustrate the method of the invention.
XX
XX SQ Sequence 1626 BP; 303 A; 585 C; 532 G; 206 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 12; Length 1626;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGTT 22
Db 814 TGAAGGTGCCCGGATCTTGTT 793

RESULT 29
AD050828/c
ID AD050828 standard; DNA; 1626 BP.
XX
XX AC AD050828;
XX DT 12-AUG-2004 (first entry)
XX DE S. coelicolor chaperonin protein 60, cpn60, gene.
XX KW Chaperonin protein 60; cpn60; ds; gene; GroEL; HSP60; heat shock protein;
XX KW food poisoning; animal processing operation; microbial load;
XX KW enteric bacteria; food-born illness.
XX OS Staphylococcus coelicolor.
XX PN US2004101917-A1.
XX PD 27-MAY-2004.
XX PF 21-MAR-2003; 2003US-00394763.
XX PR 27-NOV-2002; 2002US-00306113.
XX PA (ROBE/) ROBEY W W.
XX PA (JONE/) JONES A M.
XX PI Robey WW, Jones AM;
XX WPI; 2004-459891/43.
XX PT Management of an animal e.g. chicken processing operation comprises
XX determining microbial load of each biological sample from animal and
XX scheduling processing of the animals based on the microbial load.
XX PS Disclosure; SEQ ID NO 3; 21pp; English.
XX CC The invention relates to managing an animal processing operation
XX involving determining the microbial load, e.g. total number of enteric
XX bacteria of each biological sample, from animals and scheduling
XX processing of animals based on the microbial load. Scheduling comprises
XX ranking the animals from lowest to highest microbial load and integrating
XX the ranking with factors selected from number and weight of animals to be
XX processed, time of delivery etc. Also included are a system for
XX scheduling animals for processing and a computer readable storage medium
XX having instruction stored for causing a programmable processor to rank
XX animals from lowest to highest microbial load. The biological samples are
XX gastrointestinal tract sample (e.g. mucus, mucosal tissue and/or faeces)
XX or periodontal samples (e.g. blood, urine, saliva, sputum or semen). The
XX microbes are bacteria, protozoa or fungi. Scheduling comprises ranking
XX animals from lowest microbial load to highest microbial load and
XX integrating ranking with one or more factors selected from the group
XX consisting of number of animals to be processed, weight targets of
XX animals, proximity of animals to animal processing facility, and time of
XX delivery of animals to animal processing facility. The method further
XX comprises determining the microbial profile of each said biological
XX sample and scheduling processing of the plurality of animals based at
XX least in part on microbial load and microbial profile. Determining the
XX microbial profile comprises histological analysis, immunological
XX analysis, genetic fingerprinting, ribosomal genotyping, or cpn60

CC genotyping. The method can be used for any farmed animal that will be
CC subjected to mass processing. Effectively reduces human food-borne illness
CC i.e. food poisoning. Scheduling of animals minimises contamination during
CC the processing. The present sequence is an enteric bacteria cpn60
CC (Chaperonin protein 60 also known as Hsp60 and GroEL) gene used in the
CC method of the invention to genotype/identify enteric bacteria.

XX Sequence 1626 BP; 303 A; 585 C; 532 G; 206 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 21.6; DB 12; Length 1626;

Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22

DB 814 TGAAGTGCCCGGATCTTGT 793

RESULT 30

ADS64696/c

ID ADS64696 standard; DNA; 1626 BP.

XX AC

ADS64696;

XX DT

16-DEC-2004 (first entry)

XX DE

Streptomyces coelicolor cpn60 gene.

XX KW

GroEL; cpn60; hsp60; microbe detection; gene; ds.

XX OS

Streptomyces coelicolor.

XX FH

Key Location/Qualifiers

FT primer_bind complement(244..269)

FT /tag= a

FT primer_bind /note= "Universal cpn60 primer binds at this location"

FT 829..854

FT /tag= b

FT primer_bind /note= "Universal cpn60 primer binds at this location"

XX US2004185446-A1.

XX PD

23-SEP-2004.

XX PF

18-MAR-2003; 2003US-00392387.

XX PR

18-MAR-2003; 2003US-00392387.

XX (JONE/) JONES A M.

PA (ROBE/) ROBEY W W.

PA (HEMM/) HEMMINGSEN S.

PA (HILL/) HILL J.

PA (VKE/) VAN KESSEL A.

XX Jones AM, Robey WW, Hemmingesen S, Hill J, Van Kessel A;

XX WPI; 2004-676187/66.

DR GENBANK; AL939121.

XX Quantifying microbial species in a biological sample, comprises

FT subjecting the sample to amplification in the presence of cpn60 primers

FT and quantifying the amplified product, which correlates with the amount

PT of microbial species.

XX Disclosure; SEQ ID NO 3; 289p; English.

XX The invention relates to cpn60 (also known as hsp60 or GroEL) nucleic

CC acid-based methods for quantifying microbial species in a biological

CC sample. The method comprises subjecting the sample to amplification in

CC the presence of cpn60 primers and quantifying the amplified product,

CC which correlates with the amount of microbial species. The method is

CC useful for quantifying the amount of one or more microbial species in a

CC biological or non-biological sample. The present sequence is the

CC Streptomyces coelicolor cpn60 gene.

XX Sequence 1626 BP; 303 A; 585 C; 532 G; 206 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 21.6; DB 13; Length 1626;

Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCCGGATCTTGT 22

DB 814 TGAAGTGCCCGGATCTTGT 793

RESULT 31

ACA29800/c

ID ACA29800 standard; DNA; 1638 BP.

XX AC

ACA29800;

XX DT

19-JUN-2003 (first entry)

XX DE

Prokaryotic essential gene #11457.

XX KW

Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX OS

Corynebacterium diphtheriae.

XX PN

WO200277183-A2.

XX PD

03-OCT-2002.

XX PF

21-MAR-2002; 2002WO-US009107.

XX PR

21-MAR-2001; 2001US-00815242.

XX PR

06-SEP-2001; 2001US-00948993.

XX PR

25-OCT-2001; 2001US-0342923P.

XX PR

08-FEB-2002; 2002US-00072851.

XX PR

06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohleen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PADB; ABU25930.

XX New antisense nucleic acids, useful for identifying proteins or screening

FT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 17670; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1638 BP; 353 A; 418 C; 497 G; 370 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 8; Length 1638;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||
DB 823 TGAAGGTGCGCGGATCTTGTT 802

RESULT 32

AAH67951/c
ID AAH67951 standard; DNA; 1644 BP.

XX AAH67951;

XX 26-SEP-2001 (first entry)

DE C glutamicum coding sequence fragment SEQ ID NO: 2986.

XX Corynebacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EP1108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-00127688.

XX 16-DEC-1999; 99JP-00377484.

PR 07-APR-2000; 2000JP-00159162.

PR 03-AUG-2000; 2000JP-00280988.

XX (KYOWA) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI; 2001-376931/40.

DR P-PSDB; AAG92732.

XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.

XX Claim 8; SEQ ID NO 2986; 246pp + Sequence Listing; English.

CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of corynebacterium bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Corynebacterium bacterium, and identifying a homologue of a gene derived from
CC corynebacterium bacterium. Corynebacterium bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office

SQ Sequence 1644 BP; 346 A; 454 C; 500 G; 344 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 5; Length 1644;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGTT 22
|||||:|||||
DB 823 TGAAGTGCRCGGATCTTGTT 802

RESULT 33

AAT14265/c

ID AAT14265 standard; DNA; 1647 BP.

XX AAT14265;

XX 16-OCT-2003 (revised)

DT 16-SEP-1996 (first entry)

XX Brevibacterium flavum MJ-233 GroEL gene.

DE GroEL; coryneform bacteria; recombinant; chaperonin; protein; folding;
KW ds.

XX Brevibacterium flavum; MJ-233.

XX Key Location/Qualifiers

FT CDS 1..1650

FT /*tag= a

FT /product= "GroEL_protein"

XX JP08070873-A.

XX 19-MAR-1996.

XX 07-SEP-1994; 94JP-00213483.

XX 07-SEP-1994; 94JP-00213483.

XX (MITU) MITSUBISHI CHEM CORP.

XX WPI; 1996-203153/21.

DR P-PSDB; AAR94368.

XX DNA fragment contg. gene encoding GroEL protein - derived from Coryneform
PT bacteria, used for recombinant prodn. of GroEL protein and in genetic
PT engineering of bacteria.

XX Claim 5; Page 8-10; 11pp; Japanese.

XX AAT14265 is the GroEL gene derived from the coryneform bacterium,

CC Brevibacterium flavum strain MJ-233. The gene may be used for the

CC recombinant prodn. of the GroEL protein. The GroEL protein is a

CC chaperonin protein, the coryneform equivalent of hsp60, which ensures

CC that other cellular proteins are folded correctly. Fragments of the GroEL

CC gene are useful for genetic engineering of bacteria to increase activity,

CC extend life and increase the formation and secretion of an objective

CC protein. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 1647 BP; 349 A; 458 C; 497 G; 343 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 2; Length 1647;

Best Local Similarity 95.5%; Pred. No. 2.1;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGTT 22
|||||:|||||
DB 823 TGAAGTGCRCGGATCTTGTT 802

```
RESULT 34
AAD57198/c
ID AAD57198 standard; DNA; 1701 BP.
XX
XX AC AAD57198;
XX
XX DT 06-NOV-2003 (first entry)
XX
XX DE Mycobacterium avium subspecies paratuberculosis protein gene #11.
XX
XX KW Immunogenic fragment; vaccine; Map infection; wild-type infection;
XX KW antibacterial; gene; ds.
XX OS Mycobacterium avium.
XX
XX FH Key Location/Qualifiers
XX CDS 76..1701
XX FT /*tag= a
XX FT /product= "Protein"
XX
XX PN WO2003058248-A2.
XX
XX PD 17-JUL-2003.
XX
XX PF 13-JAN-2003; 2003WO-NL000020.
XX
XX PR 11-JAN-2002; 2002EP-00075089.
XX
XX PA (IDLE-) ID-LELYSTAD INST DIERHOUDRIJ EN DIERGEZ.
XX
XX PI Willemssen PTJ, Westerveen SP, Bakker D, Van Zijderveld FG;
XX PI Thole JER;
XX
XX DR WPI: 2003-598398/56.
XX DR P-PSDB; AAE37881.
XX
XX PT Novel Mycobacterium avium subspecies paratuberculosis protein, useful as
XX PT vaccine for combating the bacterial infection, and for diagnosing the
XX PT infection.
XX
XX PS Disclosure; Page 84-86; 88pp; English.
XX
XX CC The invention relates to Mycobacterium avium subspecies paratuberculosis
XX CC protein or an immunogenic fragment of the protein. The invention is
XX CC useful in the manufacture of a vaccine for combating Map infection. The
XX CC nucleic acids, the proteins and antibodies are also useful in
XX CC diagnostics. The vaccines are also suitable as marker vaccines, in that
XX CC it allows discrimination of vaccinated and field-infected mammals on the
XX CC basis of characteristic antibody panel induced by wild-type infection.
XX CC The present sequence is Mycobacterium avium subspecies paratuberculosis
XX CC protein gene
XX
XX SQ Sequence 1701 BP; 318 A; 569 C; 591 G; 223 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 9; Length 1701;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
DB 883 TGAAGGTGCGCGGATCTTGTT 862

RESULT 35
ACC49833/c
ID ACC49833 standard; DNA; 1752 BP.
XX
XX AC ACC49833;
XX
XX DT 27-JUN-2003 (first entry)
XX
XX DE Human recombinant protein vaccine gene.

XX
XX KW Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
XX KW antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1752
XX FT /*tag= a
XX
XX PN CN1362263-A.
XX
XX PD 07-AUG-2002.
XX
XX PF 15-NOV-2001; 2001CN-00134935.
XX
XX PR 04-JAN-2001; 2001CN-00100380.
XX
XX PA (BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
XX
XX PI Wang L, Li D, Yu Y;
XX
XX DR WPI: 2003-230415/23.
XX DR P-PSDB; ABR40246.
XX
XX PT Recombinant protein vaccine for preventing and treating human prostate
XX PT cancer.
XX
XX PS Claim 7; Page 15-19; 35pp; Chinese.
XX
XX CC The invention relates to a novel recombinant protein vaccine, a fusion
XX CC protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of
XX CC human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The
XX CC vaccine of the invention is useful for treating and preventing carcinoma
XX CC of prostate. The invention also discloses the genes encoding the
XX CC recombinant protein vaccines. The present sequence is used in the
XX CC exemplification of the invention
XX
XX SQ Sequence 1752 BP; 356 A; 535 C; 595 G; 266 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 8; Length 1752;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
DB 808 TGAAGGTGCGCGGATCTTGTT 787

RESULT 36
ADX05272/c
ID ADX05272 standard; DNA; 1761 BP.
XX
XX AC ADX05272;
XX
XX DT 21-APR-2005 (first entry)
XX
XX DE HSP65-MUC1-ME fusion protein coding sequence, SEQ ID 1.
XX
XX KW Fusion protein; Cytostatic; Gene Therapy; heat shock protein 65; HSP65;
XX KW mucin; MUC1; carcinoma; gene; ds.
XX
XX OS Mycobacterium bovis BCG.
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1761
XX FT /*tag= a
XX FT /product= "HSP65-MUC1-ME fusion protein"
XX
XX PN US2005031649-A1.
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XX PD 10-FEB-2005.
XX XX
XX PF 06-AUG-2003; 2003US-00635211.
XX XX
XX PR 06-AUG-2003; 2003US-00635211.
XX XX
XX PA (YUYV/) YU Y.
XX PA (LIHH/) LI H.
XX PA (WANG/) WANG L.
XX XX
XX PI Yu Y, Li H, Wang L;
XX XX
XX DR WPI; 2005-131970/14.
XX DR P-PSDB; ADX05273.
XX XX
XX PT New recombinant fusion protein comprises Bacillus Calmette Guerin (BCG)
XX PT heat shock protein 65 and 1-5 copies of an epitope of MUC1, useful for
XX PT treating or preventing human MUC1 expressing carcinomas.
XX XX
XX PS Claim 31; SEQ ID NO 1; 19pp; English.
XX XX
XX CC The present invention relates to a novel recombinant fusion protein
XX CC (HSP65-MUC1-ME, ADX05273) which comprises Bacillus Calmette Guerin (BCG)
XX CC heat shock protein 65 (HSP65) and an epitope of mucin protein MUC1 (MUC1-
XX CC ME). The BCG HSP65 is located at the amino terminal portion of the fusion
XX CC protein and the epitope of MUC1 is located at the carboxy terminal
XX CC portion of the fusion protein. The MUC1 epitope can generate MUC1
XX CC specific cytotoxic T lymphocytes. The recombinant fusion protein is
XX CC useful for treating or preventing human carcinomas, preferably MUC1
XX CC expressing carcinomas. The present sequence is the coding sequence for
XX CC the fusion protein of the invention.
XX XX
XX SQ Sequence 1761 BP; 338 A; 543 C; 608 G; 272 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 21.6; DB 14; Length 1761;
Best Local Similarity 95.5%; Pred. No. 2.1;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787
XX XX
RESULT 37
ADK68629/c
ID ADK68629 standard; cDNA; 1800 BP.
XX AC
XX AC ADK68629;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX
XX DE HSP65-MUC1 antigen CTL epitope related cDNA #1.
XX XX
XX KW Human breast cancer; Mycobacterium bovis; heat shock protein 65; BCG;
XX KW HSP65; cytotoxic T lymphocyte; CTL; MUC1; HSP65-MUC1 antigen CTL epitope;
XX KW gene; ss.
XX XX
XX OS Unidentified.
XX OS
XX PN CN1368384-A.
XX PN
XX PD 11-SEP-2002.
XX PD
XX PF 08-FEB-2001; 2001CN-00102614.
XX PF
XX PR 08-FEB-2001; 2001CN-00102614.
XX PR
XX PA (DIWE-) DIWEIHUAYU BIO TECHNOLOGY CO LTD BEIJING.
XX PA
XX PI Yu Y, Li H;
XX PI
XX XX WPI; 2003-854662/80.
XX XX
XX DR

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DR P-PSDB; ADK68630.
XX XX
XX PT Genetically engineered vaccine of MUC-1 antigen for human breast cancer.
XX XX
XX PS Claim 1; SEQ ID NO 1; 14pp; Chinese.
XX XX
XX CC The invention relates to a method of preparation of a genetically
XX CC engineered vaccine for preventing and treating human breast cancer. The
XX CC method comprises fusing the coding gene of the Mycobacterium bovis heat
XX CC shock protein 65 (BCG HSP65) with the cytotoxic T lymphocyte (CTL)
XX CC epitope gene of MUC1 (antigen cell expressed by human breast cancer
XX CC cells) and the HSP65-MUC1 antigen CTL epitope is expressed in Escherichia
XX CC coli cells. This sequence represents DNA used in the method of the
XX CC invention.
XX XX
XX SQ Sequence 1800 BP; 347 A; 561 C; 616 G; 276 T; 0 U; 0 Other;
XX XX
Query Match 100.0%; Score 21.6; DB 10; Length 1800;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1 TGAAGGTGCGCGGATCTTGT 22
DB 808 TGAAGGTGCGCGGATCTTGT 787
XX XX
RESULT 38
ACC49834/c
ID ACC49834 standard; DNA; 1914 BP.
XX AC
XX AC ACC49834;
XX AC
XX DT 27-JUN-2003 (first entry)
XX DT
XX DE Human recombinant protein vaccine gene.
XX XX
XX KW Human; vaccine; BCG vaccine heat shock protein 65; prostatic;
XX KW antigen cytotoxin T lymphocyte poly epitope; prostate cancer; gene; ds.
XX XX
XX OS Homo sapiens.
XX OS
XX XX Synthetic.
XX XX
XX FH Key
XX FT CDS
XX FT 1..1914
XX FT /*tag= a
XX XX
XX PN CN1362263-A.
XX PN
XX PD 07-AUG-2002.
XX PD
XX PF 15-NOV-2001; 2001CN-00134935.
XX PF
XX PR 04-JAN-2001; 2001CN-00100380.
XX PR
XX XX (BEIJ-) BEIJING DEWEIHUAYU BIOTECHNOLOGY CO LTD.
XX XX
XX PA Wang L, Li D, Yu Y;
XX XX
XX DR WPI; 2003-230415/23.
XX DR
XX DR P-PSDB; ABR40247.
XX XX
XX PT Recombinant protein vaccine for preventing and treating human prostate
XX PT cancer.
XX XX
XX PS Claim 7; Page 23-26; 35pp; Chinese.
XX XX
XX CC The invention relates to a novel recombinant protein vaccine, a fusion
XX CC protein formed from BCG vaccine heat shock protein 65 and 1-5 copies of
XX CC human prostatic specific antigen cytotoxin T lymphocyte poly epitope. The
XX CC vaccine of the invention is useful for treating and preventing carcinoma
XX CC of prostate. The invention also discloses the genes encoding the
XX CC recombinant protein vaccines. The present sequence is used in the
XX CC exemplification of the invention

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XX SQ Sequence 1914 BP; 397 A; 576 C; 633 G; 308 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 8; Length 1914;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCCGGATCTTGT 22
DB 808 TGAAGGTGCCCGGATCTTGT 787

RESULT 39
AAF25012/c
ID AAF25012 standard; DNA; 1920 BP.
XX
AC AAF25012;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of Hsp65-E7 fusion protein.
XX
KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KW E7 protein; ss.
XX
OS Synthetic.
OS Mycobacterium bovis.
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT CDS 1..1920
FT /*tag= a
FT /product= "Hsp65-E7 fusion protein"
XX
PN WO200104344-A2.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018828.
XX
PR 08-JUL-1999; 99US-0143757P.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Siegel M, Chu NR, Mizzen LA;
XX
DR WPI: 2001-138361/14.
DR P-PSDB; AAB31609.
XX
PT Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.
PS Example 5; Fig 4A-B; 88pp; English.
XX
CC The present sequence encodes a fusion protein comprising a Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial pathogens

XX SQ Sequence 1920 BP; 415 A; 551 C; 638 G; 316 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 5; Length 1920;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTCCRCGGATCTTGT 22
DB 808 TGAAGTCCRCGGATCTTGT 787

RESULT 40
AAF25019/c
ID AAF25019 standard; DNA; 1947 BP.
XX
AC AAF25019;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of Hsp65-E7 fusion protein.
XX
KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KW E7 protein; ss.
XX
OS Synthetic.
OS Mycobacterium bovis.
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT CDS 1..1947
FT /*tag= a
FT /product= "Hsp65-E7 fusion protein"
XX
PN WO200104344-A2.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018828.
XX
PR 08-JUL-1999; 99US-0143757P.
XX
PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
PI Siegel M, Chu NR, Mizzen LA;
XX
DR WPI: 2001-138361/14.
DR P-PSDB; AAB31614.
XX
PT Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.
PS Example 11; Fig 10A-B; 88pp; English.
XX
CC The present sequence encodes a fusion protein comprising a Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the Th1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial pathogens

XX SQ Sequence 1947 BP; 417 A; 557 C; 653 G; 320 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 5; Length 1947;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTCCRCGGATCTTGT 22
DB 1132 TGAAGTCCRCGGATCTTGT 1111

```
RESULT 41
ADW23606/c
ID ADW23606 standard; DNA; 1965 BP.
XX
XX AC ADW23606;
XX
XX DT 10-MAR-2005 (first entry)
XX
XX DE Hepatitis C virus related DNA SEQ ID NO 6.
XX
XX KW recombinant protein; vaccine; fusion protein; hepatitis C; ds; gene.
XX
XX OS Synthetic.
XX
XX PN CN1462636-A.
XX
XX PD 24-DEC-2003.
XX
XX PF 30-MAY-2002; 2002CN-00122116.
XX
XX PR 30-MAY-2002; 2002CN-00122116.
XX
XX PA (DIWE-) DIWEI HUAYU BIOTECHNOLOGY CO LTD BEIJING.
XX
XX PI Wang L, Sun M, Yu Y;
XX
XX WPI; 2004-239553/23.
XX
XX P-PSDB; ADW23607.
XX
XX Vaccine of recombinant albumen for preventing and treating infection of
XX human hepatitis C virus.
XX
XX Claim 9; SEQ ID NO 6; 54pp; Chinese.
XX
XX The invention relates to a recombinant protein vaccine which is a fusion
XX protein of BCG vaccine's heat shock protein 65 and the core antigen of
XX multi-epitope hepatitis C virus. Also claimed is the amino acid sequence
XX and nucleotide sequence for coding it, the expression carrier containing
XX nucleotide sequence, the host cell containing expression carrier, the
XX preparing process of recombinant protein vaccine, the vaccine containing
XX recombinant protein for preventing and treating hepatitis C and a method
XX for detecting the activity of specifically killing T-lymphocytes by the
XX hepatitis C induced by vaccine and its cell model are disclosed. The
XX present sequence represents a hepatitis C virus related DNA.
XX
XX Sequence 1965 BP; 405 A; 593 C; 658 G; 309 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 13; Length 1965;
XX Best Local Similarity 95.5%; Pred. No. 2.2;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGAAGGTGCGCGGATCTTGT 22
XX |||||:|||||
XX Db 808 TGAAGGTGCGCGGATCTTGT 787
XX
XX RESULT 42
ADN00588/c
ID ADN00588 standard; DNA; 1980 BP.
XX
XX AC ADN00588;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE BCG vaccine HSP65-MOMP fusion protein coding sequence, SEQ ID 3.
XX
XX KW Antibacterial; gynecological; protein vaccine;
XX BCG vaccine heat shock protein 65; major outer membrane protein; MOMP;
XX Chlamydia infection; urogenital infection; gene; ds.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX
XX Query Match 100.0%; Score 21.6; DB 13; Length 1965;
XX Best Local Similarity 95.5%; Pred. No. 2.2;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGAAGGTGCGCGGATCTTGT 22
XX |||||:|||||
XX Db 808 TGAAGGTGCGCGGATCTTGT 787
XX
XX RESULT 43
ADK72374/c
ID ADK72374 standard; DNA; 2016 BP.
XX
XX AC ADK72374;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE BCG-HER-2 fusion gene construct for breast cancer vaccine treatment.
XX
XX KW vaccine; fusion protein; BCG; heat-shock protein 65; HSP65; HER-2;
XX antigen; breast cancer; gene; ds.
XX
XX OS Homo sapiens.
XX OS Bacillus sp.
XX OS Chimeric.
XX
XX FH Key Location/Qualifiers
XX CDS 1..2016
XX /*tag= a
XX /product= "BCG-HER2 fusion protein"
XX
XX CN1410127-A.
XX
XX PD 16-APR-2003.
XX
XX PF 10-OCT-2001; 2001CN-00136347.
XX
```

```
CDS 1..1980
/*tag= a
/product= "BCG vaccine HSP65-MOMP fusion protein"
WO2004020471-A1.
11-MAR-2004.
03-JUN-2003; 2003WO-CN000430.
29-AUG-2002; 2002CN-00141977.
(BEIJ-) BEIJING HYDVAX BIOTECHNOLOGY CO LTD.
Wang L, Yang S, Yu Y;
WPI; 2004-248232/23.
P-PSDB; ADN00589.
Heat shock protein-based recombinant protein for vaccines against human
Chlamydia trachomatis, applicable in preventing or/and treating human
Chlamydia infections.
Claim 7; SEQ ID NO 3; 49pp; Chinese.
The present invention relates to a recombinant protein vaccine
(ADN00589), which is a fusion protein of BCG vaccine heat shock protein
(HSP) 65 with the major outer membrane protein (MOMP) of Chlamydia
trachomatis (ADN00587). The fusion protein comprises the BCG vaccine HSP
65 at the amino-end, with the MOMP protein at the carboxy-end. The
vaccine is capable of activating cytotoxic T-lymphocytes and can be used
for preventing or/and treating human Chlamydia infections, particularly
urogenital infections. The present sequence is the coding sequence for
the fusion protein, used to illustrate the invention.
Sequence 1980 BP; 407 A; 595 C; 653 G; 325 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 12; Length 1980;
XX Best Local Similarity 95.5%; Pred. No. 2.2;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGAAGGTGCGCGGATCTTGT 22
XX |||||:|||||
XX Db 808 TGAAGGTGCGCGGATCTTGT 787
XX
XX RESULT 43
ADK72374/c
ID ADK72374 standard; DNA; 2016 BP.
XX
XX AC ADK72374;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE BCG-HER-2 fusion gene construct for breast cancer vaccine treatment.
XX
XX KW vaccine; fusion protein; BCG; heat-shock protein 65; HSP65; HER-2;
XX antigen; breast cancer; gene; ds.
XX
XX OS Homo sapiens.
XX OS Bacillus sp.
XX OS Chimeric.
XX
XX FH Key Location/Qualifiers
XX CDS 1..2016
XX /*tag= a
XX /product= "BCG-HER2 fusion protein"
XX
XX CN1410127-A.
XX
XX PD 16-APR-2003.
XX
XX PF 10-OCT-2001; 2001CN-00136347.
XX
```



```
PR 05-FEB-2001; 2001US-0266733P.
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
PA Mizzen L, Liu H, Siegel M;
XX WPI; 2002-706903/76.
DR P-PSDB; ABG70776.
XX Novel isolated fusion protein useful for treating hepatitis B virus
PT infection in a subject, comprises a stress protein or its portion, and a
PT hepatitis B virus core antigen.
XX Example 1; Fig 7; 58pp; English.
XX The invention discloses an isolated fusion protein, and the
CC polynucleotide encoding it, that comprises a stress protein (e.g.
CC Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
CC hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
CC when administered to an individual, induces or enhances an immune
CC response against the HBV core antigen. HBV is a non-cytopathic DNA virus
CC against which a vaccine has been developed. However, due to the morbidity
CC and mortality arising from chronic HBV infection occurring over a period
CC of decades, the impact of vaccinations will not be apparent for some time
CC yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
CC therapy and as a pharmaceutical composition for inducing or enhancing an
CC immune response against an HBV core antigen in a subject for treating an
CC HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
CC The sequence presented is the DNA encoding the truncated hepatitis B
CC virus core antigen fused to the N-terminus of the M. bovis variant
CC Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65.
CC hisHepCorT(149/87S97P)Hsp65. The core antigen the DNA encodes has been
CC truncated to include residues 1 to 149, had an N-terminal histidine tag
CC added, had two amino acids changed from the wild-type sequence and there
CC has been an additional residue added between the HBV core protein and the
CC Hsp65 protein. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 2130 BP; 444 A; 616 C; 681 G; 389 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 2130;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCGCGATCTTGT 22
Db 1315 TGAAGGTGCCGCGATCTTGT 1294
RESULT 46
ABS54449/C
ID ABS54449 standard; DNA; 2175 BP.
XX
AC ABS54449;
XX
XX 07-AUG-2003 (revised)
DT 09-DEC-2002 (first entry)
XX BCG Hsp65/mutant HBV core antigen, HepCor(97P)Hsp65, DNA.
XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
KW Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity;
KW mortality; infection; gene therapy; hepatitis; cirrhosis;
KW hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
KW antiinflammatory; BCG; chimera; mutant.
XX
XX Hepatitis B virus.
OS Mycobacterium bovis.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 1. .2175
FT CDS /*tag= a
FT
```

```
FT XX WO200262959-A2.
XX PN /product= "HepCor(97P)Hsp65"
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX P-PSDB; ABG70778.
XX 05-FEB-2001; 2001US-0266733P.
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
PA Mizzen L, Liu H, Siegel M;
XX WPI; 2002-706903/76.
DR P-PSDB; ABG70778.
XX Novel isolated fusion protein useful for treating hepatitis B virus
PT infection in a subject, comprises a stress protein or its portion, and a
PT hepatitis B virus core antigen.
XX Example 1; Fig 11; 58pp; English.
XX The invention discloses an isolated fusion protein, and the
CC polynucleotide encoding it, that comprises a stress protein (e.g.
CC Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
CC hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
CC when administered to an individual, induces or enhances an immune
CC response against the HBV core antigen. HBV is a non-cytopathic DNA virus
CC against which a vaccine has been developed. However, due to the morbidity
CC and mortality arising from chronic HBV infection occurring over a period
CC of decades, the impact of vaccinations will not be apparent for some time
CC yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
CC therapy and as a pharmaceutical composition for inducing or enhancing an
CC immune response against an HBV core antigen in a subject for treating an
CC HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
CC The sequence presented is the DNA encoding the truncated hepatitis B
CC virus core antigen fused to the N-terminus of the M. bovis variant
CC Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65.
CC hisHepCorT(149/87S97P)Hsp65. The core antigen the DNA encodes has been
CC truncated to include residues 1 to 149, had an N-terminal histidine tag
CC added, had two amino acids changed from the wild-type sequence and there
CC has been an additional residue added between the HBV core protein and the
CC Hsp65 protein. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 2175 BP; 459 A; 628 C; 691 G; 397 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 6; Length 2175;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCGCGATCTTGT 22
Db 1360 TGAAGGTGCCGCGATCTTGT 1339
RESULT 47
ABS54446/C
ID ABS54446 standard; DNA; 2241 BP.
XX
AC ABS54446;
XX
XX 07-AUG-2003 (revised)
DT 09-DEC-2002 (first entry)
XX His tagged BCG Hsp65/mutant HBV core antigen, hisHepCor(97P)Hsp65, DNA.
XX HBV; core antigen; HBe; gene; ds; stress protein; heat shock protein;
KW Hsp65; immune response; non-cytopathic DNA virus; vaccine; morbidity;
KW mortality; infection; gene therapy; hepatitis; cirrhosis;
KW hepatocellular carcinoma; virucide; immunostimulant; hepatotropic;
KW antiinflammatory; BCG; chimera; mutant.
XX
XX Hepatitis B virus.
OS Mycobacterium bovis.
OS Synthetic.
```



```
OS Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..2241
XX FT /*tag= a
XX FT /product= "HisHepCor(97F)Hsp65"
XX
XX WO200262959-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US003460.
XX
XX 05-FEB-2001; 2001US-0266733P.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Mizzen L, Liu H, Siegel M;
XX
XX WPI; 2002-706903/76.
XX P-PSDB; ABG70775.
XX
XX Novel isolated fusion protein useful for treating hepatitis B virus
XX infection in a subject, comprises a stress protein or its portion, and a
XX hepatitis B virus core antigen.
XX
XX Example 1; Fig 5; 58pp; English.
XX
XX The invention discloses an isolated fusion protein, and the
XX polynucleotide encoding it, that comprises a stress protein (e.g.
XX Mycobacterium bovis heat shock protein, Hsp65), or a portion of it, and a
XX hepatitis B virus (HBV) core antigen (HBe), where the fusion protein,
XX when administered to an individual, induces or enhances an immune
XX response against the HBV core antigen. HBV is a non-cytopathic DNA virus
XX against which a vaccine has been developed. However, due to the morbidity
XX and mortality arising from chronic HBV infection occurring over a period
XX of decades, the impact of vaccinations will not be apparent for some time
XX yet. The polynucleotide and polypeptide can be used as a vaccine, in gene
XX therapy and as a pharmaceutical composition for inducing or enhancing an
XX immune response against an HBV core antigen in a subject for treating an
XX HBV infection such as hepatitis, cirrhosis and hepatocellular carcinoma.
XX The sequence presented is the DNA encoding the full length hepatitis B
XX virus core antigen fused to the N-terminus of the M. bovis variant
XX Bacille-Calmette-Guerin (BCG) heat shock protein (Hsp) 65,
XX hisHepCor(97F)Hsp65. The core antigen the DNA encodes has had an N-
XX terminal histidine tag added and had an amino acid changed from the wild-
XX type sequence. Two additional residues have also been added between the
XX HBV core protein and the Hsp65 protein. (Updated on 07-AUG-2003 to
XX correct OS field.)
XX
XX Sequence 2241 BP; 474 A; 650 C; 709 G; 408 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 6; Length 2241;
XX Best Local Similarity 95.5%; Pred. No. 2.2;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGAAGGTGCGCGGATCTTGTT 22
XX 1426 TGAAGGTGCGCGGATCTTGTT 1405
XX
XX Db
XX
XX RESULT 48
XX AAF25014/c
XX ID AAF25014 standard; DNA; 2847 BP.
XX
XX AC AAF25014;
XX
XX 30-APR-2001 (first entry)
XX
XX Nucleotide sequence of Hsp65-ovalbumin fusion protein.
XX
XX Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
XX lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
KW
```

```
XX ovalbumin; ss.
XX
XX Synthetic.
XX OS Mycobacterium bovis.
XX OS Gallus sp.
XX
XX Key Location/Qualifiers
XX CDS 1..2847
XX FT /*tag= a
XX FT /product= "Hsp65-ovalbumin fusion protein"
XX
XX WO200104344-A2.
XX
XX 18-JAN-2001.
XX
XX 10-JUL-2000; 2000WO-US018828.
XX
XX 08-JUL-1999; 99US-0143757P.
XX
XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX
XX Siegel M, Chu NR, Mizzen LA;
XX
XX WPI; 2001-138361/14.
XX P-PSDB; AAB31611.
XX
XX Screening for compounds that stimulate Th1-like responses in CD4+ T
XX lymphocyte cells.
XX
XX Example 8; Fig 7A-B; 89pp; English.
XX
XX The present sequence encodes a fusion protein comprising a Mycobacterium
XX bovis heat shock protein (Hsp) 65 fused at its C terminal to an ovalbumin
XX protein. The fusion protein is used in the method of the invention. The
XX specification describes a method of determining whether a compound
XX stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
XX lymphocyte cells. The method comprises contacting naive lymphocytes in
XX vitro with a fusion protein comprising at least a fragment of Hsp, and
XX then detecting the Th1-like response exhibited by the cell sample. The
XX proteins which may be used in the method of the invention are Hsp65,
XX Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
XX compounds that stimulate Th1-like responses in response to microbial
XX pathogens
XX
XX Sequence 2847 BP; 678 A; 761 C; 863 G; 545 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21.6; DB 5; Length 2847;
XX Best Local Similarity 95.5%; Pred. No. 2.3;
XX Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGAAGGTGCGCGGATCTTGTT 22
XX 868 TGAAGGTGCGCGGATCTTGTT 847
XX
XX Db
XX
XX RESULT 49
XX AAN81768/c
XX ID AAN81768 standard; DNA; 4260 BP.
XX
XX AC AAN81768;
XX
XX 25-MAR-2003 (revised)
XX DT 29-DEC-1990 (first entry)
XX
XX DE Sequence encoding Mycobacterium tuberculosis 540 and 517 AA residue
XX proteins.
XX
XX Diagnosis; assay; M. bovis; vaccine; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
XX CDS 252..1874
XX
```

```
FT FT /*tag= a
FT FT /label= 540 AA protein
FT FT /note= "AAP81351"
CDS complement(3948. .2395)
FT FT /*tag= b
FT FT /label= 517 AA protein
FT FT /note= "AAP81868"
XX
PN W08806591-A.
XX
XX 07-SEP-1988.
XX
XX 25-FEB-1988; 88WO-US000598.
XX
XX 26-FEB-1987; 87US-00019529.
XX 24-FEB-1988; 88US-00159667.
XX
XX (SCRI ) SCRIPPS CLINIC & RE.
XX
XX Shinnick T, Houghten R;
XX WPI; 1988-271136/38.
XX P-PSDB; AAP81351, AAP81868.
XX
XX Recombinant mycobacterial peptide(s) - used in assays for diagnosis of
XX infection, for producing vaccines and for producing antibodies.
XX
XX Disclosure; Fig 2a-2d; 117pp; English.
XX
XX An isolated DNA molecule that consists essentially of the nucleotide
XX sequence that corresponds to the sequence represented by position 3950 to
XX about 2390 and from position 3948 through position 2398 of AAN81768 is
XX claimed. Also claimed is a peptide sequence that consists of a 5-40 AA
XX residue sequence that corresponds to a sequence of the 540 AA residue
XX protein (AAP81351) or the 517 AA residue protein (AAP81868) coded for by
XX the DNA sequence. The proteins can be used for determining previous
XX immunological exposure of a mammal to M.tuberculosis or M.bovis and for
XX producing a vaccine. (Updated on 25-MAR-2003 to correct PR field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 4260 BP; 733 A; 1332 C; 1481 G; 714 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 1; Length 4260;
Best Local Similarity 95.5%; Pred. No. 2.4;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCRCGGATCTTGT 22
Db 1059 TGAAGGTGCCRCGGATCTTGT 1038
RESULT 50
AAN80222/c
ID AAN80222 standard; DNA; 4380 BP.
XX
XX AAN80222;
XX
XX 25-MAR-2003 (revised)
DT 19-MAR-1991 (first entry)
XX
XX Sequence of Mycobacterium tuberculosis DNA contg. gene encoding 65
DE protein.
XX
XX Antigen; vaccine; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
FT CDS 192..1874
FT /*tag= a
FT CDS complement(2398. .4101)
FT /*tag= b
XX
```

```
PN W08805823-A.
XX
XX 11-AUG-1988.
XX
XX 01-FEB-1988; 88WO-US000281.
XX
XX 02-FEB-1987; 87US-00010007.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Husson RN, Young RA, Nick TM;
XX WPI; 1988-235175/33.
XX P-PSDB; AAP80215, AAP80216.
XX
XX Genes encoding Mycobacterium tuberculosis protein antigens - useful for
XX developing reagents for diagnosis, prevention and treatment of
XX tuberculosis.
XX
XX Claim 12; Fig 8; 82pp; English.
XX
XX The gene was isolated by probing a lambda gt11 expression library of
XX M.tuberculosis DNA with monoclonal antibodies directed against
XX M.tuberculosis-specific antigens. The 19kD, 71kD and the 65kD proteins
XX CC and genes are claimed, and so is a vaccine comprising DNA encoding
XX M.tuberculosis protein in a recombinant vaccine vector. AAP80216 is
XX CC encoded on the complementary strand. (Updated on 25-MAR-2003 to correct
XX CC PA field.)
XX
XX Sequence 4380 BP; 757 A; 1373 C; 1512 G; 738 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 1; Length 4380;
Best Local Similarity 95.5%; Pred. No. 2.4;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGGTGCCRCGGATCTTGT 22
Db 1059 TGAAGGTGCCRCGGATCTTGT 1038
RESULT 51
AAV05708/c
ID AAV05708 standard; DNA; 4380 BP.
XX
XX AAV05708;
XX
XX 22-JUN-1998 (first entry)
XX
XX Mycobacterium tuberculosis 65 kDa heat shock protein gene.
XX
XX Heat shock protein; Mt Hsp65; autoimmune disease; immunotherapy;
XX gene therapy; rheumatoid arthritis; multiple sclerosis; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX Key Location/Qualifiers
FT CDS 252..1874
FT /*tag= a
FT /product= "65 kDa heat shock protein"
XX
XX W09746253-A2.
XX
XX 11-DEC-1997.
XX
XX 03-JUN-1997; 97WO-US0009427.
XX
XX 03-JUN-1996; 96US-0019100P.
XX
XX 03-JUN-1997; 97US-00019100.
XX
XX (AURA-) AURAGEN INC.
XX
XX Haynes JR, Prayaga SK, Ramshaw IA;
XX
```

DR WPI; 1998-041892/04.
 XX P-PSDB; AAW44702.
 PT Treatment of auto-immune diseases - by administering auto-antigen-coated
 XX particles or auto-antigen-encoding nucleic acid construct.
 PS Example 2; Page 55-59; 72pp; English.
 XX This DNA sequence encodes the 65 kDa heat shock protein (see AAW44702),
 CC designated Mt Hsp65, of Mycobacterium tuberculosis. This protein cross-
 CC reacts with a component of articular cartilage, human Hsp60, that is up-
 CC regulated in the joints of arthritic patients. A claimed method for
 CC treating or preventing an autoimmune disease in a mammal comprises: (a)
 CC providing a particle coated with an antigen against which an immune
 CC response is mounted in the autoimmune disease; (b) delivering the
 CC particle into the recipient cell of the mammal; and (c) repeating step
 CC (b) until either a reduction in a cytotoxic immune response or a
 CC desensitizing immune response is induced in the mammal. Alternatively,
 CC step (a) comprises providing a nucleic acid construct comprising a coding
 CC sequence for the antigen, operably linked to control elements such that
 CC the coding sequence can be transcribed and translated in a recipient
 CC cell, and delivering the construct to the recipient cell using a gene
 CC gun. The antigen of step (a) is selected from collagen, Mt Hsp65, myelin
 CC basic protein, myelin oligodendrocyte glycoprotein, proteolipid protein,
 CC and epitopes thereof. These antigens mitigate cytotoxic responses and
 CC elicit antigen desensitisation. The method is used especially for
 CC treating rheumatoid arthritis or multiple sclerosis. It represents a
 CC novel use for the known Mt Hsp65 gene
 XX
 SQ Sequence 4380 BP; 757 A; 1371 C; 1514 G; 738 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 2; Length 4380;
 Best Local Similarity 95.5%; Pred. No. 2.4;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAAGGTGCGCGGATCTTGT 22
 DB 1059 TGAAGGTGCGCGGATCTTGT 1038
 RESULT 52
 ABA99141/C
 ID ABA99141 standard; DNA; 4380 BP.
 AC ABA99141;
 XX
 DT 23-MAY-2002 (first entry)
 XX
 DE hsp65 encoding sequence.
 XX
 KW hsp65; heat shock protein; cytostatic; antibacterial; antiparasitic;
 KW MHC class I; ds.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US6331388-B1.
 XX
 PD 18-DEC-2001.
 XX
 PF 17-OCT-1997; 97US-00955565.
 XX
 PR 17-OCT-1997; 97US-00955565.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Malkovsky M, Wells AD;
 XX
 DR WPI; 2002-138381/18.
 XX
 PT Increasing expression of an MHC class I molecule in a cell, useful in
 PT increasing antigen presentation and enhancing immune recognition of cells
 PT infected with pathogens, by expressing a heat shock protein introduced by
 PT a vector.

XX Example 5; Fig 9; 89pp; English.
 PS This invention relates to increasing expression of an MHC class I
 CC molecule in a target cell, infected with a pathogen that is processed by
 CC the MHC class I endogenous pathway. The method of expressing a HSP is
 CC achieved by the introduction of an expressed vector encoding HSP to
 CC produce a transfected cell with increased expression of at least one MHC
 CC class I molecule. The method is cytostatic, antibacterial and
 CC antiparasitic. The method can be used to increase expression of an MHC
 CC class I molecule in a target cell and to increase presentation of an
 CC antigen on a cell surface by an MHC class I molecule. The method can
 CC enhance the immunogenicity of the endogenous antigen in vivo, by
 CC enhancing the generation of antibodies to an otherwise poorly immunogenic
 CC antigen or cell. The method can be used in the immunotherapy of cancer
 CC and pathogen infections, and for enhancing or reducing radiation
 CC resistance of cells. The expression of the heat shock protein in a cell
 CC enhances the presentation of endogenous antigens by MHC class I molecules
 CC onto the cell surface in vitro, and can enhance the immunogenicity of the
 CC endogenous antigen in vivo, by enhancing the generation of antibodies to
 CC an otherwise poorly immunogenic antigen or cell. This sequence represents
 CC hsp65 encoding sequence
 XX
 SQ Sequence 4380 BP; 757 A; 1372 C; 1513 G; 738 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21.6; DB 6; Length 4380;
 Best Local Similarity 95.5%; Pred. No. 2.4;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAAGGTGCGCGGATCTTGT 22
 DB 1059 TGAAGGTGCGCGGATCTTGT 1038
 RESULT 53
 ABA99143/C
 ID ABA99143 standard; DNA; 86114 BP.
 XX
 AC ABA99143;
 XX
 DT 08-APR-2003 (first entry)
 XX
 DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV265.
 XX
 KW Mycobacteriosis; survival; virulence; protective antigen; vaccine;
 KW Mycobacterial disease; tuberculosis; leprosy; ds; cosmid.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200274903-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-IB001973.
 XX
 PR 22-FEB-2001; 2001US-0270123P.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Cole S;
 XX
 DR WPI; 2002-759885/82.
 XX
 PT Identifying and selecting genes for survival or virulence of mycobacteria
 PT by a comparative genomic analysis of the sequences of Mycobacterium
 PT tuberculosis and M. leprae.
 XX
 PS Disclosure; Fig 7; 874pp; English.
 XX
 CC This invention relates to a novel method for identifying essential genes
 CC for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a

CC polynucleotide sequence that is highly conserved in both genomes with no
CC counterparts in other bacterial genomic sequences and that corresponds to
CC an essential gene for the survival or virulence of mycobacterium species.
CC The method of the invention is useful for detecting M. tuberculosis or M.
CC leprae infection. The method reduces the number of potential new targets
CC and protective antigens for new drugs and vaccine compositions to treat
CC and prevent mycobacterial diseases, particularly tuberculosis and
CC leprosy. The present sequence represents a Mycobacterial cosmid DNA
CC sequence used in the method of the invention
XX

SQ Sequence 86114 BP; 14693 A; 27103 C; 28984 G; 15334 T; 0 U; 0 Other;

Query Match 100.0%; Score 21.6; DB 6; Length 86114;
Best Local Similarity 95.5%; Pred. No. 3.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||
Db 16012 TGAAGGTGCGCGGATCTTGTT 15991

RESULT 54

AAI99682_05/c
Continuation (6 of 45) of AAI99682 from base 500001 (Mycobacterium tuberculosis strain H
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682

Fragment Name	Begin	End
AAI99682_00	1	110000
WP AAI99682_01	100001	210000
WP AAI99682_02	200001	310000
WP AAI99682_03	300001	410000
WP AAI99682_04	400001	510000
WP AAI99682_05	500001	610000
WP AAI99682_06	600001	710000
WP AAI99682_07	700001	810000
WP AAI99682_08	800001	910000
WP AAI99682_09	900001	1010000
WP AAI99682_10	1000001	1110000
WP AAI99682_11	1100001	1210000
WP AAI99682_12	1200001	1310000
WP AAI99682_13	1300001	1410000
WP AAI99682_14	1400001	1510000
WP AAI99682_15	1500001	1610000
WP AAI99682_16	1600001	1710000
WP AAI99682_17	1700001	1810000
WP AAI99682_18	1800001	1910000
WP AAI99682_19	1900001	2010000
WP AAI99682_20	2000001	2110000
WP AAI99682_21	2100001	2210000
WP AAI99682_22	2200001	2310000
WP AAI99682_23	2300001	2410000
WP AAI99682_24	2400001	2510000
WP AAI99682_25	2500001	2610000
WP AAI99682_26	2600001	2710000
WP AAI99682_27	2700001	2810000
WP AAI99682_28	2800001	2910000
WP AAI99682_29	2900001	3010000
WP AAI99682_30	3000001	3110000
WP AAI99682_31	3100001	3210000
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WP AAI99682_36	3600001	3710000
WP AAI99682_37	3700001	3810000
WP AAI99682_38	3800001	3910000
WP AAI99682_39	3900001	4010000
WP AAI99682_40	4000001	4110000
WP AAI99682_41	4100001	4210000
WP AAI99682_42	4200001	4310000
WP AAI99682_43	4300001	4410000
WP AAI99682_44	4400001	4411529

Query Match

100.0%; Score 21.6; DB 4; Length 110000;

Best Local Similarity 95.5%; Pred. No. 3.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||
Db 29413 TGAAGGTGCGCGGATCTTGTT 29392

RESULT 55

AAI99683_05/c
Continuation (6 of 44) of AAI99683 from base 500001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession AAI99683

Fragment Name	Begin	End
AAI99683_00	1	110000
WP AAI99683_01	100001	210000
WP AAI99683_02	200001	310000
WP AAI99683_03	300001	410000
WP AAI99683_04	400001	510000
WP AAI99683_05	500001	610000
WP AAI99683_06	600001	710000
WP AAI99683_07	700001	810000
WP AAI99683_08	800001	910000
WP AAI99683_09	900001	1010000
WP AAI99683_10	1000001	1110000
WP AAI99683_11	1100001	1210000
WP AAI99683_12	1200001	1310000
WP AAI99683_13	1300001	1410000
WP AAI99683_14	1400001	1510000
WP AAI99683_15	1500001	1610000
WP AAI99683_16	1600001	1710000
WP AAI99683_17	1700001	1810000
WP AAI99683_18	1800001	1910000
WP AAI99683_19	1900001	2010000
WP AAI99683_20	2000001	2110000
WP AAI99683_21	2100001	2210000
WP AAI99683_22	2200001	2310000
WP AAI99683_23	2300001	2410000
WP AAI99683_24	2400001	2510000
WP AAI99683_25	2500001	2610000
WP AAI99683_26	2600001	2710000
WP AAI99683_27	2700001	2810000
WP AAI99683_28	2800001	2910000
WP AAI99683_29	2900001	3010000
WP AAI99683_30	3000001	3110000
WP AAI99683_31	3100001	3210000
WP AAI99683_32	3200001	3310000
WP AAI99683_33	3300001	3410000
WP AAI99683_34	3400001	3510000
WP AAI99683_35	3500001	3610000
WP AAI99683_36	3600001	3710000
WP AAI99683_37	3700001	3810000
WP AAI99683_38	3800001	3910000
WP AAI99683_39	3900001	4010000
WP AAI99683_40	4000001	4110000
WP AAI99683_41	4100001	4210000
WP AAI99683_42	4200001	4310000
WP AAI99683_43	4300001	4403765

Query Match 100.0%; Score 21.6; DB 4; Length 110000;

Best Local Similarity 95.5%; Pred. No. 3.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
|||||:|||||
Db 30855 TGAAGGTGCGCGGATCTTGTT 30834

RESULT 56

AAH68533
ID AAH68533 standard; DNA; 349980 BP.
XX
AC AAH68533;
XX

DT 26-SEP-2001 (first entry)
DE C glutamicum coding sequence fragment SEQ ID NO: 7068.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN BP1108790-A2.
XX
XX 20-JUN-2001.
XX
XX 18-DEC-2000; 2000BP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Disclosure; SEQ ID NO 7068; 245pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification. But was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 U; 0 Other;
Query Match 100.0%; Score 21.6; DB 5; Length 349980;
Best Local Similarity 95.5%; Pred. No. 3.8;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTGCCTCGGATCTTGT 22
DB 189718 TGAAGTGCCTCGGATCTTGT 189739
RESULT 57
ID ADI67068/c
XX ADI67068 standard; DNA; 732 BP.
XX
AC ADI67068;
XX
DT 24-FEB-2005 (revised)
DT 22-APR-2004 (first entry)
XX
DE Novel Lactobacillus rhamnosus polynucleotide sequence #63.
XX
KW Lactic acid bacteria; vaccine; bacterial infection; microbe;
KW milk-derived product; food product; food additive;
KW nutritional supplement; bioactive substance; probiotic supplement;
KW flavour; aroma; texture, nutritional value; food; microorganism;
KW antibacterial; gene; ds.
XX

OS Lactobacillus rhamnosus; strain HN001.
XX
PN US2004009490-A1.
XX
PD 15-JAN-2004.
XX
PF 03-OCT-2002; 2002US-00264213.
XX
PR 09-AUG-1999; 99US-0147852P.
PR 09-AUG-1999; 99US-0147853P.
PR 01-SEP-1999; 99US-0152031P.
PR 01-SEP-1999; 99US-0152032P.
PR 08-AUG-2000; 2000US-00634238.
PR 02-OCT-2001; 2001US-00971536.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Glenn M, Havukkala IJ, Lubbers M, Dekker J;
PI WPI; 2004-090459/09.
XX P-PSDB; ADI67193.
XX
PT New polynucleotide from Lactobacillus rhamnosus HN001 strain, useful for
PT preparing a vaccine against bacterial infections or for modifying the
PT flavor, aroma or nutritional benefits of a bioactive or probiotic
PT supplement product.
XX
PS Claim 1; SEQ ID NO 63; 54pp; English.
XX
CC The present invention relates to the isolation of novel lactic acid
CC bacteria (Lactobacillus rhamnosus strain HN001) polynucleotide sequences,
CC and the proteins encoded by them. Also disclosed are oligonucleotide
CC probes and primers, and genetic constructs comprising the polynucleotide
CC sequences of the invention. The polynucleotide sequences are useful for
CC preparing a vaccine against bacterial infections or for improving the
CC properties of microbes used in the manufacture of milk-derived products,
CC food products, food additives, nutritional supplements, bioactive
CC substances or probiotic supplements, and for modifying the flavour,
CC aroma, texture and/or nutritional value of foods. They are also useful
CC for identifying microorganisms having a trait associated with the
CC polynucleotide sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification. The complete
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov.
XX
SQ Sequence 732 BP; 187 A; 159 C; 205 G; 181 T; 0 U; 0 Other;
Query Match 92.6%; Score 20; DB 12; Length 732;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAAGTGCCTCGGATCTTGT 22
DB 229 TGAAGTGCCTCGGATCTTGT 208
RESULT 58
ID AAQ22481/c
XX AAQ22481 standard; DNA; 1320 BP.
XX
AC AAQ22481;
XX
DT 29-JUL-1992 (first entry)
XX
DE groEL-1 gene partial sequence.
XX
KW Heat shock protein; HSP18; ss.
XX
OS Streptomyces albus.
XX
FH Key Location/Qualifiers
FT CDS 1..510

```
PT FT      /*tag= a
PT PT      /note= "groEL-1 gene encoding HSP18"
XX
XX WO9204452-A.
XX PN
XX 19-MAR-1992.
XX PD
XX 03-SEP-1991; 91WO-FR000701.
XX PF
XX 10-SEP-1990; 90FR-00011186.
XX PR
XX (INSP ) INST PASTEUR.
XX PA
XX Mazodier P, Guglielmi G;
XX PI
XX WPI; 1992-114358/14.
XX DR
XX P-PSDB; AAR22362.
XX
XX Recombinant DNA contg. heat inducible promoter and heterologous gene -
XX PT also vectors, transformed cells and new heat shock proteins of
XX PT Streptococcus albus.
XX
XX Claim 18; Fig 6; 50pp; French.
XX PS
XX
XX The sequence is a partial sequence of the groEL-1 gene which codes for the 18 kDa
XX CC heat shock protein HSP18. The gene actually codes for a 56 kDa protein
XX CC but this is subjected to post translation modification to give the 18
XX CC kDa HSP18 protein, the partial sequence given here is missing the last
XX CC 300 nucleotides encoding the C-terminal of the 56 kDa protein. See also
XX CC AAQ22477-Q22486
XX
XX Sequence 1320 BP; 237 A; 469 C; 444 G; 170 T; 0 U; 0 Other;
XX SQ
XX
XX Query Match 92.6%; Score 20; DB 2; Length 1320;
XX Best Local Similarity 90.9%; Pred. No. 13;
XX Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 TGAAGGTGCGCGGATCTTGT 22
XX QY |||||:|||||
XX DB 814 TGAACGTGCGCGGATCTTGT 793
XX
XX RESULT 59
XX AAQ22482/C
XX ID AAQ22482 standard; DNA; 1620 BP.
XX AC
XX AAQ22482;
XX AC
XX 29-JUL-1992 (first entry)
XX DT
XX groEL-1 gene coding region.
XX DE
XX Heat shock protein; HSP18; ss.
XX KW
XX Streptomyces albus.
XX OS
XX Key Location/Qualifiers
XX FH 1. 510
XX CDS /*tag= a
XX FT /note= "groEL-1 gene encoding HSP18"
XX PT
XX WO9204452-A.
XX PN
XX 19-MAR-1992.
XX PD
XX 03-SEP-1991; 91WO-FR000701.
XX PF
XX 10-SEP-1990; 90FR-00011186.
XX PR
XX (INSP ) INST PASTEUR.
XX PA
XX Mazodier P, Guglielmi G;
XX PI
XX
```

```
DR WPI; 1992-114358/14.
DR P-PSDB; AAR22363.
XX
XX Recombinant DNA contg. heat inducible promoter and heterologous gene -
XX PT also vectors, transformed cells and new heat shock proteins of
XX PT Streptococcus albus.
XX
XX Claim 18; Fig 8; 50pp; French.
XX PS
XX
XX The sequence is that of the coding region of the groEL-1 gene which codes
XX CC for the 18 kDa heat shock protein HSP18. The gene actually codes for a 56
XX CC kDa protein but this is subjected to post translation modification to
XX CC give the 18 kDa HSP18 protein. See also AAQ22477-Q22486
XX
XX Sequence 1620 BP; 287 A; 590 C; 539 G; 204 T; 0 U; 0 Other;
XX SQ
XX
XX Query Match 92.6%; Score 20; DB 2; Length 1620;
XX Best Local Similarity 90.9%; Pred. No. 13;
XX Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 TGAAGGTGCGCGGATCTTGT 22
XX QY |||||:|||||
XX DB 814 TGAACGTGCGCGGATCTTGT 793
XX
XX RESULT 60
XX ACA39632/C
XX ID ACA39632 standard; DNA; 1626 BP.
XX AC
XX ACA39632;
XX AC
XX 19-JUN-2003 (first entry)
XX DT
XX Prokaryotic essential gene #21289.
XX DE
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX KW drug design; gene.
XX KW
XX Mycobacterium leprae.
XX OS
XX WO200277183-A2.
XX PN
XX 03-OCT-2002.
XX PD
XX 21-MAR-2002; 2002WO-US009107.
XX PF
XX 21-MAR-2001; 2001US-00815242.
XX PR
XX 06-SEP-2001; 2001US-00948993.
XX PR
XX 25-OCT-2001; 2001US-0342923P.
XX PR
XX 08-FEB-2002; 2002US-00072851.
XX PR
XX 06-MAR-2002; 2002US-0362699P.
XX PR
XX (BLIT-) ELITRA PHARM INC.
XX PA
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX DR P-PSDB; ABU35762.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 27502; 1766pp; English.
XX PS
XX The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
```

CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 1626 BP; 352 A; 450 C; 540 G; 284 T; 0 U; 0 Other;

Query Match 92.6%; Score 20; DB 8; Length 1626;
 Best Local Similarity 90.9%; Pred. No. 13;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGTT 22
 ||| |||||:|||||||
 Db 808 TGAAGTGCRCGGATCTTGTT 787

Search completed: April 1, 2006, 22:21:38
 Job time : 46.7112 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
3396.840 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaaggtgccggatcttgtt 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	88.0	163	1	AW113955 MC6373 mo
C 2	19	88.0	232	1	AW111034 MT725 mou
C 3	19	88.0	341	5	EX632408 EX632408
C 4	19	88.0	459	1	AW111035 MT8449 mo
C 5	19	88.0	616	1	AW110355 ui84f03.x
C 6	19	88.0	629	2	BG081027 H3060C06-
C 7	19	88.0	858	7	CV070443 WPAEhux15
C 8	18.8	87.0	393	3	BP637291 BP637291
C 9	18.8	87.0	403	3	BP596595 BP596595
C 10	18.8	87.0	409	3	BP793678 BP793678
C 11	18.8	87.0	425	3	BP605386 BP605386
C 12	18.8	87.0	432	1	AV533334 AV533334
C 13	18.8	87.0	432	1	AV562602 AV562602
C 14	18.8	87.0	433	3	BP589232 BP589232
C 15	18.8	87.0	434	3	BP606850 BP606850
C 16	18.8	87.0	439	3	BP593318 BP593318
C 17	18.8	87.0	441	3	BP604921 BP604921
C 18	18.8	87.0	518	1	AV563537 AV563537
C 19	18.8	87.0	524	1	AV563538 AV563538
C 20	18.8	87.0	552	1	AI999651 AI999651
C 21	18.8	87.0	3509	4	CNS0ADWK
C 22	18.4	85.2	303	8	DN316919 LIB3171-0

ALIGNMENTS

RESULT 1

AW113955/c 163 bp mRNA linear EST 31-JAN-2000
LOCUS MC6373 mouse liver, vehicle control Mus musculus cDNA clone MC6373
DEFINITION 3' similar to X86561 Rat gene for alpha-fibrinogen, mRNA sequence.
ACCESSION AW113955
VERSION AW113955.1
KEYWORDS GI:6826668
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 163)
AUTHORS Thomas, R.S., Rank, D.R., Penn, S.G., Zastrow, G.M., Jovanovich, S. and
Bradfield, C.A.

McCardle Laboratory/Molecular Dynamics Dioxin EST Project
Unpublished (1999)

Contact: Bradfield CA

McCardle Laboratory for Cancer Research

University of Wisconsin

1400 University Ave., Madison, WI 53706, USA

Tel: 608 262 2034

Fax: 608 262 2824

Email: bradfield@oncology.wisc.edu

This clone was sequenced as part of a project to develop a database on gene expression changes following exposure to various environmental toxicants. The database can be accessed at <http://mccardle.oncology.wisc.edu/bradfield/>. Treatment- dioxane vehicle (400 ul/kg). Animals sacrificed- 48 hrs post-injection.

C 23	18.4	85.2	673	1	AJ808396
C 24	18.4	85.2	859	8	DR731656
C 25	18.4	85.2	889	7	CK154849
C 26	18.4	85.2	893	5	BU601986
C 27	18.4	85.2	893	7	CK152837
C 28	18	83.3	281	7	CR458933
C 29	18	83.3	335	1	AA875097
C 30	18	83.3	570	1	AA061605
C 31	18	83.3	582	3	BP294923
C 32	18	83.3	1349	1	AW727610
C 33	17.6	81.5	559	10	CL174879
C 34	17.4	80.6	179	2	BP705257
C 35	17.4	80.6	218	8	DR705480
C 36	17.4	80.6	243	8	CX223617
C 37	17.4	80.6	280	3	BJ280260
C 38	17.4	80.6	285	5	BQ752687
C 39	17.4	80.6	360	1	AJ474162
C 40	17.4	80.6	374	8	DR793683
C 41	17.4	80.6	386	6	CF646223
C 42	17.4	80.6	391	2	BI098781
C 43	17.4	80.6	397	2	BI098170
C 44	17.4	80.6	404	6	CF646224
C 45	17.4	80.6	417	2	BI098323
C 46	17.4	80.6	426	9	AQ406201
C 47	17.4	80.6	432	2	BI074698
C 48	17.4	80.6	437	1	AW666066
C 49	17.4	80.6	438	2	BF325403
C 50	17.4	80.6	447	3	BQ133585
C 51	17.4	80.6	462	6	CB541407
C 52	17.4	80.6	464	2	BG050084
C 53	17.4	80.6	474	2	BG104062
C 54	17.4	80.6	480	10	CG785031
C 55	17.4	80.6	481	10	CW368267
C 56	17.4	80.6	487	2	BG267138
C 57	17.4	80.6	487	6	CA181673
C 58	17.4	80.6	489	2	BG550996
C 59	17.4	80.6	499	6	CA182253
C 60	17.4	80.6	504	1	AA763342

AJ808396	AJ808396
DR731656	FGAS07757
CK154849	FGAS03356
BU601986	AGENCOURT
CK152837	FGAS03591
CR458933	CR458933
AA875097	UI-R-E0-C
AA061605	m133e10.r
BP294923	BP294923
AW727610	GA_Ea001
CL174879	10A_379_1
BP705257	RH122_2_G
DR705480	Asn_05659
CX223617	NNS42007
BJ280260	BJ280260
BQ752687	WHE4118_A
AJ474162	AJ474162
DR793683	ZM_BPB001
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BI098170	IP1_29_A0
CF646224	3530_1_11
BI098323	IP1_31_A0
AQ406201	HS_5047_B
BI074698	IP1_14_B0
AW666066	sk31f07_Y
BF325403	su21c08_Y
AM666066	sk31f07_Y
BQ133585	san58c04
CB541407	PVERSE203
BG050084	FW1_66_D0
BG104062	RH122_40
CG785031	RRR811_Ba
CW368267	fsbb001f0
BG267138	100011H0
CA181673	SCB8ST313
BG550996	sad31h01
CA182253	SCB8ST310
AA763342	vw53c01.r

Seq primer: dt(23)V (anchored polyT).

FEATURES

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1. 163
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/db_xref="taxon:10090"
/clone="MC6373"
/sex="male"
/lab_host="JMI09"
/clone_lib="mouse liver, vehicle control"

NotI; Site 2: EcoRI; Vector: pGEM11zf (Promega); Site 1:
NotI; Site 2: EcoRI; First strand cDNA was primed with a
NotI-polyT primer
[5'-AACTGGAAGATTGCGCGCGAGGAATTTTTTTTTTTT-3']
Double-stranded cDNA was ligated with EcoRI adapters
(Pharmacia), digested with NotI, and ligated into the
EcoRI/NotI sites of the pGEM11zf vector. The library was
NOT normalized."

ORIGIN

Query Match 88.0%; Score 19; DB 1; Length 163;
Best Local Similarity 90.5%; Pred. No. 3.1e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 21
||||| : |||||
Db 134 TGAAGGTGTCACGATCTTGT 114

RESULT 2

AW111034/c
LOCUS
DEFINITION
MW725 mouse liver, dioxin treated Mus musculus cDNA clone MT725 3'
similar to X86561 Rat gene for alpha-fibrinogen, mRNA sequence.
AW111034
VERSION
AW111034.1 GI:6823747
EST.
Mus musculus (house mouse)
ORGANISM

REFERENCE

AW111034 232 bp mRNA linear EST 31-JAN-2000
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 232)
Thomas, R.S., Rank, D.R., Penn, S.G., Zaestrow, G.M., Jovanovich, S. and
Bradfield, C.A.
McArdle Laboratory/Molecular Dynamics Dioxin EST Project
Unpublished (1999)
Contact: Bradfield CA
McArdle Laboratory for Cancer Research
University of Wisconsin
1400 University Ave., Madison, WI 53706, USA
Tel: 608 262 2024
Fax: 608 262 2824

Email: bradfield@oncology.wisc.edu
This clone was sequenced as part of a project to develop a database
on gene expression changes following exposure to various
environmental toxicants. The database can be accessed at
http://mcacrdle.oncology.wisc.edu/bradfield/. Treatment- Dioxin (10
ug/kg, ip) in a dioxane vehicle. Animals sacrificed- 48 hrs
post-injection.

Seq primer: SP6

FEATURES

source
1. 232
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MT725"
/sex="male"
/lab_host="JMI09"
/clone_lib="mouse liver, dioxin treated"
/note="Organ: liver; Vector: pGEM11zf (Promega); Site 1:

NotI; Site 2: EcoRI; First strand cDNA was primed with a
NotI-polyT primer
[5'-AACTGGAAGATTGCGCGCGAGGAATTTTTTTTTTTT-3']
Double-stranded cDNA was ligated with EcoRI adapters
(Pharmacia), digested with NotI, and ligated into the
EcoRI/NotI sites of the pGEM11zf vector. The library was
NOT normalized."

ORIGIN

Query Match 88.0%; Score 19; DB 1; Length 232;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 21
||||| : |||||
Db 122 TGAAGGTGTCACGATCTTGT 102

RESULT 3

BX632408/c
LOCUS
DEFINITION
BX632408 pBluescript Lion Mus musculus cDNA clone LIONp462C03455
3', mRNA sequence.
BX632408
VERSION
BX632408.1 GI:33612283
EST.
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM

REFERENCE

AW111034 232 bp mRNA linear EST 31-JAN-2000
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 341)
Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schlueker, T.,
Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Mouse ArrayTAG cDNA (LION)
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; LIONp462C03455.
RZPDLIB;
Mouse ArrayTAG cDNA (LION)
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=4
62 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACACGCTATGAC.
FEATURES
source
1. 341
/location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIONp462C03455"
/lab_host="DH10B"
/clone_lib="pBluescript Lion"

ORIGIN

Query Match 88.0%; Score 19; DB 5; Length 341;
Best Local Similarity 90.5%; Pred. No. 3.3e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAAGGTGCGCGGATCTTGT 21
||||| : |||||
Db 139 TGAAGGTGTCACGATCTTGT 119

RESULT 4

TITLE Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

PUBLISHED 10922068

COMMENT On Jan 26, 2001 this sequence version replaced gi:12563595. Other ESTs: H3060C06-3

Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cda@gaun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3060 row: C column: 06
Seq primer: -21M13 Reverse
High quality sequence stop: 629
POLYA=No.

FEATURES source
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:H3060C06-5"
/db_xref="taxon:10090"
/clone="H3060C06"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA libraries"
/lab_host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN
Query Match 88.0%; Score 19; DB 2; Length 629;
Best Local Similarity 90.5%; Pred. No. 3.5e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 21
|||||||:|||||||
Db 51 TGAAGGTGTCACGATCTTGT 31

RESULT 7
CV070443/c
LOCUS WPANhux1516F2.002_430126.H1_012.abl Preamplified custom cDNA library in pCMVaport6.1 (ResGen, Invitrogen Inc.) Emiliana huxleyi cDNA, mRNA sequence.

ACCESSION CV070443
VERSION CV070443.1 GI:51533607
KEYWORDS EST.
SOURCE Emiliana huxleyi
ORGANISM Emiliana huxleyi
REFERENCE 1 (bases 1 to 858)
Eukaryota; Haptophyceae; Isochrysidales; Emiliana.

Wahlund, T.W., Zhang, X. and Read, B.A.
Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying Cultures of *Emiliana huxleyi*
Micropaleontology (2004) In press
Contact: Betsy Read
Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA
Tel: 760 750 4129
Email: bread@csu-sm.edu

FEATURES source
1. .858
Location/Qualifiers
/organism="Emiliana huxleyi"
/mol_type="mRNA"
/strain="1516"
/db_xref="taxon:2903"
/dev_stage="Late log growth phase"
/clone_lib="Preamplified custom cDNA library in pCMVaport6.1 (ResGen, Invitrogen Inc.)"
/note="Emiliana huxleyi grown in Artificial Seawater (Guillard's F/2 media)."

ORIGIN
Query Match 88.0%; Score 19; DB 7; Length 858;
Best Local Similarity 90.5%; Pred. No. 3.6e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 21
|||||||:|||||||
Db 364 TGAAGGTGCGCGGATCTTGT 344

RESULT 8
BP637291
LOCUS BP637291
DEFINITION BP637291 RAPL19 Arabidopsis thaliana cDNA clone RAFL19-05-B20 3', mRNA sequence.

ACCESSION BP637291
VERSION BP637291.1 GI:49288543
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 393)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)

TITLE JOURNAL
PUBLISHED 11910074
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@tc.riken.go.jp
reversed clone; Please visit our web site (<http://pfweb.gsc.riken.go.jp/>) for further details.

FEATURES source
1. .393
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL19-05-B20"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL19"
/note="Site_1: BamHI; Site_2: SalI; Subtraction Library"

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Query Match      87.0%; Score 18.8; DB 3; Length 393;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
Db 356 TGAAGGTCTCGGATCTTGTT 377

RESULT 9
BP596595
LOCUS BP596595
DEFINITION BP596595 RAPL15 Arabidopsis thaliana cDNA clone RAFL15-36-A01 3',
mRNA sequence.
ACCESSION BP596595
VERSION BP596595.1 GI:49164063
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 403)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
reversed clone; please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.

FEATURES
source
1..403
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-36-A01"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: SalI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 403;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
Db 377 TGAAGGTCTCGGATCTTGTT 398

RESULT 11
BP605386
LOCUS BP605386
DEFINITION BP605386 RAPL16 Arabidopsis thaliana cDNA clone RAFL16-66-K06 3',
mRNA sequence.
ACCESSION BP605386
VERSION BP605386.1 GI:49252899
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 425)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
reversed clone; please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 409)
Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K.,
Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S.,
Iida, J., Kawai, J., Sasaki, D., Shiraki, T., Hayashizaki, Y. and
Shinozaki, K.
Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs
Unpublished (2005)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998, 2002). This clone is in a
modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp) and
http://rarge.gsc.riken.jp/ for further details.
reversed clone.
Location/Qualifiers
1..409
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL07-57-E07"
/dev_stage="rosette plants"
/lab_host="DH10B"
/clone_lib="RAFL7"
/note="Site_1: BamHI; Site_2: SalI; subjected to
cold-treated (1, 2, 5, 10, 24 hr)"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 409;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
Db 377 TGAAGGTCTCGGATCTTGTT 398

RESULT 11
BP605386
LOCUS BP605386
DEFINITION BP605386 RAPL16 Arabidopsis thaliana cDNA clone RAFL16-66-K06 3',
mRNA sequence.
ACCESSION BP605386
VERSION BP605386.1 GI:49252899
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 425)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
reversed clone; please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.

```

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FEATURES
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  Best Local Similarity 90.9%; Pred. No. 4.2e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGATCTTGT 22
    ||||| ||||| ||||| |||||
Db 382 TGAAGGTTCTCGATCTTGT 403

RESULT 12
AV533334
LOCUS
DEFINITION
  AV533334 Arabidopsis thaliana flower buds Columbia Arabidopsis
  thaliana cDNA clone FB059h07F 3', mRNA sequence.
ACCESSION
  AV533334
VERSION
  AV533334.1 GI:8693617
KEYWORDS
  EST.
SOURCE
  Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 432)
  Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  A large scale analysis of cDNA in Arabidopsis thaliana: Generation
  of 12,028 non-redundant expressed sequence tags from normalized and
  size-selected cDNA libraries
  DNA Res. 7 (3), 175-180 (2000)
JOURNAL
  PUBLISHED 10907847
COMMENT
  Contact: Erika Asamizu
  The First Laboratory for Plant Gene Research
  Kazusa DNA Research Institute
  Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
  Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

ORIGIN
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  Best Local Similarity 90.9%; Pred. No. 4.2e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGATCTTGT 22
    ||||| ||||| ||||| |||||
Db 357 TGAAGGTTCTCGATCTTGT 378

RESULT 14
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LOCUS
DEFINITION
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ACCESSION
  BP589232
VERSION
  BP589232.1 GI:49156700
KEYWORDS
  EST.
SOURCE
  Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 433)
  Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
  Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M.,
  Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
  Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
  Functional annotation of a full-length Arabidopsis cDNA collection
  Science 296 (5565), 141-145 (2002)
JOURNAL
  PUBLISHED 11910074
COMMENT
  Contact: Motoaki Seki
  Plant Functional Genomics Research Group
  RIKEN Genomic Sciences Center
  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
  Tel: 81-298-36-4359
  Fax: 81-298-36-9060
  Email: msekita@cc.riken.go.jp
  reversed clone; Please visit our web site
  (http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
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      1..433

FEATURES
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        /note="Site_1: BamHI; Site_2: SalI; dark-grown"

ORIGIN
  Query Match      87.0%; Score 18.8; DB 3; Length 425;
  Best Local Similarity 90.9%; Pred. No. 4.2e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGATCTTGT 22
    ||||| ||||| ||||| |||||
Db 382 TGAAGGTTCTCGATCTTGT 403

RESULT 12
AV533334
LOCUS
DEFINITION
  AV533334 Arabidopsis thaliana flower buds Columbia Arabidopsis
  thaliana cDNA clone FB059h07F 3', mRNA sequence.
ACCESSION
  AV533334
VERSION
  AV533334.1 GI:8693617
KEYWORDS
  EST.
SOURCE
  Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 432)
  Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  A large scale analysis of cDNA in Arabidopsis thaliana: Generation
  of 12,028 non-redundant expressed sequence tags from normalized and
  size-selected cDNA libraries
  DNA Res. 7 (3), 175-180 (2000)
JOURNAL
  PUBLISHED 10907847
COMMENT
  Contact: Erika Asamizu
  The First Laboratory for Plant Gene Research
  Kazusa DNA Research Institute
  Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
  Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
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        /tissue_type="flower buds"
        /clone_lib="Arabidopsis thaliana flower buds Columbia"
        /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
        XhoI"

ORIGIN
  Query Match      87.0%; Score 18.8; DB 1; Length 432;
  Best Local Similarity 90.9%; Pred. No. 4.2e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGATCTTGT 22
    ||||| ||||| ||||| |||||
Db 357 TGAAGGTTCTCGATCTTGT 378

RESULT 13
AV562602
LOCUS
DEFINITION
  AV562602 Arabidopsis thaliana green siliques Columbia Arabidopsis
  thaliana cDNA clone SQ172g05F 3', mRNA sequence.
ACCESSION
  AV562602

```

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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-49-B10"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/notes="Site_1: BamHI; Site_2: SalI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 433;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
||||| ||||| ||||| |||||
Db 358 TGAAGGTTCTCGGATCTTGTT 379

RESULT 15
BP606850 434 bp mRNA linear EST 25-JUN-2004
LOCUS BP606850 Arabidopsis thaliana cDNA clone RAFL16-72-107 3',
mRNA sequence.
ACCESSION BP606850.1 GI:49254363
VERSION BP606850
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 434)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074

COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@tc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
source
1..434
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-21-K07"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/notes="Site_1: BamHI; Site_2: SalI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 439;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
||||| ||||| ||||| |||||
Db 360 TGAAGGTTCTCGGATCTTGTT 381

RESULT 17
BP604921 441 bp mRNA linear EST 25-JUN-2004
LOCUS BP604921 Arabidopsis thaliana cDNA clone RAFL16-64-N16 3',
mRNA sequence.
ACCESSION BP604921.1 GI:49252433
VERSION BP604921
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 441)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074

COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359

```

```

/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-49-B10"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/notes="Site_1: BamHI; Site_2: SalI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 433;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
||||| ||||| ||||| |||||
Db 358 TGAAGGTTCTCGGATCTTGT 379

RESULT 15
BP606850 434 bp mRNA linear EST 25-JUN-2004
LOCUS BP606850 Arabidopsis thaliana cDNA clone RAFL16-72-107 3',
mRNA sequence.
ACCESSION BP606850.1 GI:49254363
VERSION BP606850
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 434)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074

COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@tc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
source
1..434
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-21-K07"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/notes="Site_1: BamHI; Site_2: SalI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 439;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
||||| ||||| ||||| |||||
Db 360 TGAAGGTTCTCGGATCTTGT 381

RESULT 17
BP604921 441 bp mRNA linear EST 25-JUN-2004
LOCUS BP604921 Arabidopsis thaliana cDNA clone RAFL16-64-N16 3',
mRNA sequence.
ACCESSION BP604921.1 GI:49252433
VERSION BP604921
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 441)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074

COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359

```



```

Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
    source
        1..441
            /organism="Arabidopsis thaliana"
            /mol_type="mRNA"
            /db_xref="taxon:3702"
            /clone="RAFL16-64-N16"
            /lab_host="DH10B"
            /clone_lib="RAFL16"
            /note="Site_1: BamHI; Site_2: SalI; dark-grown"

ORIGIN
Query Match      87.0%; Score 18.8; DB 3; Length 441;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 354 TGAAGGTTCTCGGATCTTGT 375

RESULT 18
AV563537
LOCUS
DEFINITION
    AV563537 Arabidopsis thaliana green siliques Columbia Arabidopsis
    thaliana cDNA clone SQ189b02F 3', mRNA sequence.
ACCESSION
    AV563537
VERSION
    AV563537.1 GI:8734963
KEYWORDS
    EST.
SOURCE
    Arabidopsis thaliana (thale cress)
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
    1 (bases 1 to 518)
    Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
    A large scale analysis of cDNA in Arabidopsis thaliana: Generation
    of 12,028 non-redundant expressed sequence tags from normalized and
    size-selected cDNA libraries
    DNA Res. 7 (3), 175-180 (2000)
    10907847
    Contact: Erika Asamizu
    The First Laboratory for Plant Gene Research
    Kazusa DNA Research Institute
    Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
    Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
    Location/Qualifiers
        1..518
            /organism="Arabidopsis thaliana"
            /mol_type="mRNA"
            /ecotype="Columbia"
            /db_xref="taxon:3702"
            /clone="SQ189b02F"
            /tissue_type="green siliques"
            /clone_lib="Arabidopsis thaliana green siliques Columbia"
            /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
            XhoI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 1; Length 524;
Best Local Similarity 90.9%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 TGAAGGTTCTCGGATCTTGT 405

RESULT 20
AV563537
LOCUS
DEFINITION
    AV563537 Arabidopsis thaliana green siliques Columbia Arabidopsis
    thaliana cDNA clone SQ189b03F 3', mRNA sequence.
ACCESSION
    AV563537
VERSION
    AV563537.1 GI:8734964
KEYWORDS
    EST.
SOURCE
    Arabidopsis thaliana (thale cress)
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
    1 (bases 1 to 524)
    Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
    A large scale analysis of cDNA in Arabidopsis thaliana: Generation
    of 12,028 non-redundant expressed sequence tags from normalized and
    size-selected cDNA libraries
    DNA Res. 7 (3), 175-180 (2000)
    10907847
    Contact: Erika Asamizu
    The First Laboratory for Plant Gene Research
    Kazusa DNA Research Institute
    Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
    Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
    Location/Qualifiers
        1..524
            /organism="Arabidopsis thaliana"
            /mol_type="mRNA"
            /ecotype="Columbia"
            /db_xref="taxon:3702"
            /clone="SQ189b03F"
            /tissue_type="green siliques"
            /clone_lib="Arabidopsis thaliana green siliques Columbia"
            /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
            XhoI"

ORIGIN
Query Match      87.0%; Score 18.8; DB 1; Length 524;
Best Local Similarity 90.9%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 TGAAGGTTCTCGGATCTTGT 405

RESULT 20
AV563537
LOCUS
DEFINITION
    AV563537 Arabidopsis thaliana green siliques Columbia Arabidopsis
    thaliana cDNA clone SQ189b03F 3', mRNA sequence.
ACCESSION
    AV563537
VERSION
    AV563537.1 GI:5846556
KEYWORDS
    EST.
SOURCE
    Arabidopsis thaliana (thale cress)
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
    1 (bases 1 to 552)
    Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
    Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P.,
    Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,
    Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,
    Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
    Nobrega,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and
    Hanson,D.
    Arabidopsis thaliana Gene Expression MicroArray
    Unpublished (1999)
    Contact: David Smoller, Ph.D.
    Genome Systems, Inc., a wholly owned subsidiary of Incyte
    Pharmaceuticals, Inc.
    4633 World Parkway Circle, St. Louis, MO 63134, USA
    Tel: 877-577-2733

TITLE
    Arabidopsis thaliana Gene Expression MicroArray
JOURNAL
COMMENT
    Contact: David Smoller, Ph.D.
    Genome Systems, Inc., a wholly owned subsidiary of Incyte
    Pharmaceuticals, Inc.
    4633 World Parkway Circle, St. Louis, MO 63134, USA
    Tel: 877-577-2733

```


Fax: 314-427-3324
Email: servicegenomesystems.com.

FEATURES

source
1. .552
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="701556873"
/tissue_type="rosette"
/dev_stage="4 - 7 weeks"
/clone_lib="A. thaliana, Columbia Col-0, rosette-3"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; cDNA library was derived from untreated rosette tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunt-ended, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."

ORIGIN

Query Match 87.0%; Score 18.8; DB 1; Length 552;
Best Local Similarity 90.9%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGGATCTTGT 22
|||||
Db 329 TGAAGTTCCTCGATCTTGT 350
|||||

RESULT 21

LOCUS CNS0ADWK/c
DEFINITION Arabidopsis thaliana Full-length cDNA complete sequence from clone GSLT1S192D05 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
BX814924
HTC; GSIT cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished
2 (bases 1 to 3509)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES

source

1. .3509
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLT1S192D05"
/tissue_type="Adult vegetative tissue"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
1. .3509
/gene="Atlg72180"

gene

ORIGIN

Query Match 87.0%; Score 18.8; DB 4; Length 3509;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TGAAGTGCRCGGATCTTGT 22
|||||
Db 3176 TGAAGTTCCTCGATCTTGT 3155
|||||

RESULT 22

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

organism

strain

db_xref

clones

tissue

lab host

clone_lib

note

vector

psport1

site_1

site_2

noti

female

query match

best local similarity

matches

conservative

mismatches

indels

gaps

qy

db

result 23

locus

definition

accession

version

keywords

source

organism

reference

authors

title

journal

comment

features

source

location/qualifiers

organism

strain

db_xref

clones

tissue

lab host

clone_lib

note

vector

psport1

site_1

site_2

noti

female

```

KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 673)
AUTHORS
Bay, M., Stuber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,
Saedler, H. and Zachgo, S.
TITLE
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
PUBMED
15539471
COMMENT
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
Location/Qualifiers
1..673
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018.6.09.b23"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 85.2%; Score 18.4; DB 1; Length 673;
Best Local Similarity 86.4%; Pred. No. 6.8e+02;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGATCTTGT 22
||||| |:|:|||||
Db 93 TGAAGGAGCCACGATCTTGT 72

RESULT 24
DR731656 859 bp mRNA linear EST 18-JUL-2005
LOCUS FGAS077576 Triticum aestivum FGAS: Talt2 Triticum aestivum cDNA,
DEFINITION mRNA sequence.
ACCESSION DR731656
VERSION DR731656.1 GI:70958035
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE
1 (bases 1 to 859)
AUTHORS Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [109,609].
Plate: Talt258 row: P column: 09.
FEATURES
source
Location/Qualifiers
1..889
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/mol_type="mRNA"
/db_xref="taxon:4565"
/lab_host="DH5 alpha"
/clone_lib="Triticum aestivum FGAS: Talt2"
/notes="Organ: Crown; Vector: pGEM-T; SSH (suppression
subtractive hybridization) cDNA library from genotype
Clt4106 cold hardened at 2 C for 1 day (24 H) (tester) and
subtracted against genotype Norstar cold hardened at 2 C
for 21 days and 49 days (equal amount of cDNA pooled
together before subtraction, driver). Nitro-pyrole
anchored oligo-dT priming and non-directional cloning."

KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 889)
AUTHORS Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [109,609].
Plate: Talt258 row: P column: 09.
FEATURES
source
Location/Qualifiers
1..889
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/lab_host="DH5 alpha"
/clone_lib="Triticum aestivum FGAS: Talt2"
/notes="Organ: Crown; Vector: pGEM-T; SSH (suppression
subtractive hybridization) cDNA library from genotype
Clt4106 cold hardened at 2 C for 1 day (24 H) (tester) and
subtracted against genotype Norstar cold hardened at 2 C
for 21 days and 49 days (equal amount of cDNA pooled
together before subtraction, driver). Nitro-pyrole
anchored oligo-dT priming and non-directional cloning."

```


Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 281)
 Henrich, J., Hermanns, J., Kranz, H., Loebert, R., Schlueter, T., Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Rat ArrayTAG cDNA

Unpublished (2004)

COMMENT

Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPD: LIONP463A10178.

RZPDLIB;

Rat ArrayTAG cDNA

http://www.rzpd.de/cgi-

bin/products/showlib.pl.cgi?response?libNo=463 Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

RP: CAGGAACAGCTATGAC

FEATURES
 source

Location/Qualifiers

1. .281

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="LIONP463A10178"

/lab_host="DH10B"

/clone_lib="Rat pBluescript Lion"

ORIGIN

Query Match 83.3%; Score 18; DB 7; Length 281;
 Best Local Similarity 90.0%; Pred. No. 9.8e+02;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGGTGCGCGGATCTTGT 21

Db 136 GAAGGTGTCGCGGATCTTGT 117

RESULT 29
 AA875097/c

LOCUS

DEFINITION

AA875097 335 bp mRNA linear EST 04-JUL-1999

UI-R-E0-cf-g-09-0-UI.81 UI-R-E0 Rattus norvegicus cDNA clone

UI-R-E0-cf-g-09-0-UI.3' similar to gi|790485|emb|X86561|RNLFIB Rat

gene for alpha-fibrinogen, mRNA sequence.

AA875097

AA875097.1 GI:4230978

EST.

Rattus norvegicus (Norway rat)

Source

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 335)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

8889548

COMMENT

On Mar 20, 1998 this sequence version replaced gi:2980045.

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: benton-soares@uiowa.edu

The sequence tag present in the cDNA between the NotI site and the

FEATURES
 source

Location/Qualifiers

1. .335

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-E0-cf-g-09-0-UI"

/dev_stage="embryonic"

/lab_host="DH10B (Life Technologies)"

/clone_lib="UI-R-E0"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: NotI; Site 2: EcoRI; This library

consists of a mixture of individually tagged normalized

libraries constructed from 8, 12 and 18-day embryo. The

tag is a string of 3-5 nucleotides present between the

Not I site and the oligo-dT track which allows

identification of the library of origin of a clone within

the mixture."

ORIGIN

Query Match 83.3%; Score 18; DB 1; Length 335;
 Best Local Similarity 90.0%; Pred. No. 1e+03;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGGTGCGCGGATCTTGT 21

Db 149 GAAGGTGTCGCGGATCTTGT 130

RESULT 30

AA061605

LOCUS

DEFINITION

AA061605 570 bp mRNA linear EST 03-FEB-1997

ml33e10.r1 Stratagene mouse testis (#937308) Mus musculus cDNA

clone IMAGE:513834 5' similar to gb:X07862 Human mRNA for protamine

2 (HUMAN); gb:X14004 Mouse protamine 2 mRNA (MOUSE); , mRNA

sequence.

AA061605

AA061605.1 GI:1555405

EST.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 570)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:307682

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 241.

FEATURES

Location/Qualifiers

```

source
1. .570
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:513834"
/sex="males"
/tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse testis (#937308)"
/notes="Organ: testis; Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Oligo adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match 83.3%; Score 18; DB 1; Length 570;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 543 AAGGGCCACGGATCTTGT 562

RESULT 31
BP294923/c
LOCUS
DEFINITION BP294923 Sugano cDNA library, macrophage Homo sapiens cDNA clone
MFB06013, mRNA sequence.
ACCESSION BP294923
VERSION BP294923.1 GI:52223883
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamaehita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
Source
Location/Qualifiers
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MFB06013"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"

ORIGIN
Query Match 83.3%; Score 18; DB 3; Length 582;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTG 20
|||||:|||||
Db 353 TGAAGTGCACGGATCTTG 334

RESULT 32
AW727610
LOCUS
DEFINITION AW727610 Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0015C14, mRNA sequence.
ACCESSION AW727610
VERSION AW727610.1 GI:7625168
KEYWORDS EST.
SOURCE Gossypium arboreum
ORGANISM Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 1349)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
High quality sequence stop: 1349.
Location/Qualifiers
1..1349
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AXA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0015C14"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 83.3%; Score 18; DB 1; Length 1349;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGTGCRCGGATCTTGT 21
|||||:|||||
Db 199 GAAGTACCACGGATCTTGT 218

RESULT 33
CL174879
LOCUS
DEFINITION CL174879 Sorghum bicolor genomic clone 10891971, genomic survey
sequence.
ACCESSION CL174879
VERSION CL174879.1 GI:40687394
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 559)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalo,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLoS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA

```

Orion Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6979
 Fax: 314 615 5975
 Email: jbedell@oriongenomics.com
 Plate: 379 row: o column: 03
 Seq primer: SWfor Forward
 Class: methylation filtered
 High quality sequence stop: 559.

FEATURES

source

1. .559
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /cultiivar="ATx623"
 /db_xref="taxon:4558"
 /clone_lib="Sorghum methylation-filtered library (LibID: 104)"
 /notes="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."

ORIGIN

Query Match 81.5%; Score 17.6; DB 10; Length 559;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGTGCCRCGGATCTTGT 22
 |||||:|||||
 Db 375 GGTGCCACGGATCTTGT 392

RESULT 34

BF705257/c

LOCUS BF705257 179 bp mRNA linear EST 29-DEC-2000
 DEFINITION RHIZ2_2_G01.b1_A003 Rhizome2 (RHIZ2) Sorghum propinquum cDNA, mRNA sequence.
 ACCESSION BF705257
 VERSION BF705257.1 GI:11996918
 KEYWORDS EST.
 SOURCE Sorghum propinquum
 ORGANISM Sorghum propinquum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 179)
 Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.
 An EST database from Sorghum: Sorghum propinquum rhizomes

Unpublished (2000)

CONTACT: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210

Email: mmpratt@uga.edu

Seq primer: JEN REV

High quality sequence stop: 141

POLYA=No.

FEATURES

source

1. .179
 /organism="Sorghum propinquum"
 /mol_type="mRNA"
 /db_xref="taxon:132711"
 /clone_lib="Rhizome2 (RHIZ2)"
 /notes="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 179;
 Best Local Similarity 85.7%; Pred. No. 1.8e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||
 Db 127 GAAGTGTCACGGATCTTGT 107

RESULT 35

DR705480

LOCUS DR705480 218 bp mRNA linear EST 14-JUL-2005
 DEFINITION Asn_05659 Aspergillus niger pBluescript (EcoRI-XhoI) Aspergillus niger cDNA clone Asn_05659, mRNA sequence.

ACCESSION DR705480

VERSION DR705480.1 GI:70821771

KEYWORDS EST.

SOURCE Aspergillus niger

ORGANISM Aspergillus niger

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE 1 (bases 1 to 218)

Teang, A., Storms, R. and Bulter, G.

Expressed sequence tags from Aspergillus niger cDNA library

Unpublished (2005)

Contact: Teang A

Centre for Structural and Functional Genomics

Concordia University

7141 Sherbrooke Street West, SP545-1, Montreal, QC H4B1R6, Canada

Tel: 514 848 2424 3405

Fax: 514 848 4504

Email: tsang@vax2.concordia.ca

POLYA=No.

FEATURES

source

1. .218
 /organism="Aspergillus niger"
 /mol_type="mRNA"
 /strain="N402"
 /db_xref="taxon:5061"
 /clone="Asn_05659"
 /dev_stage="mycelial growth"
 /lab_host="E. coli"
 /clone_lib="Aspergillus niger pBluescript (EcoRI-XhoI)"
 /note="Vector: pBluescript KS+; Site 1: XhoI; Site 2: EcoRI; Complementary DNA was synthesized with ZAP kit (Stratagene) using poly(A)+RNA isolated from Aspergillus niger cultured under different carbon sources (glucose, maltose, xylose, lactose, sorbitol, xylan, and bran). Synthesis was primed with oligo(dT)/XhoI primer. EcoRI adaptors were ligated to the blunt-ended, double-stranded cDNA. The EcoRI-XhoI-digested cDNA was ligated with EcoRI-XhoI-digested pBluescript KS+ (Invitrogen Corp)."

ORIGIN

Query Match 80.6%; Score 17.4; DB 8; Length 218;
 Best Local Similarity 85.7%; Pred. No. 1.9e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TGAAGTGCCRCGGATCTTGT 21
 |||||:|||||
 Db 52 TGAAGGTACACGGATCTTGT 72

RESULT 36

CX223617/c

LOCUS CX223617 243 bp mRNA linear EST 29-DEC-2004
 DEFINITION MNS42007 Mouse Neurosphere Normalized cDNA library Mus musculus cDNA 5', mRNA sequence.

ACCESSION CX223617

VERSION CX223617.1 GI:56878909

KEYWORDS EST.

Query Match 80.6%; Score 17.4; DB 5; Length 285;
 Best Local Similarity 85.7%; Pred. No. 1.9e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCCRGGATCTTGT 22
 |||||1:|||||
 Db 203 GAAGGTGTCACGGATGTTGT 183

RESULT 39
 AJ474162/c
 LOCUS AJ474162 360 bp mRNA linear EST 24-MAY-2002
 DEFINITION AJ474162 S00008 Hordeum vulgare cDNA clone S0000800247F08F1, mRNA sequence.

ACCESSION AJ474162
 VERSION AJ474162.1 GI:21190118
 KEYWORDS EST.
 SOURCE Hordeum vulgare

ORGANISM

Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 360)

AUTHORS Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.

TITLE Barley EST's

JOURNAL Unpublished (2002)

COMMENT Contact: Schulman AH
 Institute of Biotechnology
 University of Helsinki
 P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
 Finland.

FEATURES

source

1..360 Location/Qualifiers
 /organism="Hordeum vulgare"
 /mol_type="mRNA"
 /db_xref="taxon:4513"
 /clone="S0000800247F08F1"
 /tissue_type="Callus"
 /clone_lib="S00008"
 /note="Callus K19"

ORIGIN

Query Match 80.6%; Score 17.4; DB 1; Length 360;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCCRGGATCTTGT 22
 |||||1:|||||
 Db 62 GAAGGTGTCGGATGTTGT 42

RESULT 40
 DR793683/c
 LOCUS DR793683 374 bp mRNA linear EST 27-JUL-2005
 DEFINITION ZM_BFB001A24.f Zm_BFB Zea mays cDNA 3', mRNA sequence.

ACCESSION DR793683
 VERSION DR793683.1 GI:71314135
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 374)

AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE Zea Full-length cDNA Project

JOURNAL Unpublished (2005)

COMMENT Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585

FEATURES

source

1..374 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="mixed (silks, husks, ears, pollen, shoot
 tips, leaf, root tips, whole seed, embryo)"
 /dev_stage="varies by tissue"
 /lab_host="DH10B T1 phage resistant"

/clone_lib="ZM_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Zea Full length cDNA library (3530 library)
 created by invitrogen from multiple tissues; Organ: silks,
 husks, ears, pollen, shoot tips, leaf, root tips, whole
 seed, embryo. This is a Gateway compatible vector,
 permitting clone movement to new vector backbones for
 expression in diverse host cells using recombination
 rather than restriction enzymes. poly(A)+ mRNA was
 prepared by invitrogen, and equimolar amounts of RNA from
 each of the 12 tissue samples were mixed together for
 selection of mRNA with a 5' cap. After synthesis of cDNA,
 a normalization step was conducted against the mixture of
 RNA sources. Tissues prepared: 1. just emerging silks; 2.
 inner husks from ears of sample #1; 3. 20 day aleurone; 4.
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
 15 day old seedlings; all leaves with an expanded or
 partially expanded sheath were removed; 8. mature leaf
 tissue; 9. 0.5 cm long root tips from 15 day old
 seedlings; 10. 10 day whole seed; 11. 12 day endosperm and
 embryo; 12. 17 day endosperm and embryo. All of the
 sequenced clones in Zea Full-length cDNA Project will be
 archived at the University of Arizona. Clones, high
 density filters and amplified library can be ordered from
 the University of Arizona
 (http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 80.6%; Score 17.4; DB 8; Length 374;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCRCGGATCTTGT 22
 |||||1:|||||
 Db 307 GAAGGTGTCACGGATGTTGT 287

RESULT 41

CF646223
 LOCUS CF646223 386 bp mRNA linear EST 02-OCT-2003
 DEFINITION Invtrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION CF646223
 VERSION CF646223.1 GI:37417141
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 386)

AUTHORS Walbot,V.

TITLE Zea ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University

COMMENT Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu
 Plate: 0014 row: A column: 24.

Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3530.1.111.1 row: C column: 03.

FEATURES

SOURCE

Location/Qualifiers

1. .386
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="multiple"
 /dev_stage="varies by tissue"
 /lab_host="PH108"
 /clone_lib="3530 - Full length cDNA library created by
 Invitrogen from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
 Project contracted with Invitrogen to produce a
 normalized, full length library in a pSPORT vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZmDB in the EST library description tables. poly(A)+
 mRNA was prepared by Invitrogen, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 dap aleurone; 4. immature tassels, stages from
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
 vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
 12 dap endosperm and embryo; 12. 17 dap endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 Unigene clones from the Maize Gene Discovery EST
 sequencing projects. Clones can be ordered through the
 ZmDB web site or directly from the University of Arizona
 (<http://www.genome.arizona.edu/orders/>). High density
 filters containing over 18,000 clones can also be ordered
 from the University of Arizona."

ORIGIN

Query Match 80.6%; Score 17.4; DB 6; Length 386;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAAGTGCCRCGGATCTGTT 22
 ||||| : |||||
 Db 100 GAAGGTGTCACGGATGTTT 120

RESULT 42

BI098781/c

LOCUS

DEFINITION IPI 33_B04.b1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
 mRNA sequence.

ACCESSION

BI098781

VERSION

EST.

KEYWORDS

Sorghum bicolor (sorghum)

ORGANISM

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 391)

AUTHORS

Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and

TITLE

JOURNAL

COMMENT

Pratt,L.H.
 An EST database from Sorghum: developing preanthesis pannicles
 Unpublished (2001)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for high quality sequence is
 20. Three-prime sequences, which are obtained with PolyTmix or T7
 sequencing primer, are presented as the reverse complement.
 Seq primer: JEN REV
 High quality sequence stop: 239
 POLYA=No.

FEATURES

SOURCE

Location/Qualifiers

1. .391
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /clone_lib="Immature pannicle 1 (IP1)"
 /note="Organ: Developing preanthesis pannicles; Vector:
 pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
 Site 2: EcoRI; The library was made from poly-A RNA in the
 cloning vector lambda ZAP II. Clones to be sequenced were
 prepared by mass excision."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 391;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAAGTGCCRCGGATCTGTT 22

||||| : |||||

Db 58 GAAGGTGTCACGGATATTGTT 38

||||| : |||||

RESULT 43

BI098170/c

LOCUS

DEFINITION IPI 29_A02.b1_A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
 mRNA sequence.

ACCESSION

BI098170

VERSION

BI098170.1

KEYWORDS

EST.

SOURCE

Sorghum bicolor (sorghum)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 397)

AUTHORS

Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and
 Pratt,L.H.

An EST database from Sorghum: developing preanthesis pannicles

Unpublished (2001)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions

below Phred quality 16. The threshold for high quality sequence is

20. Three-prime sequences, which are obtained with PolyTmix or T7

sequencing primer, are presented as the reverse complement.

Seq primer: JEN REV

High quality sequence stop: 389

POLYA=No.

Location/Qualifiers

```

source
1. .397
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IPI)"
/notes="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Query Match      80.6%; Score 17.4; DB 2; Length 397;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGTCRCGCGATCTTGT 22
||||| 1:|||||
Db 330 GAAGGTGTCGCGATCTTGT 310

RESULT 44
CF646224/c
LOCUS CF646224 404 bp mRNA linear EST 02-OCT-2003
DEFINITION 3530.1_l11.1_C03.Y.1_3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION CF646224
VERSION CF646224.1 GI:37417143
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 404)
Walbot V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530.1_l11.1 row: C column: 03.

FEATURES
source
1. .404
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH10B"
/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/notes="Organ: silks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSport vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
RNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the

```

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mixture of RNA sources. This step effected a 20X to 80X
reduction in common transcript types. Tissues prepared: 1.
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 dap aleurone; 4. Immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
vegetative shoot tips from 15 day old seedlings; all
leaves with an expanded or partially expanded sheath
were removed; 8. mature leaf tissue; 9. 0.5 cm long root
tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
12 dap endosperm and embryo; 12. 17 dap endosperm and
embryo. All of the sequenced clones in project 3530 will
be archived at the University of Arizona along with the
Unigene clones from the Maize Gene Discovery EST
sequencing projects. Clones can be ordered through the
ZmDB web site or directly from the University of Arizona
(http://www.genome.arizona.edu/orders/). High density
filters containing over 18,000 clones can also be ordered
from the University of Arizona."

ORIGIN
Query Match      80.6%; Score 17.4; DB 6; Length 404;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGTCRCGCGATCTTGT 22
||||| 1:|||||
Db 305 GAAGGTGTCGCGATCTTGT 285

RESULT 45
BI098323/c
LOCUS BI098323 417 bp mRNA linear EST 26-JUN-2001
DEFINITION IPI_31_A02.b1_A002 Immature pannicle 1 (IPI) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BI098323
VERSION BI098323.1 GI:14569905
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 417)
Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and
Pratt, L.H.
An EST database from Sorghum: developing preanthesis pannicles
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTmix or T7
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 402
POLYA=No.

FEATURES
source
1. .417
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IPI)"
/notes="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

```

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 417;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCGCGGATCTTGT 22
 |||||:|||||
 Db 330 GAAGGTGCGCGGATCTTGT 310

RESULT 46

LOCUS AQ406201
 DEFINITION HS_5047_B2_F08_SP68_RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=623 Col=16 Row=L, genomic survey sequence.

ACCESSION AQ406201
 VERSION AQ406201.1 GI:4411566

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 426)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

JOURNAL

High Throughput Sequencing Center

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACpac Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (<http://www.htsc.washington.edu>)

Plate: 623 row: L column: 16

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 426.

FEATURES

source

1. .426

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=623 Col=16 Row=L"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBAC3.6 vector at EcoRI sites"

ORIGIN

Query Match 80.6%; Score 17.4; DB 9; Length 426;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 21
 |||||:|||||

Db 77 TGAAGTGCRCGGATCTTGT 97

RESULT 47

LOCUS BI074698/c

DEFINITION

RNA sequence.

ACCESSION BI074698

VERSION BI074698.1

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 432)

Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and

Pratt,L.H.

An EST database from Sorghum: developing preanthesis pannicles

Unpublished (2001)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions

below Phred quality 16. The threshold for high quality sequence is

20. Three-prime sequences, which are obtained with PolyTwix or 77

sequencing primer, are presented as the reverse complement.

Seq primer: JEN REV

High quality sequence stop: 429

POLYA=No.

Location/Qualifiers

1. 432

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="BTx623"

/db_xref="taxon:4558"

/clone_lib="Immature pannicle 1 (ipl)"

/note="Organ: Developing preanthesis pannicles; Vector:

pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;

Site 2: EcoRI; The library was made from poly-A RNA in the

cloning vector lambda ZAP II. Clones to be sequenced were

prepared by mass excision."

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 432;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 |||||:|||||

Db 105 GAAGTGCCRCGGATCTTGT 85

Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 2036 Std Error: 0.00
High quality sequence stop: 421.

FEATURES

Location/Qualifiers
1. .437
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Supernod"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-3806"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH108"
/clone_lib="Gm-cl028"

/notes="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicum, strain USDA110 prior to harvest. Stratagene's cDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGACTAGTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

ORIGIN

Query Match 80.6%; Score 17.4; DB 1; Length 437;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAAGGTGCGCGGATCTTGTT 22
||||| |:|||||
Db 363 GAAGGTGACGGATGTTGT 343
||||| |:|||||

RESULT 49
BF325403/c
LOCUS

438 bp mRNA linear EST 13-JUL-2004

DEFINITION

su21c08.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl066-2056 5' similar to TR:024052 024052
3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE PRECURSOR ;
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF325403
BF325403.1 GI:11275080
EST.
Glycine max (soybean)
Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1. (bases 1 to 438)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Corvelli,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1931 Std Error: 0.00
High quality sequence stop: 421.

TITLE

JOURNAL
COMMENT

Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

FEATURES

Location/Qualifiers
1. .438
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-2056"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week old seedling"
/lab_host="DH108"
/clone_lib="Gm-cl066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

source

1. .438
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-2056"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week old seedling"
/lab_host="DH108"
/clone_lib="Gm-cl066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 438;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAAGGTGCGCGGATCTTGTT 22
||||| |:|||||
Db 342 GAAGGTGACGGATGTTGT 322
||||| |:|||||

RESULT 50

```

BQ133585/c
LOCUS       BQ133585               447 bp    mRNA    linear    EST 05-JUL-2004
DEFINITION  3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE PRECURSOR ;
            Gm-c1052-3943 5' similar to TR:024052 024052
            mRNA sequence.
ACCESSION   BQ133585
VERSION     BQ133585.1  GI:20207496
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 447)
AUTHORS    Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvett,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Stepcos,M., Theising,B., Allen,M.,
            Bowers,I., Person,B., Swallier,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
            Public Soybean EST Project
            Unpublished (1999)
            Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. This clone is
            available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
            57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES    Location/Qualifiers
             1..447
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Harosoy"
                /db_xref="taxon:3847"
                /clone="SOYBEAN CLONE ID: Gm-c1052-3943"
                /tissue_type="whole seedlings of greenhouse grown plants"
                /dev_stage="1 week old"
                /lab_host="DH10B"
                /clone_lib="Gm-c1052"
                /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                XhoI; The Harosoy NIL was constructed and seed was
                provided by Dr. J. Specht, University of Nebraska
                (Shoemaker and Specht, 1995). The cDNA library was
                constructed from mRNA isolated from whole seedlings of 1
                week old greenhouse grown plants. Complementary DNA was
                synthesized from mRNA using a primer consisting of a
                poly(dT) sequence with a XhoI restriction site and a 3'
                anchor. EcoRI adapters were ligated to the blunt-ended
                cDNA fragments followed by XhoI digestion. The cDNA
                fragments were directionally cloned into the EcoRI-XhoI
                restriction site of the pBluescript vector. The ligated
                cDNA fragments were transformed into DH10B host cells
                (GibcoBRL). The library was constructed in cooperation
                with Dr. Paul Keim's laboratory at Northern Arizona
                University."
ORIGIN
Query Match      80.6%; Score 17.4; DB 3; Length 447;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAAGGTGCGCGGATCTTGTT 22
        ||||| |:|||||
DB      380 GAAGGTGTCACGGATGTTGTT 360

```

RESULT 51
CB541407/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB541407
PVPSE2033C10.9 Common bean seedling EST Library - PVPSE2
Phaseolus vulgaris cDNA clone PVPSE2033C10 5', mRNA sequence.
CB541407
EST.
CB541407.1 GI:59935970

Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 462)
Melotto,M., Monteiro-Vitorello,C.B., Bruschi,A.G. and
Camargo,L.E.A.
Comparative bioinformatic analysis of genes expressed in common
bean (Phaseolus vulgaris L.) seedlings
Genome 48 (3), 562-570 (2005)
Contact: Maeli Melotto
Laboratory of Molecular Genetics, Dept. of Plant Pathology
ESALQ - University of Sao Paulo
Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil
Tel: 55 19 3429 4124
Fax: 55 19 3434 3839
Email: melottom@msu.edu
PCR Primers

BACKWARD: M13 reverse
High quality sequence stop: 461.
Location/Qualifiers
1..462
/organism="Phaseolus vulgaris"
/mol_type="mRNA"
/cultivar="SEL 1308"
/db_xref="taxon:3885"
/clone="PVPSE2033C10"
/tissue_type="shoot"
/dev_stage="10 days after seed germination"
/lab_host="E. coli DH10B"
/clone_lib="Common bean seedling EST Library - PVPSE2"
/note="Vector: pSPORT 1; Site 1: Not I; Site 2: Sal I;
mRNA from bean tissue was extracted with the FastTrack 2.0
kit (Invitrogen) and mRNA sample quality was checked in
1.2% formaldehyde-agarose gel. cDNA was synthesized and
cloned into either pCMV Sport 6 or the pSPORT 1 vector
with the SuperScript Plasmid System with Gateway
Technology kit (Gibco BRL) as indicated by the
manufacturer. Recombinant colonies were cultured in
96-well plates and maintained in liquid LB medium with
ampicillin (100ug/ml) and 8% glycerol at -80°C. Plasmid
miniprep was conducted in 96-well plates using standard
procedure and sequencing of the cDNA was performed in
96-well PCR plates using the Big Dye Terminator Cycle
Sequencing Ready Reaction Kit (Applied Biosystems). Clones
were sequenced from the 5' end using either M13 Reverse or
the T7 primer. PCR file consisted of 25 cycles of 10 sec.
at 96°C, 5 sec. at 50°C, and 4 min. at 60°C. After PCR
product precipitation, large-scale automated sequencing
was carried out in a capillary system (3700 ABI Sequencer,
Applied Biosystems). Raw data from sequencing was
validated in a series of automated routine analyses
including Phred/CAP3/Consed programs and Perl scripts
created by our team. Reads that did not have at least 300
bases with Phred quality of 20 were not included in the
analysis."

FEATURES
source

ORIGIN

Query Match 80.6%; Score 17.4; DB 6; Length 462;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 2 GAAGGTGCCRCGGATCTTGT 22
Db 403 GAAGGTGTACCGATGTTGT 383

RESULT 52
BG050084/c 464 bp mRNA linear EST 25-JAN-2001
LOCUS FMI_66_D09_b1_A003 Floral-Induced Meristem 1 (FMI) Sorghum
DEFINITION propinquum cDNA, mRNA sequence.
ACCESSION BG050084
VERSION BG050084.1 GI:12502451
KEYWORDS EST.
SOURCE Sorghum propinquum
ORGANISM Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 464)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and
Pratt,L.H.
TITLE An EST database from Sorghum: floral-induced meristems
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 400
POLYA=No.
FEATURES
source Location/Qualifiers
1..464
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Floral-Induced Meristem 1 (FMI)"
/note="Organ: Floral-Induced Meristem 1; Site_1: XhoI; Site_2:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excision."
ORIGIN
Query Match 80.6%; Score 17.4; DB 2; Length 464;
Best Local Similarity 85.7%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 2;
QY 2 GAAGGTGCCRCGGATCTTGT 22
Db 134 GAAGGTGTACCGATGTTGT 114

RESULT 53
BG104062/c 474 bp mRNA linear EST 30-JAN-2001
LOCUS RHIZ2_40_A12_b1_A003 Rhizome2 (RHIZ2) Sorghum propinquum cDNA, mRNA
DEFINITION sequence.
ACCESSION BG104062
VERSION BG104062.1 GI:12618895
KEYWORDS EST.
SOURCE Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 474)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and
Pratt,L.H.
TITLE An EST database from Sorghum: floral-induced meristems
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 400
POLYA=No.
FEATURES
source Location/Qualifiers
1..474
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Floral-Induced Meristem 1 (FMI)"
/note="Organ: Floral-Induced Meristem 1; Site_1: XhoI; Site_2:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excision."
ORIGIN
Query Match 80.6%; Score 17.4; DB 2; Length 464;
Best Local Similarity 85.7%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 2;
QY 2 GAAGGTGCCRCGGATCTTGT 22
Db 127 GAAGGTGTACCGATGTTGT 107

RESULT 54
CG785031/c 480 bp mRNA linear GSS 16-JUN-2004
LOCUS RRR811 BayGenomics Gene Trap Library pGTOLxf Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION CG785031
VERSION CG785031.1 GI:38157591
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 480)
AUTHORS BayGenomics.
TITLE http://baygenomics.ucsf.edu/
JOURNAL Unpublished (2001)
COMMENT Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=RRR811
Class: Gene Trap.
FEATURES
source Location/Qualifiers
1..480
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"

```

ORGANISM

Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE
AUTHORS

Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and
Pratt,L.H.

TITLE

An EST database from Sorghum: Sorghum propinquum rhizomes

JOURNAL

Unpublished (2000)

COMMENT

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Seq primer:

JEN REV

High quality sequence stop:

395

POLYA=No.

FEATURES

source

1..474

/organism="Sorghum propinquum"

/mol_type="mRNA"

/db_xref="taxon:132711"

/clone_lib="Rhizome2 (RHIZ2)"

/note="Organ: Rhizomes; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda Zap II. "
Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 80.6%; Score 17.4; DB 2; Length 474;

Best Local Similarity 85.7%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;

Matches 18; Conservative 1; Mismatches 2;

QY

2 GAAGGTGCCRCGGATCTTGT 22

Db

127 GAAGGTGTACCGATGTTGT 107

RESULT 54

CG785031/c

LOCUS

RRR811 BayGenomics Gene Trap Library pGTOLxf Mus musculus cDNA,

DEFINITION

mRNA sequence.

ACCESSION

CG785031

VERSION

CG785031.1 GI:38157591

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 480)

AUTHORS

BayGenomics.

TITLE

http://baygenomics.ucsf.edu/

JOURNAL

Unpublished (2001)

COMMENT

Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)

Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from BayGenomics. Annotation

information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=

CELL_LINE&KEY=RRR811

Class: Gene Trap.

FEATURES

source

1..480

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

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/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/notes="Vector: pGT0Lxf"

ORIGIN
Query Match      80.6%; Score 17.4; DB 10; Length 480;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 21
||||| : |||||
Db 390 TGAAGGTGCTGCGAATCTTGT 370

RESULT 55
CW368267/c
LOCUS
DEFINITION
  481 bp DNA linear GSS 01-NOV-2004
  f8bb001f042c11f0 Sorghum methylation filtered library (LibID: 104)
  Sorghum bicolor genomic clone f8bb001f042c11, genomic survey
  sequence.
ACCESSION
  CW368267
VERSION
  GSS
KEYWORDS
  Sorghum bicolor (sorghum)
SOURCE
  Sorghum bicolor
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
  1 (bases 1 to 481)
  Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
  Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
  McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F.,
  Rabnowicz,P.D., Lakey,N., McCombie,W.R., Jeddloh,J.A. and
  Martienssen,R.A.
  Sorghum genome sequencing by methylation filtration
  PLoS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 5979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Seq primer: f Forward
Class: methylation filtered
High quality sequence stop: 481.
Location/Qualifiers
  1..481
  /organism="Sorghum bicolor"
  /mol_type="genomic DNA"
  /cultivar="ATx623"
  /db_xref="taxon:4558"
  /clone="f8bb001f042c11"
  /clone_lib="Sorghum methylation filtered library (LibID:
  104)"
  /note="Organ: Leaf; Vector: pBCSK(-); Site 1: HincII; DNA
  prepared from purified nuclei was randomly sheared,
  end-repaired, size fractionated to enrich for the 0.5 to 5
  kb fraction, ligated into HincII-digested pBCSK(-) vector
  and electroporated into E. coli cells. This is a
  methylation filtered library."

ORIGIN
Query Match      80.6%; Score 17.4; DB 10; Length 481;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 21
||||| : |||||
Db 59 TGAAGGTTCACGAATCTTGT 39

/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/notes="Vector: pGT0Lxf"

ORIGIN
Query Match      80.6%; Score 17.4; DB 10; Length 480;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 21
||||| : |||||
Db 390 TGAAGGTGCTGCGAATCTTGT 370

RESULT 56
CW367138/c
LOCUS
DEFINITION
  487 bp mRNA linear EST 20-FEB-2001
  100011H09.x3 1000 - Unigene 1 from Maize Genome Project Zea mays
  cDNA, mRNA sequence.
ACCESSION
  BG267138
VERSION
  BG267138.1
KEYWORDS
  EST.
SOURCE
  Zea mays
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 487)
  Walbot,V.
  Maize ESTs from various cDNA libraries sequenced at Stanford
  University
  Unpublished (1999)
  Contact: Walbot V
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 723 2227
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Plate: 1000111 row: H column: 09.
  Location/Qualifiers
    1..487
    /organism="Zea mays"
    /mol_type="mRNA"
    /db_xref="dbEST:605050H10.x1"
    /db_xref="taxon:4577"
    /clone_lib="1000 - Unigene 1 from Maize Genome Project"
    /note="This library represents the unique ESTs found in
    the first round of EST sequencing at Stanford University
    for the maize genome project. Sequences are present from
    libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
    683, 687, 707, and 945. Contigs were assembled using
    TIGR's CAP program and a representative EST from each
    contig was selected for the Unigene set. All singlets were
    also selected."

ORIGIN
Query Match      80.6%; Score 17.4; DB 2; Length 487;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCCRCGGATCTTGT 22
||||| : |||||
Db 39 GAAGGTGTCACGAATCTTGT 19

RESULT 57
CA181673/c
LOCUS
DEFINITION
  487 bp mRNA linear EST 24-SEP-2003
  SCBFST3135C05.g ST3 Saccharum officinarum cDNA clone SCBFST3135C05
  5', mRNA sequence.
ACCESSION
  CA181673
VERSION
  CA181673.1
KEYWORDS
  EST.
SOURCE
  Saccharum officinarum
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
  complex.
REFERENCE
  1 (bases 1 to 487)
  Vettore,A.L., da Silva,F.R., Kemper,B.L. and Arruda,P.
  The libraries that made SUCEST
  Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
  Contact: Arruda P
  Centro de Biologia Molecular e Engenharia Genetica

```


Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccc.br/facv.unesp.br
Plate: 135 row: C column: 05
Seq primer: T7 Promoter Primer.

FEATURES

source

```
1. .487
  Location/Qualifiers
    /organism="Saccharum officinarum"
    /mol_type="mRNA"
    /db_xref="taxon:4547"
    /clone="SCBFS3135C05"
    /lab_host="DH10B"
    /clone_lib="ST3"
    /notes="Organ: Fourth apical internodes of adult
  plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An
  undirectional cDNA library generated from [Fourth apical
  stalk internodes of adult plants]. cDNA was prepared from
  polyA+ mRNA using SuperScript Plasmid System Kit
  (Invitrogen). The double-strand cDNAs were fractionated
  in a sepharose CL-2B 40cm-columns and fragments sizing
  between 0.8 and 1.5 Kb were directionally cloned into the
  vector. Details of each source of RNA and library
  construction can be obtained at
  http://sucest.lad.ic.unicamp.br/public"
```

ORIGIN

```
Query Match      80.6%; Score 17.4; DB 6; Length 487;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCCCGGATCTTGT 22
    |||||1:|||||
Db 52 GAAGGTGCCCGGATCTTGT 32
```

RESULT 58

BG550996/c

LOCUS

DEFINITION

BG550996 489 bp mRNA linear EST 22-JUL-2004
ead31h01.y1 Gm-cl074 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl074-1898 5' similar to TR:Q42921 Q42921
3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE ; mRNA
sequence.

ACCESSION

BG550996.1 GI:13562776

VERSION

EST.

Glycine max (soybean)

SOURCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 489)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 400.

FEATURES

source

```
1. .489
  Location/Qualifiers
    /organism="Glycine max"
    /mol_type="mRNA"
    /cultivar="Williams 82"
    /db_xref="taxon:3847"
    /clone="GENOME SYSTEMS CLONE ID: Gm-cl074-1898"
    /tissue type="seedlings induced for HR (hypersensitive
  response)"
    /dev stage="9-11 day old"
    /lab_host="DH10B"
    /clone_lib="Gm-cl074"
    /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
  XhoI; The cDNA library was constructed from mRNA isolated
  from 9-11 day old seedlings that were induced for HR
  (hypersensitive response) by vacuum infiltrating plant
  tissue with Pseudomonas syringae pv. glycinea carrying the
  avrB gene (Genetics 141:1597-1604). Plant tissue (expanded
  unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
  and 53 hrs after inoculation and their mRNA pooled equally
  for cDNA construction. The library was prepared using the
  Stratagene pBluescript II SK(+) library construction kit.
  Complementary DNA was synthesized from mRNA using a primer
  consisting of a poly(dT) sequence with an XhoI restriction
  site. EcoRI adaptors were ligated to the blunt-ended cDNA
  fragments followed by XhoI digestion. The cDNA insert is
  protected from XhoI digestion via methylation during first
  strand synthesis. The cDNA fragments were directionally
  cloned into the EcoRI-XhoI restriction site of the
  pBluescript vector. The ligated cDNA fragments were
  transformed into E.coli ElectroMax DH10B host cells. Plant
  care, inoculations, and library construction were
  performed by Steve Clough (Lila Vodkin lab, University of
  Illinois)."
```

ORIGIN

```
Query Match      80.6%; Score 17.4; DB 2; Length 489;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGGTGCCCGGATCTTGT 22
    |||||1:|||||
Db 30 GAAGGTGCCCGGATCTTGT 10
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RESULT 59

CA182253/c

LOCUS

DEFINITION

CA182253 499 bp mRNA linear EST 24-SEP-2003
SCBGS3109D03.g S73 Saccharum officinarum cDNA clone SCBGS3109D03
5', mRNA sequence.

ACCESSION

CA182253

VERSION

CA182253.1 GI:35117838

KEYWORDS

EST.

SOURCE

Saccharum officinarum

ORGANISM

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

1 (bases 1 to 499)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>
 Plate: 109 row: D column: 03
 Seq primer: T7 Promoter Primer.
 Location/Qualifiers

FEATURES

source
 1. .499
 /organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SCBGST3109D03"
 /lab_host="DH10B"
 /clone_lib="ST3"

/note="Organ: Fourth apical stalk internodes of adult
 plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An
 unidirectional cDNA library generated from [Fourth apical
 stalk internodes of adult plants]. cDNA was prepared from
 polyA+ mRNA using Superscript Plasmid System Kit
 (Invitrogen). The double-strand cDNAs were fractionated
 in a sepharose CL-2B 40cm-columns and fragments sizing
 between 0.8 and 1.5 Kb were directionally cloned into the
 vector. Details of each source of RNA and library
 construction can be obtained at
<http://sucet.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 80.6%; Score 17.4; DB 6; Length 499;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
 ||||| : |||||
 Db 119 GAAGTGTCGCGGATGTTGT 99

RESULT 60

AA763342
 LOCUS 504 bp mRNA linear EST 27-JAN-1998
 DEFINITION vw53c01.r1 Soares mammary gland NLMG Mus musculus cDNA clone
 IMAGE:1247520 5' similar to TR:Q12845 Q12845 HYPOTHETICAL PROTEIN
 ; mRNA sequence.

ACCESSION AA763342
 VERSION AA763342.1 GI:2813089
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 504)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:661208

Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 495.

FEATURES

Location/Qualifiers

1. .504

source

/organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1247520"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"

/clone_lib="Soares mammary gland NLMG"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from mammary
 gland tissue from a lactating female, and was then primed
 with a Not I - oligo(dT) primer. Double-stranded cDNA was
 ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the
 modified pT7T3 vector. Library is normalized. Library
 was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 80.6%; Score 17.4; DB 1; Length 504;
 Best Local Similarity 85.7%; Pred. No. 2e+03;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 21
 ||||| : |||||
 Db 8 TGAAGTGCTGTGGATCTTGT 28

Search completed: April 2, 2006, 00:09:46
 Job time : 308.022 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:17:36 ; Search time 59.2198 Seconds
(without alignments)
3072.051 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaagtgccrcggatctgtt 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : Published Applications_NA_Main:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*

8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*

9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	100.0	22	US-10-824-527-2	Sequence 2, Appli
2	21.6	100.0	337	US-09-880-503-77	Sequence 77, Appl
3	21.6	100.0	337	US-10-051-643-77	Sequence 77, Appl
4	21.6	100.0	927	US-09-880-503-116	Sequence 116, App
5	21.6	100.0	927	US-10-051-643-116	Sequence 116, App
6	21.6	100.0	985	US-09-880-505-161	Sequence 161, App
7	21.6	100.0	985	US-10-051-643-161	Sequence 161, App
8	21.6	100.0	985	US-10-205-979-16	Sequence 16, Appl
9	21.6	100.0	1569	US-09-880-505-113	Sequence 113, App
10	21.6	100.0	1569	US-10-051-643-113	Sequence 113, App
11	21.6	100.0	1620	US-10-282-122A-26142	Sequence 26142, A
12	21.6	100.0	1623	US-09-712-363-23	Sequence 23, Appli
13	21.6	100.0	1623	US-10-267-311-3	Sequence 3, Appli
14	21.6	100.0	1623	US-10-156-761-3915	Sequence 3915, Ap
15	21.6	100.0	1623	US-10-282-122A-25595	Sequence 25595, A
16	21.6	100.0	1623	US-10-282-122A-28196	Sequence 28196, A
17	21.6	100.0	1623	US-10-679-956-3	Sequence 3, Appli
18	21.6	100.0	1626	US-09-880-505-159	Sequence 159, App
19	21.6	100.0	1626	US-10-051-643-159	Sequence 159, App
20	21.6	100.0	1626	US-10-205-979-14	Sequence 14, Appl
21	21.6	100.0	1626	US-10-392-041-3	Sequence 3, Appli
22	21.6	100.0	1626	US-10-394-763-3	Sequence 3, Appli
23	21.6	100.0	1626	US-10-392-387-3	Sequence 3, Appli

C 24	21.6	100.0	1626	9	US-10-491-300-1	Sequence 1, Appli
C 25	21.6	100.0	1638	7	US-10-282-122A-17670	Sequence 17670, A
C 26	21.6	100.0	1644	3	US-09-738-626-2986	Sequence 2986, Ap
C 27	21.6	100.0	1701	9	US-10-501-127A-21	Sequence 21, Appl
C 28	21.6	100.0	1761	8	US-10-635-211-1	Sequence 1, Appli
C 29	21.6	100.0	1920	5	US-10-267-311-16	Sequence 16, Appl
C 30	21.6	100.0	1920	5	US-10-679-956-16	Sequence 16, Appl
C 31	21.6	100.0	1947	5	US-10-267-311-28	Sequence 28, Appl
C 32	21.6	100.0	1947	5	US-10-679-956-28	Sequence 28, Appl
C 33	21.6	100.0	2073	5	US-10-068-059-9	Sequence 9, Appli
C 34	21.6	100.0	2073	9	US-10-941-049-9	Sequence 9, Appli
C 35	21.6	100.0	2130	5	US-10-068-059-7	Sequence 7, Appli
C 36	21.6	100.0	2130	9	US-10-941-049-7	Sequence 7, Appli
C 37	21.6	100.0	2175	5	US-10-068-059-11	Sequence 11, Appl
C 38	21.6	100.0	2175	9	US-10-941-049-11	Sequence 11, Appl
C 39	21.6	100.0	2241	5	US-10-068-059-5	Sequence 5, Appli
C 40	21.6	100.0	2241	9	US-10-941-049-5	Sequence 5, Appli
C 41	21.6	100.0	2847	5	US-10-267-311-20	Sequence 20, Appl
C 42	21.6	100.0	2847	9	US-10-679-956-20	Sequence 20, Appl
C 43	21.6	100.0	86114	6	US-10-080-170-648	Sequence 648, App
C 44	21.6	100.0	86114	7	US-10-080-170-648	Sequence 648, App
C 45	21.6	100.0	86114	8	US-10-468-356-648	Sequence 648, App
C 46	21.6	100.0	3309400	3	US-09-738-626-1	Sequence 1, Appli
C 47	21.6	100.0	9025608	6	US-10-156-761-1	Sequence 1, Appli
C 48	20	92.6	732	6	US-10-264-213-63	Sequence 63, Appl
C 49	20	92.6	1626	6	US-10-156-761-4976	Sequence 4976, Ap
C 50	20	92.6	1626	7	US-10-282-122A-27502	Sequence 27502, A
C 51	20	92.6	1728	6	US-10-369-493-32009	Sequence 32009, A
C 52	20	92.6	2256646	7	US-10-470-565-1	Sequence 1, Appli
C 53	20	92.6	9025608	6	US-10-156-761-1	Sequence 1, Appli
C 54	19.6	90.7	20	8	US-10-500-586-56	Sequence 56, Appl
C 55	18.4	85.2	552	8	US-10-857-542-18	Sequence 18, Appl
C 56	18.4	85.2	552	8	US-10-857-542-27	Sequence 27, Appl
C 57	18.4	85.2	552	8	US-10-857-542-35	Sequence 35, Appl
C 58	18.4	85.2	552	8	US-10-857-542-38	Sequence 38, Appl
C 59	18.4	85.2	552	8	US-10-857-542-39	Sequence 39, Appl
C 60	18.4	85.2	552	8	US-10-857-542-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-10-824-527-2
; Sequence 2, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823_0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer

US-10-824-527-2

Query Match 100.0%; Score 21.6; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||

RESULT 2

US-09-880-505-77/c
; Sequence 77, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-77

Query Match 100.0%; Score 21.6; DB 3; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.6; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

RESULT 3

US-10-051-643-77/c
; Sequence 77, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-77

Query Match 100.0%; Score 21.6; DB 5; Length 337;
Best Local Similarity 95.5%; Pred. No. 0.6; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

RESULT 4

US-09-880-505-116/c
; Sequence 116, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-116

Query Match 100.0%; Score 21.6; DB 3; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.65; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

RESULT 5

US-10-051-643-116/c
; Sequence 116, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-116

Query Match 100.0%; Score 21.6; DB 5; Length 927;
Best Local Similarity 95.5%; Pred. No. 0.65; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
|||||:|||||
Db 166 TGAAGGTGCGCGGATCTTGT 145
|||||:|||||

RESULT 6
US-09-880-505-161/c
; Sequence 161, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-161

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Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 167 TGAAGTGCCCGGATCTTGT 146

RESULT 7
US-10-051-643-161/c
; Sequence 161, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-161

Query Match 100.0%; Score 21.6; DB 5; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 167 TGAAGTGCCCGGATCTTGT 146

RESULT 8
US-10-205-979-16/c
; Sequence 16, Application US/10205979
; Publication No. US20030147861A1

; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; TITLE OF INVENTION: of Immune Responses
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-205-979-16

Query Match 100.0%; Score 21.6; DB 6; Length 985;
Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 167 TGAAGTGCCCGGATCTTGT 146

RESULT 9
US-09-880-505-113/c
; Sequence 113, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-113

Query Match 100.0%; Score 21.6; DB 3; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCCGGATCTTGT 22
Db 808 TGAAGTGCCCGGATCTTGT 787

RESULT 10
US-10-051-643-113/c
; Sequence 113, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2

; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-113

Query Match 100.0%; Score 21.6; DB 5; Length 1569;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCRCGGATCTTGT 787

RESULT 11
US-10-282-122A-26142/c
; Sequence 26142, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26142
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-282-122A-26142

Query Match 100.0%; Score 21.6; DB 7; Length 1620;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCRCGGATCTTGT 787

RESULT 12
US-09-712-363-23/c
; Sequence 23, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match 100.0%; Score 21.6; DB 3; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGGTGCCRCGGATCTTGT 787

RESULT 13
US-10-267-311-3/c
; Sequence 3, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08

; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 1623
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match 100.0%; Score 21.6; DB 5; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 14
US-10-156-761-3915/c
; Sequence 3915, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3915
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
US-10-156-761-3915

Query Match 100.0%; Score 21.6; DB 6; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 15
US-10-282-122A-25595/c
; Sequence 25595, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25595
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25595

Query Match 100.0%; Score 21.6; DB 7; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
DB 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 16
US-10-282-122A-28196/c
; Sequence 28196, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

```
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28196
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28196

Query Match      100.0%; Score 21.6; DB 7; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 17
US-10-679-956-3/c
; Sequence 3, Application US/10679956
; Publication No. US2005009841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-679-956-3

Query Match      100.0%; Score 21.6; DB 9; Length 1623;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 18
US-09-880-505-159/c
```

```
; Sequence 159, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-880-505-159

Query Match      100.0%; Score 21.6; DB 3; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 19
US-10-051-643-159/c
; Sequence 159, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-643-159

Query Match      100.0%; Score 21.6; DB 5; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 20
US-10-205-979-14/c
; Sequence 14, Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
```



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; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-205-979-14

Query Match      100.0%; Score 21.6; DB 6; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
    |||||:|||||:|||||
Db 808 TGAAGGTGCGCGGATCTTGTT 787

RESULT 21
US-10-392-041-3/c
; Sequence 3, Application US/10392041
; Publication No. US20040101826A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Alison M.
; APPLICANT: Robey, W. Wade
; TITLE OF INVENTION: Monitoring High-Risk Environments
; FILE REFERENCE: 12794/010001
; CURRENT APPLICATION NUMBER: US/10/392,041
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 10/306,113
; PRIOR FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Staphylococcus coelicolor
US-10-392-041-3

Query Match      100.0%; Score 21.6; DB 7; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
    |||||:|||||:|||||
Db 814 TGAAGGTGCGCGGATCTTGTT 793

RESULT 22
US-10-394-763-3/c
; Sequence 3, Application US/10394763
; Publication No. US20040101917A1
; GENERAL INFORMATION:
; APPLICANT: Robey, W. Wade
; APPLICANT: Jones, Alison M.
; TITLE OF INVENTION: Methods for Managing Animal Processing
; FILE REFERENCE: 12794/012001
; CURRENT APPLICATION NUMBER: US/10/394,763
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 10/306,113
; PRIOR FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Staphylococcus coelicolor
US-10-394-763-3

Query Match      100.0%; Score 21.6; DB 7; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
    |||||:|||||:|||||
Db 814 TGAAGGTGCGCGGATCTTGTT 793

RESULT 23
US-10-392-387-3/c
; Sequence 3, Application US/10392387
; Publication No. US20040185446A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Alison M.
; APPLICANT: Robey, W. Wade
; APPLICANT: Hemmingsen, Sean
; APPLICANT: Hill, Janet
; APPLICANT: Van Kessel, Andrew
; TITLE OF INVENTION: Cpns60 Targets for Quantification of
; FILE REFERENCE: 16671-009001
; CURRENT APPLICATION NUMBER: US/10/392,387
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-392-387-3

Query Match      100.0%; Score 21.6; DB 8; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
    |||||:|||||:|||||
Db 814 TGAAGGTGCGCGGATCTTGTT 793

RESULT 24
US-10-491-300-1/c
; Sequence 1, Application US/10491300
; Publication No. US20050063984A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTH AUSTRALIA
; APPLICANT: MEDVET SCIENCE PTY LTD
; APPLICANT: RURAL INDUSTRIES RESEARCH AND DEVELOPMENT CORPORATION
; TITLE OF INVENTION: GroEL Chimeric Protein and Vaccine
; FILE REFERENCE: A20-061
; CURRENT APPLICATION NUMBER: US/10/491,300
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Rhodococcus equi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
; OTHER INFORMATION: groEL gene
US-10-491-300-1

Query Match      100.0%; Score 21.6; DB 9; Length 1626;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGTT 22
```

Db 808 TGAAGGTGCCACGAGTCTTGT 787
|||||||:|||||||

RESULT 25

US-10-282-122A-17670/c
; Sequence 17670, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Cheryl
; APPLICANT: Malone, Cheryl
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/131,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17670
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Corynebacterium diptheriae

US-10-282-122A-17670

Query Match 100.0%; Score 21.6; DB 7; Length 1638;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCACGAGTCTTGT 22
|||||||:|||||||
Db 823 TGAAGGTGCCACGAGTCTTGT 802

RESULT 26

US-09-738-626-2986/c
; Sequence 2986, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO

; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2986
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-2986

Query Match 100.0%; Score 21.6; DB 3; Length 1644;
Best Local Similarity 95.5%; Pred. No. 0.68;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCACGAGTCTTGT 22
|||||||:|||||||
Db 823 TGAAGGTGCCACGAGTCTTGT 802

RESULT 27

US-10-501-127A-21/c
; Sequence 21, Application US/10501127A
; Publication No. US20050232937A1
; GENERAL INFORMATION:
; APPLICANT: ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid.
; TITLE OF INVENTION: Paramycobacterial diagnostics and vaccines
; FILE REFERENCE: 2002-032-US
; CURRENT APPLICATION NUMBER: US/10/501,127A
; CURRENT FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: mycobacterium avium paratuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1701)
; US-10-501-127A-21

Query Match 100.0%; Score 21.6; DB 9; Length 1701;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCACGAGTCTTGT 22
|||||||:|||||||
Db 883 TGAAGGTGCCACGAGTCTTGT 862

RESULT 28

US-10-635-211-1/c
; Sequence 1, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein
; FILE REFERENCE: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant gene
; NAME/KEY: CDS
; LOCATION: (1)..(1761)
US-10-635-211-1

Query Match 100.0%; Score 21.6; DB 8; Length 1761;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 29

US-10-267-311-16/c
; Sequence 16, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-267-311-16

Query Match 100.0%; Score 21.6; DB 5; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 30

US-10-679-956-16/c
; Sequence 16, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303

; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1917)
US-10-679-956-16

Query Match 100.0%; Score 21.6; DB 9; Length 1920;
Best Local Similarity 95.5%; Pred. No. 0.69;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 808 TGAAGTGCCRCGGATCTTGT 787

RESULT 31

US-10-267-311-28/c
; Sequence 28, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-267-311-28

Query Match 100.0%; Score 21.6; DB 5; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||
Db 1132 TGAAGTGCCRCGGATCTTGT 1111

RESULT 32

US-10-679-956-28/c
; Sequence 28, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001

```
; CURRENT APPLICATION NUMBER: US/10/679,956
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1944)
US-10-679-956-28

Query Match      100.0%; Score 21.6; DB 9; Length 1947;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 1132 TGAAGTGCCGCGGATCTTGT 1111

RESULT 33
US-10-068-059-9/c
; Sequence 9, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match      100.0%; Score 21.6; DB 5; Length 2073;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 1258 TGAAGTGCCGCGGATCTTGT 1237

RESULT 34
US-10-941-049-9/c
; Sequence 9, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-9

Query Match      100.0%; Score 21.6; DB 9; Length 2073;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 1258 TGAAGTGCCGCGGATCTTGT 1237

RESULT 35
US-10-068-059-7/c
; Sequence 7, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-7

Query Match      100.0%; Score 21.6; DB 5; Length 2130;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 1315 TGAAGTGCCGCGGATCTTGT 1294

RESULT 36
US-10-941-049-7/c
; Sequence 7, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
```

; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2127)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-7

Query Match 100.0%; Score 21.6; DB 9; Length 2130;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1315 TGAAGTGCCRCGGATCTTGT 1294

RESULT 37
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 100.0%; Score 21.6; DB 5; Length 2175;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1360 TGAAGTGCCRCGGATCTTGT 1339

RESULT 38
US-10-941-049-11/c
; Sequence 11, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14

; PRIOR APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-11

Query Match 100.0%; Score 21.6; DB 9; Length 2175;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1360 TGAAGTGCCRCGGATCTTGT 1339

RESULT 39
US-10-068-059-5/c
; Sequence 5, Application US/10068059
; Publication No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match 100.0%; Score 21.6; DB 5; Length 2241;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
Db 1426 TGAAGTGCCRCGGATCTTGT 1405

RESULT 40
US-10-941-049-5/c
; Sequence 5, Application US/10941049
; Publication No. US20050152917A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/941,049
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/10/068,059

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; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-941-049-5

Query Match      100.0%; Score 21.6; DB 9; Length 2241;
Best Local Similarity 95.5%; Pred. No. 0.7;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 1426 TGAAGTGCCRCGGATCTTGT 1405

RESULT 41
US-10-267-311-20/c
; Sequence 20, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
; US-10-679-956-20

Query Match      100.0%; Score 21.6; DB 9; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.72;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 868 TGAAGTGCCRCGGATCTTGT 847

RESULT 42
US-10-679-956-20/c
; Sequence 20, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/679,956

; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
; US-10-679-956-20

Query Match      100.0%; Score 21.6; DB 9; Length 2847;
Best Local Similarity 95.5%; Pred. No. 0.72;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 868 TGAAGTGCCRCGGATCTTGT 847

RESULT 43
US-10-080-170-648/c
; Sequence 648, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-10-080-170-648

Query Match      100.0%; Score 21.6; DB 6; Length 86114;
Best Local Similarity 95.5%; Pred. No. 0.97;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||:|||||:|||||
Db 16012 TGAAGTGCCRCGGATCTTGT 15991

RESULT 44
US-10-080-170-648/c
; Sequence 648, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-648

Query Match          100.0%; Score 21.6; DB 7; Length 86114;
Best Local Similarity 95.5%; Pred. No. 0.97;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:
Db 16012 TGAAGGTGCCRCGGATCTTGT 15991

RESULT 45
US-10-468-356-648/c
; Sequence 648, Application US/10468356
; Publication No. US20040197896A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.0019
; CURRENT APPLICATION NUMBER: US/10/468,356
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 10/080,170
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 648
; LENGTH: 86114
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-468-356-648

Query Match          100.0%; Score 21.6; DB 8; Length 86114;
Best Local Similarity 95.5%; Pred. No. 0.97;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:
Db 16012 TGAAGGTGCCRCGGATCTTGT 15991

RESULT 46
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988

; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match          100.0%; Score 21.6; DB 3; Length 3309400;
Best Local Similarity 95.5%; Pred. No. 1.3;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:
Db 2889718 TGAAGGTGCCRCGGATCTTGT 2889739

RESULT 47
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match          100.0%; Score 21.6; DB 6; Length 9025608;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||:
Db 4855012 TGAAGGTGCCRCGGATCTTGT 4855033

RESULT 48
US-10-264-213-63/c
; Sequence 63, Application US/10264213
; Publication No. US20040009490A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J
; APPLICANT: Lubbers, Mark William
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043c
; CURRENT APPLICATION NUMBER: US/10/264,213
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 253
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-10-264-213-63

Query Match 92.6%; Score 20; DB 6; Length 732;
Best Local Similarity 90.9%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
||| ||||| : |||||
Db 229 TGAAGGTGCCACGATCTTGT 208

RESULT 49
US-10-156-761-4976/c
; Sequence 4976, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4976
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1626)
US-10-156-761-4976

Query Match 92.6%; Score 20; DB 6; Length 1626;
Best Local Similarity 90.9%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
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Db 814 TGAAGGTGCGCGGATCTTGT 793

RESULT 50
US-10-282-122A-27502/c
; Sequence 27502, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27502
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-282-122A-27502

Query Match 92.6%; Score 20; DB 7; Length 1626;
Best Local Similarity 90.9%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
||| ||||| : |||||
Db 808 TGAAGTGCCACGATCTTGT 787

RESULT 51
US-10-369-493-32009/c
; Sequence 32009, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32009
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Thermobifida fusca
US-10-369-493-32009

Query Match 92.6%; Score 20; DB 6; Length 1728;
Best Local Similarity 90.9%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCGGATCTTGT 22
||| ||||| : |||||
Db 916 TGAAGGTACCGCGGATCTTGT 895

RESULT 52

US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/WO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: BP 01102050.0
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1

Query Match 92.6%; Score 20; DB 7; Length 2256646;
Best Local Similarity 90.9%; Pred. No. 8.8;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 1640 TGAAGTGCCACGGATGTGTT 1619

RESULT 53

US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 92.6%; Score 20; DB 6; Length 9025608;
Best Local Similarity 90.9%; Pred. No. 9.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 6041755 TGAAGTGCCGCGGATCTTGTT 6041734

RESULT 54

US-10-500-586-56
; Sequence 56, Application US/10500586

; Publication No. US20050014157A1

; GENERAL INFORMATION:
; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIES
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSPR3
US-10-500-586-56

Query Match 90.7%; Score 19.6; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.1;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 1 AAGGTGCCRCGGATCTTGTT 20

RESULT 55

US-10-857-542-18/c
; Sequence 18, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
US-10-857-542-18

Query Match 85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGTT 22
|||||:|||||
Db 538 TGAATGTGCCACGAATCTTGTT 517

RESULT 56

US-10-857-542-27/c
; Sequence 27, Application US/10857542
; Publication No. US20050026188A1

```
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-27

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCCGATCTTGT 22
   ||||| ||||| |||||
Db 538 TGAAGGTACCAACGAATCTTGT 517

RESULT 57
US-10-857-542-35/c
; Sequence 35, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-35

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCCGATCTTGT 22
   ||||| ||||| |||||
Db 538 TGAAGGTACCAACGAATCTTGT 517

RESULT 58
US-10-857-542-38/c
; Sequence 38, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-38

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCCGATCTTGT 22
   ||||| ||||| |||||
Db 538 TGAAGGTACCAACGAATCTTGT 517

RESULT 59
US-10-857-542-39/c
; Sequence 39, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-39

Query Match      85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCGCCGATCTTGT 22
   ||||| ||||| |||||
Db 538 TGAAGGTACCAACGAATCTTGT 517

RESULT 60
US-10-857-542-41/c
; Sequence 41, Application US/10857542
; Publication No. US20050026188A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Janet E
; APPLICANT: Hemmingsen, Sean M
; APPLICANT: Van Kessel, Andrew G
; TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
; FILE REFERENCE: 3015-5840.1US
; CURRENT APPLICATION NUMBER: US/10/857,542
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/474471
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: CA 2,430,586
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured human vaginal bacterium
; US-10-857-542-41
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APPLICANT: Hemmingen, Sean M
APPLICANT: Van Kessel, Andrew G
TITLE OF INVENTION: Methods of Identifying, Characterizing and Comparing Microorganisms
FILE OF INVENTION: Communities
FILE REFERENCE: 3015-5840.1US
CURRENT APPLICATION NUMBER: US/10/857,542
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: US 60/474471
PRIOR FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: CA 2,430,586
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.2
SEQ ID NO 41
LENGTH: 552
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Uncultured human vaginal bacterium
US-10-857-542-41

Query Match 85.2%; Score 18.4; DB 8; Length 552;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 22
|||||
Db 538 TGAAGGTACCGCGATCTTGT 517
|||||

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Job time : 68.2198 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:19:05 ; Search time 54.3836 Seconds
(without alignments)
1615.302 Million cell updates/sec

Title: US-10-824-527-2

Perfect score: 21.6

Sequence: 1 tgaaggcgccggatctgtt 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

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- 1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.4	85.2	555	14	US-11-055-637-99
C 2	18.4	85.2	1654	11	US-11-201-916-3
C 3	18	83.3	1400	14	US-11-136-527-8176
C 4	18	83.3	9176	14	US-11-136-527-4080
C 5	17.4	80.6	399	6	US-09-925-065A-141335
C 6	17.4	80.6	401	10	US-10-301-480-236251
C 7	17.4	80.6	401	10	US-10-301-480-849660
C 8	17.4	80.6	1587	9	US-10-897-981-11
C 9	17.4	80.6	1683	14	US-11-131-479-37
C 10	17.4	80.6	1836	11	US-11-096-568A-7645
C 11	17.4	80.6	1997	11	US-11-096-568A-19419
C 12	17.4	80.6	2590	9	US-10-897-981-3
C 13	17.2	79.6	2619	9	US-10-932-182A-78771
C 14	17.2	79.6	2619	9	US-10-932-182A-78771
C 15	17	78.7	25	14	US-11-136-527-294718
C 16	17	78.7	1400	14	US-11-136-527-6229
C 17	17	78.7	1415	14	US-11-136-527-2133
C 18	16.8	77.8	25	14	US-11-136-527-238844

C 19	16.8	77.8	25	14	US-11-136-527-238846
C 20	16.8	77.8	486	14	US-11-136-527-964
C 21	16.8	77.8	486	14	US-11-136-527-5060
C 22	16.8	77.8	547	6	US-09-925-065A-390792
C 23	16.8	77.8	547	6	US-09-925-065A-390793
C 24	16.8	77.8	547	6	US-09-925-065A-390794
C 25	16.8	77.8	547	6	US-09-925-065A-390795
C 26	16.8	77.8	552	14	US-11-055-637-112
C 27	16.8	77.8	559	10	US-10-301-480-459081
C 28	16.8	77.8	559	10	US-10-301-480-459082
C 29	16.8	77.8	559	10	US-10-301-480-459083
C 30	16.8	77.8	559	10	US-10-301-480-459084
C 31	16.8	77.8	559	10	US-10-301-480-1072490
C 32	16.8	77.8	559	10	US-10-301-480-1072491
C 33	16.8	77.8	559	10	US-10-301-480-1072492
C 34	16.8	77.8	559	10	US-10-301-480-1072493
C 35	16.8	77.8	637	6	US-09-925-065A-697497
C 36	16.8	77.8	637	6	US-09-925-065A-697498
C 37	16.8	77.8	1562	11	US-11-096-568A-5292
C 38	16.8	77.8	1626	14	US-11-074-176-29
C 39	16.8	77.8	1661	11	US-11-201-916-7
C 40	16.8	77.8	3534	9	US-10-932-182A-940
C 41	16.8	77.8	3534	9	US-10-932-182A-940
C 42	16.6	76.9	25	8	US-10-310-944A-1061804
C 43	16.4	75.9	803	11	US-11-096-568A-1453
C 44	16.4	75.9	1402	11	US-11-072-512-1108
C 45	16.4	75.9	1750	14	US-11-091-883-407
C 46	16.4	75.9	2886	11	US-11-050-857-678
C 47	16.4	75.9	2886	11	US-11-051-720-55
C 48	16.4	75.9	3100	11	US-11-050-857-679
C 49	16.4	75.9	3164	11	US-11-051-720-56
C 50	16.4	75.9	3164	11	US-11-050-857-677
C 51	16.4	75.9	3164	11	US-11-051-720-54
C 52	16.4	75.9	3254	11	US-11-050-857-680
C 53	16.4	75.9	3254	11	US-11-051-720-57
C 54	16.4	75.9	3256	11	US-11-050-857-676
C 55	16.4	75.9	3256	11	US-11-051-720-53
C 56	16.4	75.9	3263	11	US-11-050-857-675
C 57	16.4	75.9	3263	11	US-11-051-720-52
C 58	16.4	75.9	6208	11	US-11-181-330-5
C 59	16.4	75.9	6237	14	US-11-076-074-14
C 60	16.4	75.9	6240	9	US-10-912-971-5

ALIGNMENTS

RESULT 1

US-11-055-637-99/c

; Sequence 99, Application US/11055637

; Publication No. US20050260619A1

; GENERAL INFORMATION:

; APPLICANT: BROUSSEAU, Roland

; APPLICANT: DUBOIS, Jason

; APPLICANT: EDGE, Tom

; APPLICANT: MASSON, Luc

; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND

; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES

; FILE REFERENCE: 2139-33US

; CURRENT APPLICATION NUMBER: US/11/055,637

; PRIOR FILING DATE: 2005-02-11

; PRIOR APPLICATION NUMBER: US 60/543,288

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 99

; LENGTH: 555

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

; US-11-055-637-99

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141335
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-141335

Query Match 80.6%; Score 17.4; DB 6; Length 399;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 21
|||||||:|||||||
DB 324 TGAAGTGTGCAGATCTTGT 304

RESULT 6

US-10-301-480-236251/c
; Sequence 236251, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236251
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-236251

Query Match 80.6%; Score 17.4; DB 10; Length 401;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 21
|||||||:|||||||
DB 326 TGAAGTGTGCAGATCTTGT 306

RESULT 7

US-10-480-849660/c
; Sequence 849660, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 849660
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-849660

Query Match 80.6%; Score 17.4; DB 10; Length 401;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCRCGGATCTTGT 21
|||||||:|||||||
DB 326 TGAAGTGTGCAGATCTTGT 306

RESULT 8

US-10-897-981-11/c
; Sequence 11, Application US/10897981
; Publication No. US20060019354A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Armentrout, Richard W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USING A
; TITLE OF INVENTION: REGULATOR OF BIOPOLYMER PRODUCTION
; FILE REFERENCE: 850136.421
; CURRENT APPLICATION NUMBER: US/10/897,981
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Sphingomonas sp.
US-10-897-981-11

Query Match 80.6%; Score 17.4; DB 9; Length 1587;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
DB 471 GAAGTGTGCGGATGTGT 451

RESULT 9

US-11-131-479-37/c
; Sequence 37, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Coding Region Encoding IBV NP Protein
US-11-131-479-37

Query Match 80.6%; Score 17.4; DB 14; Length 1683;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 22
|||||||:|||||||
DB 462 GAAGTGCCGCGGTCTTGT 442

```
RESULT 10
US-11-096-568A-7645/c
; Sequence 7645, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 7645
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1836)
; OTHER INFORMATION: Ceres Seq. ID no. 15174547
; US-11-096-568A-7645

Query Match      80.6%; Score 17.4; DB 11; Length 1836;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAAGGTGCCRCGGATCTTGT 22
Db      413 GAAGGTGTCACGGATGTTGT 393

RESULT 11
US-11-096-568A-19419/c
; Sequence 19419, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19419
; LENGTH: 1997
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1997)
; OTHER INFORMATION: Ceres Seq. ID no. 12373118
; US-11-096-568A-19419

Query Match      80.6%; Score 17.4; DB 11; Length 1997;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAAGGTGCCRCGGATCTTGT 22
Db      569 GAAGGTGTCACGGATGTTGT 549

RESULT 12
US-10-897-981-3
; Sequence 3, Application US/10897981
; Publication No. US20060019354A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Motohide
; APPLICANT: Armentrout, Richard W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USING A
; TITLE OF INVENTION: REGULATOR OF BIOPOLYMER PRODUCTION
```

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; FILE REFERENCE: 850136.421
; CURRENT APPLICATION NUMBER: US/10/897,981
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Spingomonas sp.
; US-10-897-981-3

Query Match      80.6%; Score 17.4; DB 9; Length 2590;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAAGGTGCCRCGGATCTTGT 22
Db      1402 GAAGGTGTCGGGATGTTGT 1422

RESULT 13
US-10-932-182A-78771/c
; Sequence 78771, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78771
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-10-932-182A-78771

Query Match      79.6%; Score 17.2; DB 9; Length 2619;
Best Local Similarity 86.4%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TGAAGTGCCRCGGATCTTGT 22
Db      2408 TGAAGTTGCCCGGATGTTGT 2387

RESULT 14
US-10-932-182A-78771/c
; Sequence 78771, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78771
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-10-932-182A-78771
```


Query Match 79.6%; Score 17.2; DB 9; Length 2619;
Best Local Similarity 86.4%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||:|||||:|||||
DB 2408 TGAAGTTGCCCGGATGTTGT 2387

RESULT 15

US-11-136-527-294718/c
; Sequence 294718, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 294718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-294718

Query Match 78.7%; Score 17; DB 14; Length 25;
Best Local Similarity 89.5%; Pred. No. 38;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGGATCTTGT 21
|||||:|||||:|||||
DB 21 AAGGTGCCACGGATGTTGT 3

RESULT 16

US-11-136-527-6229/c
; Sequence 6229, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6229
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6229

Query Match 78.7%; Score 17; DB 14; Length 1400;
Best Local Similarity 89.5%; Pred. No. 55;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGGATCTTGT 21
|||||:|||||:|||||
DB 436 AAGGTGCCACGGATGTTGT 418

RESULT 17

US-11-136-527-2133/c

; Sequence 2133, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2133
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2133

Query Match 78.7%; Score 17; DB 14; Length 1415;
Best Local Similarity 89.5%; Pred. No. 55;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGTGCCRCGGATCTTGT 21
|||||:|||||:|||||
DB 451 AAGGTGCCACGGATGTTGT 433

RESULT 18

US-11-136-527-238844/c
; Sequence 238844, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-238844

Query Match 77.8%; Score 16.8; DB 14; Length 25;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
|||||:|||||:|||||
DB 25 TGAAGTGCCCAAGATCTTGCT 4

RESULT 19

US-11-136-527-238846/c
; Sequence 238846, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
; US-11-136-527-238846

Query Match 77.8%; Score 16.8; DB 14; Length 25;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGATCTTGT 22
|||||: |||||
Db 23 TGAAGTGCCCAAGATCTTGT 2

RESULT 20
US-11-136-527-964
; Sequence 964, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 964
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-964

Query Match 77.8%; Score 16.8; DB 14; Length 486;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGATCTTGT 22
|||||: |||||
Db 211 TGAAGTGCCCAAGATCTTGT 232

RESULT 21
US-11-136-527-5060/c
; Sequence 5060, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5060
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-5060

Query Match 77.8%; Score 16.8; DB 14; Length 486;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGATCTTGT 22
|||||: |||||
Db 276 TGAAGTGCCCAAGATCTTGT 255

RESULT 22
US-09-925-065A-390792/c
; Sequence 390792, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390792
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-390792

Query Match 77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGATCTTGT 22
|||||: |||||
Db 221 TGAAGTGGAAGTCTTGT 200

RESULT 23
US-09-925-065A-390793/c
; Sequence 390793, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390793
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-390793

```
Query Match          77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 221 TGAAGTGGAACTGATCTTGT 200

RESULT 24
US-09-925-065A-390794/c
; Sequence 390794, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390794
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390794

Query Match          77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 221 TGAAGTGGAACTGATCTTGT 200

RESULT 25
US-09-925-065A-390795/c
; Sequence 390795, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390795
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390795

; ORGANISM: Homo sapiens
US-09-925-065A-390795

Query Match          77.8%; Score 16.8; DB 6; Length 547;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 221 TGAAGTGGAACTGATCTTGT 200

RESULT 26
US-11-055-637-112/c
; Sequence 112, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-112

Query Match          77.8%; Score 16.8; DB 14; Length 552;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 538 TGAAGTACCACGAATCTTGT 517

RESULT 27
US-10-301-480-459081/c
; Sequence 459081, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459081
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459081

Query Match          77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
```

```
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 226 TGAAGTGGAAGTGAATCTTGT 205

RESULT 28
US-10-301-480-459082/c
; Sequence 459082, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459082
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459082

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 226 TGAAGTGGAAGTGAATCTTGT 205

RESULT 29
US-10-301-480-459083/c
; Sequence 459083, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459083
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459083

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 226 TGAAGTGGAAGTGAATCTTGT 205

RESULT 30
US-10-301-480-459084/c
; Sequence 459084, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459084
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459084

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 226 TGAAGTGGAAGTGAATCTTGT 205
```

```
; Sequence 459084, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459084
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-459084

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 226 TGAAGTGGAAGTGAATCTTGT 205

RESULT 31
US-10-301-480-1072490/c
; Sequence 1072490, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072490
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072490

Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTGCCRCGGATCTTGT 22
Db 226 TGAAGTGGAAGTGAATCTTGT 205

RESULT 32
US-10-301-480-1072491/c
; Sequence 1072491, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
```

```
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072491
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072491
```

```
Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TGAAGTGCCRCGGATCTTGT 22
||||| : |||||
Db 226 TGAAGTGGAACTGATCTTGT 205
```

RESULT 33

```
US-10-301-480-1072492/c
; Sequence 1072492, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072492
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1072492
```

```
Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TGAAGTGCCRCGGATCTTGT 22
||||| : |||||
Db 226 TGAAGTGGAACTGATCTTGT 205
```

RESULT 34

```
US-10-301-480-1072493/c
; Sequence 1072493, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1072493
; LENGTH: 559
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
US-10-301-480-1072493
```

```
Query Match 77.8%; Score 16.8; DB 10; Length 559;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TGAAGTGCCRCGGATCTTGT 22
||||| : |||||
Db 226 TGAAGTGGAACTGATCTTGT 205
```

RESULT 35

```
US-09-925-065A-697497/c
; Sequence 697497, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697497
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-697497
```

```
Query Match 77.8%; Score 16.8; DB 6; Length 637;
Best Local Similarity 81.8%; Pred. No. 65;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TGAAGTGCCRCGGATCTTGT 22
||||| : |||||
Db 388 TGAAGTGGAACTGATCTTGT 367
```

RESULT 36

```
US-09-925-065A-697498/c
; Sequence 697498, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 697498
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-697498

Query Match          77.8%; Score 16.8; DB 6; Length 637;
Best Local Similarity 81.8%; Pred. No. 65;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 388 TGAAGTGGAAGTGAATCTTGT 367

RESULT 37
US-11-096-568A-5292
; Sequence 5292, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5292
; LENGTH: 1562
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1562)
; OTHER INFORMATION: Ceres Seq. ID no. 14307879
US-11-096-568A-5292

Query Match          77.8%; Score 16.8; DB 11; Length 1562;
Best Local Similarity 81.8%; Pred. No. 71;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 1260 TGAAGTGCCAGGAGATCTTGT 1281

RESULT 38
US-11-074-176-29/c
; Sequence 29, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAnuliffe, Olivia
; APPLICANT: Peril, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1626)
; FEATURE:
```

```
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: ORF 406; GroEL - 60 kDa chaperonin
US-11-074-176-29

Query Match          77.8%; Score 16.8; DB 14; Length 1626;
Best Local Similarity 81.8%; Pred. No. 71;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 808 TGAAGTACCAGCATCTTGT 787

RESULT 39
US-11-201-916-7/c
; Sequence 7, Application US/11201916
; Publication No. US20060039922A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: STREPTOCOCAL HEAT SHOCK PROTEINS OF THE
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/201,916
; FILING DATE: 11-AUG-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,737
; FILING DATE: 31-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 870109.408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1649
US-11-201-916-7

Query Match          77.8%; Score 16.8; DB 11; Length 1661;
Best Local Similarity 81.8%; Pred. No. 71;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
    ||||| : |||||
Db 822 TGAAGTACCAGCATCTTGT 801

RESULT 40
US-10-932-182A-940
```

```
; Sequence 940, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 940
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-940

Query Match      77.8%; Score 16.8; DB 9; Length 3534;
Best Local Similarity 81.8%; Pred. No. 77;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 1929 TAAAGTGCCGCGGAATTGTT 1950

RESULT 41
US-10-932-182A-940
; Sequence 940, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 940
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-940

Query Match      77.8%; Score 16.8; DB 9; Length 3534;
Best Local Similarity 81.8%; Pred. No. 77;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTGT 22
   |||||:|||||
Db 1929 TAAAGTGCCGCGGAATTGTT 1950

RESULT 42
US-10-914A-1061804/c
; Sequence 1061804, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1061804
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1061804

Query Match      76.9%; Score 16.6; DB 8; Length 25;
Best Local Similarity 94.1%; Pred. No. 61;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGGTGCGCGGATCTTGT 20
   |||||:|||||
Db 19 AGGTGCGCGGATCTTGT 3

RESULT 43
US-11-096-568A-1453/c
; Sequence 1453, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1453
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(803)
; OTHER INFORMATION: Ceres Seq. ID no. 14308995
US-11-096-568A-1453

Query Match      75.9%; Score 16.4; DB 11; Length 803;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAAGTGCCRCGGATCTTGT 21
   |||||:|||||
Db 171 GACGTCGCGTGATCTGT 152

RESULT 44
US-11-072-512-1108/c
; Sequence 1108, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YANAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: OTSUKA, MOTOTOMU
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072.512
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; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1108
; LENGTH: 1402
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-1108

Query Match 75.9%; Score 16.4; DB 11; Length 1402;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 170 TGGAGGTGACCGGATCTTG 151

RESULT 45

US-11-091-883-407/c
; Sequence 407, Application US/11091883
; Publication No. US20060024693A1

; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.

; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; FILE REFERENCE: 53942US

; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 407

; LENGTH: 1750
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-407

Query Match 75.9%; Score 16.4; DB 14; Length 1750;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 172 TGGAGGTGACCGGATCTTG 153

RESULT 46

US-11-050-857-678/c
; Sequence 678, Application US/11050857
; Publication No. US20060040278A1

; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150

; SEQ ID NO 678
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-050-857-678

Query Match 75.9%; Score 16.4; DB 11; Length 2886;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 360 TGGAGGTGACCGGATCTTG 341

RESULT 47

US-11-051-720-55/c
; Sequence 55, Application US/11051720
; Publication No. US20060046257A1

; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780

; SEQ ID NO 55
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-720-55

Query Match 75.9%; Score 16.4; DB 11; Length 2886;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 360 TGGAGGTGACCGGATCTTG 341

RESULT 48

US-11-050-857-679/c
; Sequence 679, Application US/11050857
; Publication No. US20060040278A1

; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150

; SEQ ID NO 679
; LENGTH: 3100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-857-679

Query Match 75.9%; Score 16.4; DB 11; Length 3100;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGGTGCCRCGGATCTTG 20
||| ||||| : ||||| |||||
Db 360 TGGAGGTGACCGGATCTTG 341

RESULT 49

US-11-051-720-56/c
; Sequence 56, Application US/11051720
; Publication No. US20060046257A1

; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 56
; LENGTH: 3100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-720-56

Query Match 75.9%; Score 16.4; DB 11; Length 3100;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 50
US-11-050-857-677/c
; Sequence 677, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 677
; LENGTH: 3164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-857-677

Query Match 75.9%; Score 16.4; DB 11; Length 3164;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 51
US-11-051-720-54/c
; Sequence 54, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 54
; LENGTH: 3164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-720-54

Query Match 75.9%; Score 16.4; DB 11; Length 3164;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 52
US-11-050-857-680/c
; Sequence 680, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 680
; LENGTH: 3254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-857-680

Query Match 75.9%; Score 16.4; DB 11; Length 3254;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 53
US-11-051-720-57/c
; Sequence 57, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 57
; LENGTH: 3254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-720-57

Query Match 75.9%; Score 16.4; DB 11; Length 3254;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 54
US-11-050-857-676/c
; Sequence 676, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 676
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-857-676

Query Match 75.9%; Score 16.4; DB 11; Length 3256;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 56
; LENGTH: 3100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-720-56

Query Match 75.9%; Score 16.4; DB 11; Length 3254;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 53
US-11-051-720-57/c
; Sequence 57, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 57
; LENGTH: 3254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-720-57

Query Match 75.9%; Score 16.4; DB 11; Length 3254;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 54
US-11-050-857-676/c
; Sequence 676, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 676
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-857-676

Query Match 75.9%; Score 16.4; DB 11; Length 3256;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 55
US-11-051-720-58/c
; Sequence 58, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 58
; LENGTH: 3254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-720-58

Query Match 75.9%; Score 16.4; DB 11; Length 3254;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

RESULT 56
US-11-050-857-677/c
; Sequence 677, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 677
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-857-677

Query Match 75.9%; Score 16.4; DB 11; Length 3256;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAAGTGCCRCGGATCTTG 20
||| ||||| :||| |||||
DB 360 TGGAGGTGACGCGGATCTTG 341

Qy 3 AAGTGCCRCGGATCTTGT 22
| | | | | : | | | | |
Db 778 ATGGTGCTCGGATCTTGT 759

RESULT 60
US-10-912-971-5/c
; Sequence 5, Application US/10912971
; Publication No. US20060029546A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING ANTI-SCHIZOPHRENIC AGENTS
; FILE REFERENCE: 30847/40237
; CURRENT APPLICATION NUMBER: US/10/912,971
; CURRENT FILING DATE: 2004-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 6240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-912-971-5

Query Match 75.9%; Score 16.4; DB 9; Length 6240;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAGTGCCRCGGATCTTGT 22
| | | | | : | | | | |
Db 778 ATGGTGCTCGGATCTTGT 759

Search completed: April 1, 2006, 22:39:10
Job time : 56.3836 secs

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BA000030_23	2300001	2410000	
BA000030_24	2400001	2510000	
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BA000030_30	3000001	3110000	
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BA000030_90	9000001	9025608	
Continuation (49 of 91) of BA000030 from base 4800001 (BA000030 Streptomyces avermitilis			
96.2%; Score 404; DB 1; Length 110000;			
Query Match			
RESULT 2			
STMGROELY 1814 bp DNA linear BCT 26-APR-1993			
LOCUS Streptomyces albus open reading frame (GROEL2) gene, complete cds.			
DEFINITION M76658			
ACCESSION M76658			
VERSION M76658.1 GI:153293			
KEYWORDS heat shock protein.			
SOURCE Streptomyces albus			
ORGANISM			
REFERENCE 1 (bases 1 to 1814)			
AUTHORS Mazodier, P., Guglielmi, G., Davies, J. and Thompson, C. J.			
TITLE Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
JOURNAL J. Bacteriol. 173 (22), 7382-7386 (1991)			
PUBMED 1682304			
COMMENT Original source text: Streptomyces albus (strain G) DNA.			
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/mol_type="genomic DNA"			
/strain="G"			
/db_xref="taxon:1888"			
101..1723			
/gene="GROEL2"			
101..1723			
/gene="GROEL2"			
/note="open reading frame; GROEL1 encodes two gene			
products, related to a second GROEL-like gene (GROEL2) in			
S. albus"			
/codon_start=1			
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/protein_id="AA26754.1"			
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AEMDKVKGEGVITVESQFGLTELETEGMPFDKGYISAYFATDMERWASDDPYI			
LVINSKIGNKOLLPLEKVMQSGKPLLIADVEGEALSTLVNKKITGTFKSVAVKA			
PFGDRKAMGLDIALITGTVISEEVKLEKNAGLDLLGRARKVITDKETTVIDGA			
GDTDQVNGRVAQIRAEIENSDDYDREKLQERLANVAGGVAVIKAGAAATEVELKERKH			

RIEDAVRNAAKAAVEGIVAGGVALLOASSVFEKLEBGEDEATGAANVKLALAEAPLKQ
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ORIGIN	Query Match 93.5%; Score 392.8; DB 1; Length 1814; Best Local Similarity 96.0%; Pred. No. 1.2e-32; Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY	1 AAGAAGACGAGCGACGTCGCGGTGACGCGTAGCACACCGCGACCGTTCCTCGCCCGAGCG 60
DB	332 AAGAAGACGAGCGACGTCGCGGTGACGCGTAGCACACCGCGACCGTTCCTCGCCCGAGCG 391
QY	61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCGCATGCTCTCAAGCGC 120
DB	392 CTCGTCCGCGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCGCATGCTCTCAAGCGC 451
QY	121 GGCATCGAGAAGCGCTCGAGCGCGTCTCGCGCGCGTCTCGCGCGCGTCTCGCGCGCGTCTC 180
DB	452 GGCATCGAGAAGCGCGTCTCGAGCGCGTCTCTCGCGCGCGTCTCGCGCGCGTCTCGCGCGCGTCTC 511
QY	181 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB	512 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 571
QY	241 GAGCTCATCGCGAGCGCATGACAAAGTTCGCGAAGGAGGCGTTCATCAGTTCGAGGAG 300
DB	572 GAGCTCATCGCGAGCGCATGACAAAGTTCGCGAAGGAGGCGTTCATCAGTTCGAGGAG 631
QY	301 TCCGAGACCTTCGCTGAGGCTCGAGCTCAGCGAGGATCGCTTCGACAGGCGCTAC 360
DB	632 TCCGAGACCTTCGCTGAGGCTCGAGCTCAGCGAGGATCGCTTCGACAGGCGCTAC 691
QY	361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGTTCGACGACCGCTAC 420
DB	692 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGTTCGACGACCGCTAC 751

RESULT 3	SC0939119	299050 bp	DNA	linear	BCT 16-APR-2005
LOCUS	Streptomyces coelicolor A3(2)	complete genome; segment 16/29.			
DEFINITION	AL939119 AL160331 AL353816 AL356612 AL357432 AL357524 AL358592				
ACCESSION	AL358818 AL359988 AL391406 AL391541 AL392149 AL392150 AL392178				
	AL645882				
VERSION	AL939119.1	GI:24427855			
KEYWORDS	Streptomyces coelicolor A3(2)				
SOURCE	Streptomyces coelicolor A3(2)				
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
REFERENCE	1				
AUTHORS	Bentley, S.D., Chater, K.F., Cerdano-Tarraga, A.M., Challis, G.L., Thomson, N.N., James, K.D., Harris, D.E., Quail, M.A., Kieser, H., Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M., Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S., Huang, C.H., Kieser, T., Larke, L., Murphy, L., Oliver, K., O'Neill, S., Rabinowitz, E., Rajandream, M.A., Rutherford, K., Rutter, S., Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S., Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrall, B.G., Parkhill, J., and Hopwood, D.A.				
TITLE	Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)				
JOURNAL	Nature 417 (6885), 141-147 (2002)				
PUBMED	1200953				
REFERENCE	2 (bases 1 to 299050)				
AUTHORS	Bentley, S.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: sds@sanger.ac.uk				
COMMENT	On or before Oct 30, 2002 this sequence version replaced gi:7242748, gi:7636006, gi:8248766, gi:8249971, gi:8388712,				

gi:8439477, gi:8894718, gi:9857143, gi:9886716, gi:10129746, gi:11595528.	Location/Qualifiers
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200..1727	gene="rRNA"
	/note="rRNA, 16S ribosomal RNA. Coordinates based on comparison with rrmB from Streptomyces coelicolor (EMBL:AL109848)." .
2004..5126	gene="rRNA"
2004..5126	gene="rRNA"
	/note="rRNA, 23S ribosomal RNA. Coordinates based on comparison with rrmB from Streptomyces coelicolor (EMBL:AL109848)." .
5228..5348	gene="rRNA"
5228..5348	gene="rRNA"
	/note="rRNA, 5S ribosomal RNA. Coordinates based on comparison with rrmB from Streptomyces coelicolor (EMBL:AL109848)." .
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	/gene="SCO4123"
	/note="synonym: SCD72A.09c"
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	/gene="SCO4123"
	/note="SCD72A.09c, possible two-component system response regulator, len: 222aa; similar to many eg. FR:086632 (EMBL:AL031155) possible two-component regulator from Streptomyces coelicolor (222 aa) fasta scores; opt: 973, z-score: 1128.5, E(): 0, 69.1% identity in 220 aa overlap. Contains pfam match to entry PF00072 response reg. Response regulator receiver domain, pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family and Prosite match to PS00622 Bacterial regulatory proteins, luxR family signature."
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	/note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 61.00, E-value 2.6e-14"
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	/gene="SCO4123"
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	/note="Pfam match to entry PF00072 response reg. Response regulator receiver domain, score 126.30, E-value 5.7e-34"
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complement(6077..7447)
/gene="SCO4124"
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len: 456aa; similar to many eg. TR:O86631 (EMBL:AL031155),
putative two-component sensor kinase from Streptomyces
coelicolor (429 aa) fasta scores; opt: 929, z-score:
995.1, E(): 0, 42.7% identity in 422 aa overlap. Contains
pfam match to entry PF00512 signal, Histidine kinase and
possible membrane-spanning hydrophobic regions. Contains
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/notes="SCD72A.11, possible acetyltransferase, len: 177 aa;
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maltophilia (153 aa) fasta scores; opt: 128, z-score:
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PLEGGPDHSELYLIER"
7476..7934
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Acetyltransferase (GNAT) family, score 34.50, E-value
2.4e-06"
complement(8054..9541)
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complement(8054..9541)
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similar in regions to others from actinomycetes eg.
TR:Q9X8A2 (EMBL:AL049645) hypothetical protein from
Streptomyces coelicolor (427 aa) fasta scores; opt: 266,
z-score: 260.7, E(): 4.7e-07, 27.7% identity in 296 aa
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overlap. Contains possible membrane-spanning hydrophobic
region."
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HQDALETEPPASAAKRLGCGWETHRAEAGVHYGPGESRSTAVQTLRDAGAAALVI
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Best Local Similarity 95.2%; Pred. No. 7.4e-33;
Matches 400; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 AAGNAGACGAGCAGCTCCCGGTGACGTCAGCACCGCGACCGTCTTCCGCCAGGCG 60
DB 180896 AAGAAGACGAGCAGCTCCCGGTGACGTCAGCACCGCGACCGTCTTCCGCCAGGCG 180955

QY 61 CTCGTACGCGAGGCGCTGCGCAACGTTCGCGCGCGTCCCAACCCGATGCTCTCAAGCGC 120
DB 180956 CTGCTCAAGNAGAGCTTCGCAACGTTCGCGCGCGCGCCCAACCCGATGCTCTCAAGCGC 181015

QY 121 GGCATCGAAGAGCGCGCTCGAGCGCTCTCCGCGCGCTCTCGAGCAGCGAGGATGTC 180
DB 181016 GGTATCGAAGAGCGCGCTCGAGCGCTCTCCGCGCGCTCTCGAGCAGCGAGGATGTC 181075

QY 181 GAGACCAAGGACGATCGCTTCACGGCTCCATCTCCGCCCGCGACACCCAGATCGCG 240
DB 181076 GAGACCAAGGACGATCGCTTCACGGCTCCATCTCCGCCCGCGACACCCAGATCGCG 181135

QY 241 GAGCTCATCGCGAGGCGATGCAACAGGTTCGGCAAGGAGGCGTCAATACCGTTCGAGGAG 300
DB 181136 GAGCTCATCGCGAGGCGATGCAACAGGTTCGGCAAGGAGGCGTCAATACCGTTCGAGGAG 181195

QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATGCGGTTTCGACAGGCGCTAC 360
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QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGAGCGCTCGCTCGACACCGCTAC 420
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RESULT 4
SLGROEL2G LOCUS 2192 bp DNA linear BCT 18-APR-2005
DEFINITION S.lividans groEL2 gene.
ACCESSION X95971
VERSION X95971.1 GI:2558615
KEYWORDS groEL2 gene; groEL2 protein; promoter region.
SOURCE Streptomyces lividans
ORGANISM Streptomyces lividans
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1
AUTHORS de Leon,P., Marco,S., Isiegas,C., Marina,A., Carrascosa,J.L. and
Mellado,R.P.
TITLE Streptomyces lividans groES, groEL1 and groEL2 genes
JOURNAL Microbiology (Reading, Engl.) 143 (Pt 11), 3563-3571 (1997)
PUBMED 9387235
REFERENCE 2 (bases 1 to 2192)
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AUTHORS Mellado, R.P.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-1996) R.P. Mellado, Centro Nacional de Biotecnología (CSIC), Campus de la Universidad Autónoma, Cantoblanco, 28049 Madrid, SPAIN

FEATURES Location/Qualifiers
source 1..2192

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ORIGIN

Query Match 91.6%; Score 384.8; DB 1; Length 2192;
Best Local Similarity 94.8%; Pred. No. 7.6e-32;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGAGCTGCGCGGTGACGGTACAGCACCGCCACCGTTCGCCCCAGGG 60

DB 702 AAGAAGACGACGAGCTGCGCGGTGACGGTACAGCACCGCCACCGTTCGCCCCAGGG 761

QY 61 CTGCTACGCGAGGGCTGCGCAACGCTGCGCGCGGTGCGCAACCCGATGCGCTCTCAAGCGC 120

DB 762 CTGGTCAAGGAAGGCTGCGCAACGCTGCGCGCGGTGCGCAACCCGATGCGCTCTCAAGCGC 821

QY 121 GCATCGAAGCGCGTTCGAGCGGCTCTCGCGCGGTGCGCAACCCGATGCGCTCTCAAGCGC 180

DB 822 GGTATCGAAGCGCGTTCGAGCGGCTCTCGCGCGGTGCGCAACCCGATGCGCTCTCAAGCGC 881

QY 181 GAGACCAAGGACGATGCTTCCAGCGCTCCATCTCGCGCGGTGCGCAACCCGATGCGCTCTCAAGCGC 240

DB 882 GAGACCAAGGACGATGCTTCCAGCGCTCCATCTCGCGCGGTGCGCAACCCGATGCGCTCTCAAGCGC 941

QY 241 GAGCTCATCGCGAGGCGATGACCAAGGTGCGCAAGGAGGCGGTCTATCACCGTTCGAGGAG 300

DB 942 GAGCTCATCGCGAGGCGATGACCAAGGTGCGCAAGGAGGCGGTCTATCACCGTTCGAGGAG 1001

QY 301 TCCCAAGCTTCGCTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 360

DB 1002 TCCCAAGCTTCGCTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 1061

QY 361 ATCTCGGGTACTTCCGACACGACATGAGCGGATGAGGGGTGCGCTTCGACGACCGCTTAC 420

DB 1062 ATCTCGGGTACTTCCGACACGACATGAGCGGATGAGGGGTGCGCTTCGACGACCGCTTAC 1121

RESULT 5
AY691305

LOCUS
DEFINITION

Streptomyces thermoviolaceus subsp. thermoviolaceus 60 kDa
chaperonin (cpn60) gene, partial cds.

ACCESSION
AY691305

VERSION
KEYWORDS

SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL

PUBMED
REFERENCE

Hill, J.E., Penny, S.L., Crowell, K.G., Goh, S.H. and Hemmingsen, S.M.
cpnDB: a chaperonin sequence database

Genome Res. 14 (8), 1659-1675 (2004)

15289485

2 (bases 1 to 552)

cpnDB - a chaperonin sequence database

ConsRTM

Direct Submission

TITLE

JOURNAL

Submitted (20-JUL-2004) NRC Plant Biotechnology Institute, 110
Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada

Location/Qualifiers

1..552

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Db      301  ATGGCTTCACAGGAGGTATCATCTCGCGTACTTCGCCACCCACCATGGAGCGCATGGAG 360
Qy      400  GCGTGCCTCGACGACCGCGTAC 420
Db      361  GCGTGCCTCGAGGACCGGTAC 381

RESULT 6
AF233387
LOCUS   AF233387
DEFINITION Rhodococcus equi GroEL (groEL), gene, complete cds, and unknown
genes.
VERSION AF233387
KEYWORDS AF233387.1 GI:15321579
SOURCE   Rhodococcus equi (Corynebacterium equi)
ORGANISM Rhodococcus equi
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
REFERENCE 1 (bases 1 to 4713)
AUTHORS Vanniasinkam,T., Barton,M.D. and Heuzenroeder,M.W.
TITLE The immunogenicity of Rhodococcus equi GroEL2-based vaccines in a
murine model
JOURNAL Vet. Immunol. Immunopathol. 98 (1-2), 91-100 (2004)
REFERENCE 2 (bases 1 to 4713)
AUTHORS Vanniasinkam,T., Barton,M.D. and Heuzenroeder,M.W.
TITLE Characterization of the groEL gene of Rhodococcus equi
Unpublished
JOURNAL 3 (bases 1 to 4713)
REFERENCE Vanniasinkam,T., Barton,M.D. and Heuzenroeder,M.W.
AUTHORS Direct Submission
TITLE Submitted (10-FEB-2000) Microbiology, University of South
JOURNAL Australia, Frone Road, Adelaide, SA 5000, Australia

FEATURES
source Location/Qualifiers
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RESULT 7
AF456472
LOCUS AF456472
DEFINITION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

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DEFINITION Mycobacterium sp. 'graecum DL049' heat shock protein 65 (hsp65)
gene, partial cds.
ACCESSION AF456472
VERSION AF456472.1 GI:24571116
SOURCE Mycobacterium sp. 'graecum DL049'
ORGANISM Mycobacterium sp. 'graecum DL049'
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1651)
AUTHORS Ucko, M., Colomni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED 12406715
REFERENCE 2 (bases 1 to 1651)
AUTHORS Ucko, M., Colomni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2001) Genetics, IOLR the National Center for Mariculture, P.O. Box 1212, Eilat 88112, Israel
LOCATION/Qualifiers
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Best Local Similarity 84.5%; Pred. No. 1.3e-24;
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DB 314 CTCGTGCGCGAGGGCTGCGCAACGTCGCGCGCGCGCGCAACCGCATGGCGCTGAAGCGC 373
QY 121 GGCATCGAGAGCGCGCTGAGGCGCTCTCGCGCGCGCTGCGAGCGCGAGGATGTC 180
DB 374 GGCATCGAGAGCGCGCTGAGGCGCTCTCGCGCGCGCTGCGAGCGCGAGGATGTC 433
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DB 494 GAGCTCATCGCGCGCGATGGAAGGTTCGCAAGGAGGCGTCTATCACCGTCGAGGAG 553
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DB 554 TCCACACACTTCGGCTCGAGCTCGAGCTCACCGAGGGCATGCGCTTCGACAAGGGCTAC 613
QY 361 ATCTCGGGTACTTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGACGACCGCTAC 420
DB 614 ATCTCGGGTACTTTCGTGACCGACCGCGCGAGGAAGCGTCTCTGAGGAGCGCTAC 673
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AF352578 1623 bp DNA linear BCT 13-MAR-2001
LOCUS Tsukamurella paurometabola heat shock protein 60 (hsp60) gene,
complete cds.
ACCESSION AF352578
VERSION AF352578.1 GI:13310800
KEYWORDS
SOURCE Tsukamurella paurometabola
ORGANISM Tsukamurella paurometabola
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Tsukamurellaceae; Tsukamurella.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Zimmermann, O.S. and Koechel, H.G.
TITLE Tsukamurella paurometabola heat shock protein 60 (hsp60) gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1623)
AUTHORS Zimmermann, O.S. and Koechel, H.G.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2001) Virology, Univ. Goettingen, Kreuzbergstr
57, Goettingen D-37075, Germany
LOCATION/Qualifiers
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ORIGIN
Query Match 74.9%; Score 314.4; DB 1; Length 1623;
Best Local Similarity 84.3%; Pred. No. 2e-24;
Matches 354; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 1 AAGAGACGACGACGTCGCCGGTACGCGTACGACACCGACCGTCTCGCCCGAGCG 60
DB 232 AAGAGACCGACGACGTCGCCGGCGACGACCAACCGACCGTCTCGCCCGAGCG 291
QY 61 CTCGTACGCGAGGGCTGCGCAACGTCGCGCGCGTGCACACCGCATGGCTCTCAAGCGC 120
DB 292 CTCGTGCGCGAGGGCTGCGCAACATGGCTGCGGTGCGACCGCTCGGCGCTCAAGCGG 351
QY 121 GGCATCGAGAGCGCGCTGAGGCGCTCTCGCGCGCGCTCTGCGAGCGCGAGGATGTC 180

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Db      352  GGCAATCGAAGGCGCTCGAGGCGGTGACCGAGACACTGCTCAAGGAGCGCAAGGAGGTC 411
Qy      181  GAGACCAAGAGAGAGATCGTTTCCAGGCGCTTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
Db      412  GAGACCAAGAGAGAGATCGTTTCCAGGCGCTTCCATCTCCGCGCGCGCCGACACCCAGATCGGT 471
Qy      241  GAGCTCATCGCCGAGGCGATGAGCAAGGTCGCGCAAGGTCGCGCAAGGCGCTCATCACCGTCGAGGAG 300
Db      472  GAGCTCATCGCCGAGGCGATGAGCAAGGTCGCGCAAGGTCGCGCAAGGCGCTCATCACCGTCGAGGAG 531
Qy      301  TCCAGACCTTCGCTCGGAGCTGAGGCTCACCGAGGATGATCGCTTCGACCAAGGCGCTAC 360
Db      532  AGCAACACCTTCGCTTCAGCTGAGGCTCACCGAGGATGATCGCTTCGACCAAGGCGCTTC 591
Qy      361  ATCTCGGCGTACTTCGCCACCGATGAGGCGATGAGGCGCTTCGACGACCCGCTAC 420
Db      592  ATCTCGGCGTACTTCGCCACCGAGCGTCAAGGCGCTCGAGGAGCGCTGCTCGAGGAGCGCTAC 651

RESULT 9
AF281650      1624 bp      DNA      linear      BCT 02-APR-2002
LOCUS      Mycobacterium avium heat shock protein Hsp65 gene, partial cds.
DEFINITION
ACCESSION      AF281650
VERSION
KEYWORDS
SOURCE
ORGANISM      Mycobacterium avium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
avium complex (MAC).
REFERENCE
1 (bases 1 to 1624)
Nagabhushanam, V., Praszkier, J. and Cheers, C.
Molecular and immunological characterization of Mycobacterium avium
65 kDa heat shock protein (Hsp65)
Immunol. Cell Biol. 79 (5), 454-461 (2001)
11564153
REFERENCE
2 (bases 1 to 1624)
Nagabhushanam, V., Praszkier, J. and Cheers, C.
Direct Submission
Submitted (23-JUN-2000) Microbiology and Immunology, Melbourne
University, Royal Parade, Melbourne, Victoria 3052, Australia
JOURNAL
Location/Qualifiers
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ORIGIN
Query Match      74.9%; Score 314.4; DB 1; Length 1624;
Best Local Similarity 84.3%; Pred. No. 2e-24; Mismatches 0; Indels 0; Gaps 0;
Matches 354; Conservative 0;

Qy      1  AAGAAGACCGACGCTCGCGGCTGACGGTACGACACCGACCGACCGCTTCGCGCCAGCG 60
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Db      352  GGCATCGAAGAGCGCGCTCGAAGAGGTCACCGAGACCCCTGCTCAAGTCGCGCAAGGAGGTC 411
Qy      181  GAGACCAAGGAGCAGATCGCTTCAGGCGCTTCATCTCCGCGCGCGCGACACCCAGATCGCG 240
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Qy      241  GAGCTCATCGCGAGGCGATGAGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCTCATCACCGTCGAGGAG 300
Db      472  GACCTGATCGCGAGGCGATGAGCAAGGTCGCGCAAGGTCGCGCGCGCGCGCGCGCGCGCGCG 531
Qy      301  TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGATCGCTTCGCAAGGCGCTAC 360
Db      532  TCCAGACCTTCGCGCTTCGAGCTTCGAGCTCACCGAGGATGATCGCTTCGCAAGGCGCTAC 591
Qy      361  ATCTCGGCGTACTTCGCCACCGATGAGGCGATGAGGCGCTTCGCTCGACGACCGCTAC 420
Db      592  ATCTCGGCGTACTTCGCTCACCGACCGCGCGCTCAGAGGCGCGCTCCTCGAGGACCGCGTTC 651

RESULT 10
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LOCUS      Sequence 21 from Patent WO03058248.
DEFINITION
ACCESSION      AX802868
VERSION      AX802868.1 GI:38501565
KEYWORDS
SOURCE
ORGANISM      Mycobacterium avium subsp. paratuberculosis
Mycobacterium avium subsp. paratuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
avium complex (MAC).
REFERENCE
1
Willemse, P. T., Westerveen, S. F., Bakker, D., van Zijderveld, F. G. and
Thole, J. E.
Paramycobacterial diagnostics and vaccines
Patent: WO 03058248-A 21 17-JUL-2003;
ID-labeled, Instituut voor Dierhouderij en Diergezondheid B.V.
(NL)
Location/Qualifiers
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Query Match      74.9%; Score 314.4; DB 6; Length 1701;
Best Local Similarity 84.3%; Pred. No. 1.9e-24;

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Query Match 74.9%; Score 314.4; DB 1; Length 1751;
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416	TTGGTCCGCGAGGGCTCGCGCAACGTCGCGCGCGCGCCCAACCCGCTGGGTCTCAAGCGC	475
121	GGCATTCGAGAAGCCCGTCGAGGCCGTCTCCGGCGCCCTGCTCGAGCAGCGCAAGGATGTC	180
476	GGCATCGAGAAGCCCGTCGAGAAGGTCAACCGAGACCCCTGCTCAAGTCGCGCCAAGGAGTTC	535
181	GAGACCAAGGACGATCGCTTTCCAGGCGCTCCATCTCCGCGCCGACACCCAGATCGGC	240
536	GAGACCAAGGACGATCGCTGCCACCGGGCCATCTCCGCGGGCGACCACTCGATCGGC	595
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596	GACCTGATCGCCGAGCGCATGACAAAGGTCGGCAACGAGGGGGCTCATCAACCGTCGAGGAG	655
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656	TCCAACACCTTCGGCTGCAGCTCAGAGTCAACGAGGGGTATCGGGTTCGACAAGGGTTAC	715
361	ATCTCGGGCGTATTTCCGACACCGACATGAGCGGATGGAGGGCGTCTCGACGACCCGGTAC	420
716	ATCTCGGGGTATTTGGTCAGGACCGCGAGCGTCAGGAAGCGGTCTTCGAGACCCGGTTC	775

MPU15989	2641 bp	DNA	linear	BCT 02-MAR-2000
LOCUS				
DEFINITION	Mycobacterium paratuberculosis	65 kDa	heat shock protein	PTB65K
	gene, complete cds.			

RECESSION
U15989.1
VERSION U15989.1 GI:559802

SOURCE	ORGANISM
Myxobacterium avium subsp. paratuberculosis	Myxobacterium avium subsp. paratuberculosis
Myxobacterium avium subsp. paratuberculosis	Myxobacterium avium subsp. paratuberculosis

Corynebacterineae; Mycobacteriaceae; Mycobacterium

AUTHORS
el-Zaatar, F. A., Naser, S. A., Engstrand, L., Burch, P. E., Hachem, C. Y.,
Whipple, D. L. and Graham, D. Y.

JOURNAL
PURCHASED
8574825
Clin. Diagn. Lab. Immunol. 2 (6), 657-664 (1995)
SHOCK PROTEIN FROM MYCOBACTERIUM PARATUBERCULOSIS

AUTHORS	El-Zaatari, F.A.K.
TITLE	Direct Submission

FEATURES

Location/Qualifiers

Holcombe Blvd., Houston, TX 77030, USA

source

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ORIGIN

Query Match 74.9%; Score 314.4; DB 1; Length 2641;
Best Local Similarity 84.3%; Pred. No. 1.7e-24;
Matches 354; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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DB 503 AAGAAGACGACGACGCGCGGTGACGATACGACACCGCGACCGGTCTCGCCAGGCG 562
QY 61 CTGCTACGAGGCGCTTGCACACGTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 120
DB 563 TTGCTCGCGAGGCGCTTGCACACGTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 622
QY 121 GGCATCGAGAGGCGCTGAGGCGGTCTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 180
DB 623 GGCATCGAGAGGCGCTGAGGCGGTCTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 682
QY 181 GAGACCAAGGACGATGCGCTTCCACGCGCTTCCACGCGCGGTGACACCGCGATGGCTCTCAAGCGC 240
DB 683 GAGACCAAGGACGATGCGCTTCCACGCGCTTCCACGCGCGGTGACACCGCGATGGCTCTCAAGCGC 742
QY 241 GAGCTCATCGCGAGGCGATGACAGGTGCGCAAGGAGGCGGTCTATCACCGTCGAGGAG 300
DB 743 GACCTGATCGCGAGGCGATGACAGGTGCGCAAGGAGGCGGTCTATCACCGTCGAGGAG 802
QY 301 TCCAGACCTTGGCTTGGAGCTGAGGCTCACCGAGGATGCGCTTCCAGCAAGGCGGTAC 360
DB 803 TCCAGACCTTGGCTTGGAGCTGAGGCTCACCGAGGATGCGCTTCCAGCAAGGCGGTAC 862
QY 361 ATCTCGGCGTACTTCGCCACCGCATGAGGCGGTGAGGCGGTGCGCTCGACGACCGGTAC 420
DB 863 ATCTCGGCGTACTTCGCCACCGCATGAGGCGGTGAGGCGGTGCGCTCGACGACCGGTTC 922
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RESULT 13
CP000088_02
WPCOMMENT

Sequence split into 37 fragments LOCUS CP000088 Accession CP000088

Fragment Name	Begin	End
CP000088_00	1	110000
CP000088_01	100001	210000
CP000088_02	200001	310000
CP000088_03	300001	410000
CP000088_04	400001	510000
CP000088_05	500001	610000
CP000088_06	600001	710000
CP000088_07	700001	810000

RESULT 14

AE017241
LOCUS
DEFINITION
Mycobacterium avium subsp. paratuberculosis str. k10, section 15 of 16 of the complete genome.
ACCESSION
AE017241 AE016958
VERSION
AE017241.1 GI:41398721
KEYWORDS
Mycobacterium avium subsp. paratuberculosis str. k10

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CP000088_09 900001 1010000
CP000088_10 100001 1110000
CP000088_11 110001 1210000
CP000088_12 120001 1310000
CP000088_13 130001 1410000
CP000088_14 140001 1510000
CP000088_15 150001 1610000
CP000088_16 160001 1710000
CP000088_17 170001 1810000
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CP000088_28 280001 2910000
CP000088_29 290001 3010000
CP000088_30 300001 3110000
CP000088_31 310001 3210000
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CP000088_33 330001 3410000
CP000088_34 340001 3510000
CP000088_35 350001 3610000
CP000088_36 360001 3642249
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Continuation (3 of 37) of CP000088 from base 200001 (CP000088 Thermobifida fusca YX.

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Query Match 74.9%; Score 314.4; DB 1; Length 110000;
Best Local Similarity 84.3%; Pred. No. 5.2e-25;
Matches 354; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGGTCTCGCCAGGCG 60
DB 57157 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGGTCTCGCCAGGCG 57216
QY 61 CTGCTACGAGGCGCTTGCACACGTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 120
DB 57217 CTGCTACGAGGCGCTTGCACACGTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 57276
QY 121 GGCATCGAGAGGCGCTTGCACACGTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 180
DB 57277 GGCATCGAGAGGCGCTTGCACACGTCGCGCGCGGTGACACCGCGATGGCTCTCAAGCGC 57336
QY 181 GAGACCAAGGACGATGCGCTTCCACGCGCTTCCACGCGCGGTGACACCGCGATGGCTCTCAAGCGC 240
DB 57337 GAGACCAAGGACGATGCGCTTCCACGCGCTTCCACGCGCGGTGACACCGCGATGGCTCTCAAGCGC 57396
QY 241 GAGCTCATCGCGAGGCGATGACAGGTGCGCAAGGAGGCGGTCTATCACCGTCGAGGAG 300
DB 57397 GAGCTCATCGCGAGGCGATGACAGGTGCGCAAGGAGGCGGTCTATCACCGTCGAGGAG 57456
QY 301 TCCAGACCTTGGCTTGGAGCTGAGGCTCACCGAGGATGCGCTTCCAGCAAGGCGGTAC 360
DB 57457 GGCACACCTTGGCTTGGAGCTGAGGCTCACCGAGGATGCGCTTCCAGCAAGGCGGTAC 57516
QY 361 ATCTCGGCGTACTTCGCCACCGCATGAGGCGGTGAGGCGGTGCGCTCGACGACCGGTAC 420
DB 57517 ATCTCGGCGTACTTCGCCACCGCATGAGGCGGTGAGGCGGTGCGCTCGACGACCGGTAC 57576
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QY 121 GGCATCGAGAGGCCGTGAGGCGCTCTCGGCGCCCTGCTGAGAGCAGGCGAAGGATGTC 180
DB 352 GGCATCGAAAGCCGTGGAAGCCGTACCGAACACCTGTGAAAGCCGCAAGGAGGTC 411
QY 181 GAGACCAAGAGCAGATCGTCTCACGGCTCCATCTCCGCGCGCCGACACCCAGATCGGC 240
DB 412 GAGACCAAGATCAGATCGTCTACCGGGGATCTCGCGCGCGACCCCGCCATCGGC 471
QY 241 GAGCTCATCGCGAGCGCATGGACAAGGTGCGCAAGGAAGGCGTCATCACCGTCGAGGAG 300
DB 472 GAGCTCATCGCGAGCGCATGGACAAGGTGCGCAAGGAAGGCGTCATCACCGTCGAGGAG 531
QY 301 TCCACAGCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGCTTAC 360
DB 532 AGCAACACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGCTTAC 591
QY 361 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCGGTAC 420
DB 592 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCGGTAC 651
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RESULT 16
AF352019 1629 bp DNA linear BCT 11-APR-2001
LOCUS Nocardia asteroides heat shock protein 60 (hsp60) gene, complete cds.
DEFINITION AF352019
ACCESSION AF352019.1 GI:13591780
VERSION AF352019.1
KEYWORDS Nocardia asteroides
SOURCE Nocardia asteroides
ORGANISM Nocardia asteroides
REFERENCE Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
AUTHORS Corynebacterineae; Nocardiaaceae; Nocardia.
TITLES Zimmermann, O.S. and Koehel, H.G.
JOURNAL Direct Submission
SUBMITTED (21-FEB-2001) Department of Virology, University of
Goettingen, Kreuzberg 57, Goettingen D-37075, Germany
FEATURES
1..1629
source /organism="Nocardia asteroides"
1..1629 /mol_type="genomic DNA"
1..1629 /db_xref="taxon:1824"
1..1629 /gene="hsp60"
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1..1629 /codon_start=1
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1..1629 /product="heat shock protein 60"
1..1629 /protein_id="AAK31351.1"
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LNNVAGNPLKRGKIGKAVATKLLDTAKEVTEKQIAATAGISAGDAAGELI
AEAMDKVGEVITVEENFTGLQLETEGMEFDKGYISGFATDPERQEAFLDPYI
LIVGSKSVTKLLPLEKVIQAGKPLLI IADVEGEALSTLVKKILGTFSVAVKA
PGGRRRAQLADILITGGOVI SEEVGLSLETAGIELLGQARKVVTVDSTIVEGA
GDPAIAGRVASQIRAEIENSDDYDREKQLERKLAKGVAIVKAGATEVELKERKH
RIEDAVRNKAASVEGI VAGGVAVFLQSPALDDPKLEGDEATGANIVRVALSAPLKQ
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Query Match 73.7%; Score 309.6; DB 1; Length 1629;
Best Local Similarity 83.6%; Pred. No. 6.2e-24;
Matches 351; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 AAGAGACGAGCAGCTCGCGGTGACCGTACGACACCGGACCGGTCGCGCCAGCGG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACCGTACGACACCGGACCGGTCGCGCTCAGCG 291
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QY 61 CTCGTACGCGAGGCGCTCGGCAACGTCGCGCGCGTGCACACCGATGGCTCTCAAGCGC 120
DB 292 CTGGTGCAGGCGCTCGGCAACGTCGCGCGCGTGCACACCGATGGCTCTCAAGCGC 351
QY 121 GGCATCGAGAGGCCGTGAGGCGCTCTCCGCGCGCCCTGCTGAGAGCAGGCGAAGGATGTC 180
DB 352 GGCATCGAAAGCCGTGGAAGCCGTACCGAACACCTGTGAAAGCCGCAAGGAGGTC 411
QY 181 GAGACCAAGAGCAGATCGTCTCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 412 GAGACCAAGAGCAGATCGTCTCACGGCTTACCGCGCGCGACCGGCGCATCGGT 471
QY 241 GAGCTCATCGCGAGCGCATGGACAAGGTGCGCAAGGAAGGCGTCATCACCGTCGAGGAG 300
DB 472 GAGCTCATCGCGAGCGCATGGACAAGGTGCGCAAGGAAGGCGTCATCACCGTCGAGGAG 531
QY 301 TCCACAGCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGCTTAC 360
DB 532 AGCAACACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGCTTAC 591
QY 361 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCGGTAC 420
DB 592 ATCTCGGCTACTTCCGACCGACATGAGCGGATGAGGCGTTCGCTCGACGACCGGTAC 651
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RESULT 17
AR080017
LOCUS Sequence 113 from patent US 5968524.
DEFINITION AR080017
ACCESSION AR080017
VERSION AR080017.1 GI:10006752
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Watson, J.D. and Tan, P.L.J.
TITLES Methods and compounds for the treatment of immunologically-mediated
psoriasis
JOURNAL Patent: US 5968524-A 113 19-OCT-1999;
FEATURES Location/Qualifiers
1..1569 /organism="unknown"
1..1569 /mol_type="unassigned DNA"

ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCAGCTCGCGGTGACCGTACGACACCGGACCGGTCGCGCCAGCGG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACCGTACGACACCGGACCGGTCGCGCTCAGGCT 291
QY 61 CTCGTACGCGAGGCGCTCGGCAACGTCGCGCGCGTGCACACCGATGGCTCTCAAGCGC 120
DB 292 CTGGTTCGGAAGCCGTGCGCAACGTCGCGCGCGCCGCAACCGCTCGGCTCAAGCGT 351
QY 121 GGCATCGAGAGGCCGTGAGGCGCTCTCCGCGCGCCCTGCTGAGAGCAGGCGAAGGATGTC 180
DB 352 GGCATCGAAAGCCGTGGAAGCCGTACCGAACACCTGTGAAAGCCGCAAGGAGGTC 411
QY 181 GAGACCAAGAGCAGATCGTCTCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 412 GAGACCAAGAGCAGATCTTCCACCGCGCGGATTTCCCGCGCGGACACCCAGATCGGC 471
QY 241 GAGCTCATCGCGAGGCGATGGACAAGGTGCGCAAGGAAGGCGTCATCACCGTCGAGGAG 300
DB 472 GAGCTCATCGCGAGGCGATGGACAAGGTGCGCAAGGAAGGCGTCATCACCGTCGAGGAG 531
QY 301 TCCACAGCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGCTTAC 360
DB 532 TCGAACACCTTCGGCGCTGAGCTCAGCTCAGGCGTACCGAGGATGCGCTTCGACAGGCGCTTAC 591

Qy	361	ATCTCGGCTACTTTCGCCACCGACATGAGCGGATGGAGCGTCTCGCTCGACGACCGCTAC	420
Db	592	ATCTCGGTTACTTCTGTGACCGACCGCGCGGCGGAGCGCTCTCGAGGATCCCTAC	651
RESULT 18			
LOCUS	AR085943	1569 bp	DNA linear PAT 07-SEP-2000
DEFINITION	Sequence 113 from patent US 5985287.		
ACCESSION	AR085943		
VERSION	AR085943.1	GI:10012709	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1569)		
AUTHORS	Tan, P., Skinner, M. and Prestidge, R.		
TITLE	Compounds and methods for treatment and diagnosis of mycobacterial infections		
JOURNAL	Patent: US 5985287-A 113 16-NOV-1999;		
FEATURES	Location/Qualifiers		
source	1..1569		
	/organism="unknown"		
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ORIGIN			
Query Match 73.3%; Score 308; DB 6; Length 1569;			
Best Local Similarity 83.3%; Pred. No. 9.3e-24; Indels 0; Gaps 0;			
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;			
Qy	1	AAGAAGACGACGACGCTCGCGGTGACGCTACGACACCGGACCGCTTCTCGCCACGGCG	60
Db	232	AAGAAGACGACGACGCTCGCGGGGACGCGCACCAACCGCCACGCTCGCTCAGGCT	291
Qy	61	CTCGTACGAGGGCTTCGCAACGTCGCGCGGTGCAACCCGATGGCTCTCAAGGCG	120
Db	292	CTGGTTTCGCAAGGCGCTGCGCAACGTCGACGCGCGCGCAACCCGCTCGGCTCAAGCGT	351
Qy	121	GGCATCGAAGCGCTCGAGGCGCTCTCGGCGCGCTCTGGAGCGGCGAAGGATGTC	180
Db	352	GGCATCGAAGGCTGTGAGGCTGTGACCCAGTCGCTGCTGTAAGTCGGCCAGGAGGTC	411
Qy	181	GAGACCAAGGACGATCGCTTCCACGGCTCTCATCTCGCGCGCGACACCCAGATCGGC	240
Db	412	GAGACCAAGGACGATTTCTGCCACCGGGCGATTTCCGCGGGCGACACCCAGATCGGC	471
Qy	241	GAGCTCATCGGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGCGTCAACCGTCGAGGAG	300
Db	472	GAGCTCATCGGAGCGCATGCAAGGTCGCAAGGTCGCAAGGAGGTCATCAACCGTCGAGGAG	531
Qy	301	TCCAGACCTTGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGCTAC	360
Db	532	TCGAACACCTTGGCTCGAGCTCGAGCTCACCGAGGATGCGCTTCGACAGGCGCTAC	591
Qy	361	ATCTCGGCTACTTTCGCCACCGACATGAGCGGATGGAGCGTCTCGCTCGACGACCGCTAC	420
Db	592	ATCTCGGTTACTTCTGTGACCGACCGCGGAGCGCGGAGGCGCTCTCGAGGATCCCTAC	651
RESULT 19			
LOCUS	AR121709	1569 bp	DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 113 from patent US 6160093.		
ACCESSION	AR121709		
VERSION	AR121709.1	GI:14105285	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1569)		
AUTHORS	Visser, E.		
TITLE	Compounds and methods for treatment and diagnosis of mycobacterial infections		

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G01N33/68//
PC      (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
CC      Compositions derived from mycobacterium
       vaccae and methods for
       their use
FH      Key              Location/Qualifiers
FT      source          1..1569
                        /organism='Mycobacterium vaccae'
FEATURES             Location/Qualifiers
     source          1..1569
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                     /mol_type="genomic DNA"
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ORIGIN
Query Match       73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0

Qy 1 AAGAAACGGACGACGTTCGCCGGTACCGGTACGACCAACCGACCGATGGCTTCGAAGGC 120
    |||
Db 232 AAGAAACGGACGACGTTCGCCGGCGACGSCACCACCGCACCGCTCGCTCAGGCT 291
    |||

Qy 61 CTCGTACCGAGGGGCTCGGCACACTCGCCGGCGGTGCCAACCGCATGGCTTCGAAGGC 120
    |||
Db 292 CTGGTTCCGGAAGGCTTCGGCAAACGTGCGAGCCGGCGCCAACCCGCTCGGCTCAAGCGT 351
    |||

Qy 121 GGCAATCGAAGAAGCCCGTCGAGGCCGTCTCTCGCGGCCCTGCTGGAGCAGCGCAAGGATGTC 180
    |||
Db 352 GGCATCGAAGAGGCTGTTCGAGGCTGTCAACCACTGCTGTGTAAGTCGGCCAAAGAGGTC 411
    |||

Qy 181 GAGACCAAGAGACAGATCGCTTCCAGGCGCTCCATCTCGCGCGCGACACCCAGATCGGC 240
    |||
Db 412 GAGACCAAGAGACAGATTCTGCCACC CGCGGCGATTTCGCGCGGCGACACCCAGATCGGC 471
    |||

Qy 241 GAGCTCATCGCGAGGCCATGGAAGAAGTCGGCAAGGAAGGCTCATCACGTCGAGGAG 300
    |||
Db 472 GAGCTCATCGCGAGGCCATGGAAGAAGTCGGAACGAGGCGTGTATCACCGTCGAGGAG 531
    |||

Qy 301 TCCAGAGCTTCGGTCTCGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
    |||
Db 532 TCGAACACTTCGGGCTCGAGCTCGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 591
    |||

Qy 361 ATCTCGGCGTACTTCGCCACCAGACATGGAGCGGATGAGGCGGTCGCTCGACACCGCTAC 420
    |||
Db 592 ATCTCGGCTTACTTCGTGACCGAGCGCGAGGCCAGGAAGCGGTCCTTGAGGATCCCTAC 651
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RESULT 21
AR213755 LOCUS               1569 bp DNA linear PAT 25-SEP-2000
DEFINITION Sequence 113 from patent US 6406704.
ACCESSION AR213755
VERSION AR213755.1 GI:23311042
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 113 18-JUN-2002;
        Genesis Research and Development Corporation Limited;;
        NZX;

FEATURES             Location/Qualifiers
     source          1..1569
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                     /mol_type="genomic DNA"

ORIGIN
Query Match       73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;

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QY 241 GAGCTCATCCGAGGCGATGGACAGGTGCGCAAGGAGCGCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCCGAGGCGCATGGACAGGTGCGCAAGGAGCGCTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTTCGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCTTACTTCGCGACCGACATGGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 420
Db 592 ATCTCGGCTTACTTCGCGACCGACCGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 651

RESULT 23
BD008540
LOCUS BD008540 1569 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial
infections.
ACCESSION BD008540
VERSION BD008540.1 GI:18636913
KEYWORDS JP 2001503969-A/43.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1569)
AUTHORS Tan, P., Hiyama, J., Visser, E.S., Skinner, M.A., Scott, L.M. and
Prestidge, R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial
infections
JOURNAL Patent: JP 2001503969-A 43 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT OS Unidentified
PN JP 2001503969-A/43
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI PAUL TAN, JUN HIYAMA, ELIZABETH S VISSER, MARGOT A SKINNER, PI
LINDA W SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04, A61K35/74, C07K14/35, C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1..1569
FT Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1569;
Best Local Similarity 83.3%; Pred. No. 9.3e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGCAGGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 60
Db 232 AAGAAGCAGGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 291
QY 61 CTGCTAGCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 120
Db 292 AAGAAGCAGGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 351
QY 121 GGCATCGAGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 240
Db 412 GGCATCGAGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 471
QY 241 GAGCTCATCCGAGGCGATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCCGAGGCGCATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTTCGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCTTACTTCGCGACCGACATGGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 420
Db 592 ATCTCGGCTTACTTCGCGACCGACCGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 651

RESULT 24
AR080045
LOCUS AR080045 1626 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 159 from patent US 598524.
ACCESSION AR080045
VERSION AR080045.1 GI:10006780
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Watson, J.D. and Tan, P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated
psoriasis
JOURNAL Patent: US 598524-A 159 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..1626
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity 83.3%; Pred. No. 9.2e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGCAGGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 60
Db 232 AAGAAGCAGGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 291
QY 61 CTGCTAGCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 120
Db 292 CTGCTAGCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 351
QY 121 GGCATCGAGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 180
Db 352 GGCATCGAGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 411
QY 181 GAGACCAAGGAGCGATCGCTTCACGCGCTCCATCTCGCGCGCGACACCGAGATCGGC 240
Db 412 GAGACCAAGGAGCGATCGCTTCACGCGCTCCATCTCGCGCGCGACACCGAGATCGGC 471
QY 241 GAGCTCATCCGAGGCGATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCCGAGGCGCATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTTCGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCTTACTTCGCGACCGACATGGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 420
Db 592 ATCTCGGCTTACTTCGCGACCGACCGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 651

RESULT 25
AR085971
LOCUS AR085971 1626 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 159 from patent US 5985287.
ACCESSION AR085971
VERSION AR085971.1 GI:10012737
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QY 241 GAGCTCATCCGAGGCGATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCCGAGGCGCATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTTCGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCTTACTTCGCGACCGACATGGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 420
Db 592 ATCTCGGCTTACTTCGCGACCGACCGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 651

RESULT 24
AR080045
LOCUS AR080045 1626 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 159 from patent US 598524.
ACCESSION AR080045
VERSION AR080045.1 GI:10006780
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Watson, J.D. and Tan, P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated
psoriasis
JOURNAL Patent: US 598524-A 159 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..1626
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity 83.3%; Pred. No. 9.2e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 AAGAAGCAGGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 60
Db 232 AAGAAGCAGGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 291
QY 61 CTGCTAGCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 120
Db 292 CTGCTAGCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 351
QY 121 GGCATCGAGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 180
Db 352 GGCATCGAGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 411
QY 181 GAGACCAAGGAGCGATCGCTTCACGCGCTCCATCTCGCGCGCGACACCGAGATCGGC 240
Db 412 GAGACCAAGGAGCGATCGCTTCACGCGCTCCATCTCGCGCGCGACACCGAGATCGGC 471
QY 241 GAGCTCATCCGAGGCGATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATCCGAGGCGCATGGACAGGTGCGCAAGGAGCGGTCTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTTCGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 360
Db 532 TCGAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGGTATGGCTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCTTACTTCGCGACCGACATGGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 420
Db 592 ATCTCGGCTTACTTCGCGACCGACCGAGCGGATGGAGCGGTCGCTCCAGACCGCTAC 651

RESULT 25
AR085971
LOCUS AR085971 1626 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 159 from patent US 5985287.
ACCESSION AR085971
VERSION AR085971.1 GI:10012737
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Tan, P., Skinner, M. and Prestidge, R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 159 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..1626
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity 83.3%; Pred. No. 9.2e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAAGCGAGCGAGCGTCCGCGGTGACGGTACGACCAACCGGACCGCTTCTCCGCCAGGCG 60
DB 232 AAGAAGCGAGCGAGCGTCCGCGGTGACGGTACGACCAACCGGACCGCTTCTCCGCCAGGCGT 291
QY 61 CTCGTACCGAGGGGCTCGGCAACCTCCCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
DB 292 CTGGTTCCGGAAGGCTCGGCAACCTCGAGCGCGGCGCAACCGCTCGGCTCAAGCGT 351
QY 121 GGCATCGAGAAGCGCGTCCGAGCGCTCTCCGCGCGCTCTCGAGCAGGCGAAGGATGTC 180
DB 352 GGCATCGAGAGGCTGTGAGGCTGTACCCAGTCTGCTGAAAGTGGCCAGGAGGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGATTTCCGCGCGCGACACCCAGATCGGC 471
QY 241 GAGCTCATCGCGAGGCGATGAGCAAGGTCCGCAAGGAAGGCGTATCAACCGTTCGAGG 300
DB 472 GAGCTCATCGCGAGGCGATGAGCAAGGTCCGCAAGGAAGGCGTATCAACCGTTCGAGG 531
QY 301 TCCAGACCTTCGGTCTGAGCTGAGGCTCACCGAGGGTATCGCTTCGACAAAGGCTAC 360
DB 532 TCGACACCTTCGGCTGAGCTGAGCTCACCGAGGGTATCGCTTCGACAAAGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGGAGGCGTCCGTCGACGACCCGTCAC 420
DB 592 ATCTCGGCGTACTTCGTCACCGACCGCGGCGCGAGGAGCGTCTCTCGAGGATCCCTAC 651

RESULT 26
AR121737
LOCUS AR121737 1626 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 159 from patent US 6160093.
ACCESSION AR121737
VERSION AR121737.1 GI:14105313
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Visser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 159 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..1626
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 73.3%; Score 308; DB 6; Length 1626;
Best Local Similarity 83.3%; Pred. No. 9.2e-24;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAAGCGAGCGAGCGTCCGCGGTGACGGTACGACCAACCGGACCGCTTCTCCGCCAGGCG 60
DB 232 AAGAAGCGAGCGAGCGTCCGCGGTGACGGTACGACCAACCGGACCGCTTCTCCGCCAGGCGT 291
QY 61 CTCGTACCGAGGGGCTCGGCAACCTCCCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
DB 292 CTGGTTCCGGAAGGCTCGGCAACCTCGAGCGCGGCGCAACCGCTCGGCTCAAGCGT 351
QY 121 GGCATCGAGAAGCGCGTCCGAGCGCTCTCCGCGCGCTCTCGAGCAGGCGAAGGATGTC 180
DB 352 GGCATCGAGAGGCTGTGAGGCTGTACCCAGTCTGCTGAAAGTGGCCAGGAGGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGATTTCCGCGCGCGACACCCAGATCGGC 471
QY 241 GAGCTCATCGCGAGGCGATGAGCAAGGTCCGCAAGGAAGGCGTATCAACCGTTCGAGG 300
DB 472 GAGCTCATCGCGAGGCGATGAGCAAGGTCCGCAAGGAAGGCGTATCAACCGTTCGAGG 531
QY 301 TCCAGACCTTCGGTCTGAGCTGAGGCTCACCGAGGGTATCGCTTCGACAAAGGCTAC 360
DB 532 TCGACACCTTCGGCTGAGCTGAGCTCACCGAGGGTATCGCTTCGACAAAGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGGAGGCGTCCGTCGACGACCCGTCAC 420
DB 592 ATCTCGGCGTACTTCGTCACCGACCGCGGCGCGAGGAGCGTCTCTCGAGGATCCCTAC 651

RESULT 27
BD218146
LOCUS BD218146 1626 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION BD218146
VERSION BD218146.1 GI:33027916
KEYWORDS JP 2002514385-A/71.
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
REFERENCE 1 (bases 1 to 1626)
AUTHORS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
TITLE Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
JOURNAL Compositions derived from mycobacterium vaccae and methods for their use.
COMMENT Patent: JP 2002514385-A 71 21-MAY-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Mycobacterium vaccae
PN JP 2002514385-A/71
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
PC A61P17/00,
PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
PC C07K19/00,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC (C12N15/09, C12R1:32), C12N15/00, C12N5/00, (C12N15/00, C12R1:32)
CC Compositions derived from mycobacterium
vaccae and methods for
their use
CC Key Location/Qualifiers
FH source 1..1626
FT /organism="Mycobacterium vaccae".
FEATURES Location/Qualifiers
source 1..1626
/organism="Mycobacterium vaccae"
/mol_type="genomic DNA"

RESULT 30
LOCUS AR080018 647 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 115 from patent US 5968524.
ACCESSION AR080018
VERSION AR080018.1 GI:10006753
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Watson, J.D. and Tan, P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated psoriasis
JOURNAL Patent: US 5968524-A 115 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..647
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGACCGGTCCTCGCCCGAGGG 60
|||
Db 232 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGACCGGTCCTCGCTCAGGCT 291
|||
QY 61 CTCGTACCGGAGGGCTCGGCAACGTCGCCCGGTGCGCAACCCCGATGGCTCTCAAGGCG 120
|||
Db 292 CTGGTTCCGGAAGGCTCGGCAACGTCGACGCGGCGCAACCCGCTCGGCTCAAGCGT 351
|||
QY 121 GGCATCGAAGAGCGCTCGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 180
|||
Db 352 GGCATCGAAGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 411
|||
QY 181 GAGACCAAGGACGACGATCGCTTCCACGGCTTCCATCTCCGCGCGGACACCCAGATCGGC 240
|||
Db 412 GAGACCAAGGACGACGATCTTCCACCGCGGGATTTCCGCGGCGACACCCAGATCGGC 471
|||
QY 241 GAGCTCATCGCGAGGGCGATGACAAAGTTCGCGCGGTGCGCAACCCCGATGGCTCTCAAGGCG 300
|||
Db 472 GAGCTCATCGCGAGGGCGATGACAAAGTTCGCGCGGTGCGCAACCCCGATGGCTCTCAAGGCG 531
|||
QY 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCACCAGGGGTATGCGTTTCGACNAGGGCTAC 360
|||
Db 532 TCGAACACCTTCGGCTTCGAGCTCAGCTCACCAGGGGTATGCGTTTCGACNAGGGCTAC 591
|||
QY 361 ATCTCGGCTACTTCCGACACCATGAGCGGATGAGGGGTGCTCGACGACCC 416
|||
Db 592 ATCTCGGCTACTTCTGTGACCGACCGCGGACCGGACCGGTCCTCGAGGATCC 647
|||

RESULT 31
LOCUS AR085944 647 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 115 from patent US 5985287.
ACCESSION AR085944
VERSION AR085944.1 GI:10012710
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Tan, P., Skinner, M. and Prestidge, R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 115 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..647
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGTCCTCGCCCGAGGG 60
|||
Db 232 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGTCCTCGCTCAGGCT 291
|||
QY 61 CTCGTACCGGAGGGCTCGGCAACGTCGCCCGGTGCGCAACCCCGATGGCTCTCAAGGCG 120
|||
Db 292 CTGGTTCCGGAAGGCTCGGCAACGTCGACGCGGCGCAACCCGCTCGGCTCAAGCGT 351
|||
QY 121 GGCATCGAAGAGCGCTCGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 180
|||
Db 352 GGCATCGAAGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 411
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGTCCTCGCCCGAGGG 60
|||
Db 232 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGTCCTCGCTCAGGCT 291
|||
QY 61 CTCGTACCGGAGGGCTCGGCAACGTCGCCCGGTGCGCAACCCCGATGGCTCTCAAGGCG 120
|||
Db 292 CTGGTTCCGGAAGGCTCGGCAACGTCGACGCGGCGCAACCCGCTCGGCTCAAGCGT 351
|||
QY 121 GGCATCGAAGAGCGCTCGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 180
|||
Db 352 GGCATCGAAGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 411
|||
QY 181 GAGACCAAGGACGACGATCGCTTCCACGGCTTCCATCTCCGCGCGGACACCCAGATCGGC 240
|||
Db 412 GAGACCAAGGACGACGATTTCTGCCACCGCGGGATTTCCGCGGCGACACCCAGATCGGC 471
|||
QY 241 GAGCTCATCGCGAGGGCGATGACAAAGTTCGCGCGGTGCGCAACCCCGATGGCTCTCAAGGCG 300
|||
Db 472 GAGCTCATCGCGAGGGCGATGACAAAGTTCGCGCGGTGCGCAACCCCGATGGCTCTCAAGGCG 531
|||
QY 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCACCAGGGGTATGCGTTTCGACNAGGGCTAC 360
|||
Db 532 TCGAACACCTTCGGCTTCGAGCTCAGCTCACCAGGGGTATGCGTTTCGACNAGGGCTAC 591
|||
QY 361 ATCTCGGCTACTTCCGACACCATGAGCGGATGAGGGGTGCTCGACGACCC 416
|||
Db 592 ATCTCGGCTACTTCTGTGACCGACCGCGGACCGGACCGGTCCTCGAGGATCC 647
|||

RESULT 32

LOCUS AR121710 647 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 115 from patent US 6160093.
ACCESSION AR121710
VERSION AR121710.1 GI:14105286
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 647)
AUTHORS Viesser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 115 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..647
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGTCCTCGCCCGAGGG 60
|||
Db 232 AAGAAGACGGACGACGTCGCCGGTGACGGGTACGACACCGCGGACCGGTCCTCGCTCAGGCT 291
|||
QY 61 CTCGTACCGGAGGGCTCGGCAACGTCGCCCGGTGCGCAACCCCGATGGCTCTCAAGGCG 120
|||
Db 292 CTGGTTCCGGAAGGCTCGGCAACGTCGACGCGGCGCAACCCGCTCGGCTCAAGCGT 351
|||
QY 121 GGCATCGAAGAGCGCTCGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 180
|||
Db 352 GGCATCGAAGAGCGCTCTCCGGCGCCCTGCTGGAGCAGCGGCAAGATGTC 411
|||

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QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCCGCGACACCCAGATCGGC 471
QY 241 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 300
Db 472 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGAGAGCTCACGAGGATATGCGCTTCGACAAAGGCGTAC 360
Db 532 TCGAACACCTTCGCGCTCGAGCTCGAGCTCACGAGGATATGCGCTTCGACAAAGGCGTAC 591
QY 361 ATCTCGGCTTACTTCGTCGACCGAGCGCGGAGGAGGCGCTTCGAGAGGCC 416
Db 592 ATCTCGGCTTACTTCGTCGACCGAGCGCGGAGGAGGCGCTTCGAGAGGCC 647

RESULT 33
LOCUS BD218119 647 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for
their use.
ACCESSION BD218119
VERSION BD218119 1 GI:33027889
KEYWORDS JP 2002514385-A/44.
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
REFERENCE 1 (bases 1 to 647)
AUTHORS Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for
their use
JOURNAL Patent: JP 2002514385-A 44 21-MAY-2002;
GENESTS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT OS Mycobacterium vaccae
PN JP 2002514385-A/44
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
A61P17/00,
PC A61P17/06, A61P31/00, A61P37/04, C07K14/35, C07K16/12,
PC C07K19/00,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC (C12N15/09, C12R1.32), C12N15/00, C12N5/00, (C12N15/00, C12R1.32)
CC Compositions derived from mycobacterium
vaccae and methods for
CC their use
FH Key Location/Qualifiers
FT source 1..647
/organism="Mycobacterium vaccae"
FEATURES source 1..647
Location/Qualifiers
1..647
/organism="Mycobacterium vaccae"
/mol_type="genomic DNA"
/db_xref="taxon:1810"
ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 AAGAAGACCGAGCGTCCGCGGCGAGCGGACCGACCGTTCGCTCGCTCAGGCT 291
Db 232 AAGAAGACCGAGCGTCCGCGGCGAGCGGACCGACCGTTCGCTCGCTCAGGCT 291

QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCCGCGACACCCAGATCGGC 471
QY 241 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 300
Db 472 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGAGAGCTCACGAGGATATGCGCTTCGACAAAGGCGTAC 360
Db 592 ATCTCGGCTTACTTCGTCGACCGAGCGCGGAGGAGGCGCTTCGAGAGGCC 647
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QY 61 CTCTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCCAACCCGATGCTCTCAAGCGC 120
Db 292 CTGTTTCGCGAAGGCTTCGCAACGTCGCGCGCGGTGCCAACCCGCTCGGCTCAAGCGT 351
QY 121 GGCATCGAAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCTGAGCAGGCGGAGGATGTC 180
Db 352 GGCATCGAAGAGGCTTCGAGGCTGTCAACCCAGTCTGCTGAAGTTCGCGCCCAAGGAGGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCCGCGACACCCAGATCGGC 471
QY 241 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 300
Db 472 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGAGAGCTCACGAGGAGTATGCGCTTCGACAAAGGCGTAC 360
Db 532 TCGAACACCTTCGCGCTCGAGCTCGAGCTCACGAGGAGTATGCGCTTCGACAAAGGCGTAC 591
QY 361 ATCTCGGCTTACTTCGTCGACCGAGCGCGGAGGAGGCGCTTCGAGAGGCC 416
Db 592 ATCTCGGCTTACTTCGTCGACCGAGCGCGGAGGAGGCGCTTCGAGAGGCC 647

RESULT 34
LOCUS AR213756 647 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 115 from patent US 6406704.
ACCESSION AR213756
VERSION AR213756.1 GI:23311043
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 647)
AUTHORS Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6406704-A 115 18-JUN-2002;
GENESTS Research and Development Corporation Limited;;
NZX;
FEATURES source 1..647
Location/Qualifiers
1..647
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 AAGAAGACCGAGCGTCCGCGGCGAGCGGACCGACCGTTCGCTCGCTCAGGCT 291
Db 232 AAGAAGACCGAGCGTCCGCGGCGAGCGGACCGACCGTTCGCTCGCTCAGGCT 291
QY 61 CTCTACGCGAGGCGCTTCGCAACGTCGCGCGCGGTGCCAACCCGATGCTCTCAAGCGC 120
Db 292 CTGTTTCGCGAAGGCTTCGCAACGTCGCGCGCGGTGCCAACCCGCTCGGCTCAAGCGT 351
QY 121 GGCATCGAAGAGGCGCTCGAGGCGCTTCGCGCGCGCTTCGCTGAGCAGGCGGAGGATGTC 180
Db 352 GGCATCGAAGAGGCTTCGAGGCTGTCAACCCAGTCTGCTGAAGTTCGCGCCCAAGGAGGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCCGACACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCCGCGACACCCAGATCGGC 471
QY 241 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 300
Db 472 GAGCTCATCTCCCGGAGGCGATGAGCAAGGTTCGCAAGAGGCGCTCATCAGCTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGAGAGCTGAGAGCTCACGAGGAGTATGCGCTTCGACAAAGGCGTAC 360
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Db 532 TCACACACCTTCGCGCTCGAGCTCGAGCTCACGAGGATATGCGCTTCGACCAAGGCTAC 591
Qy 361 ATCTCGCGTACTTCGCGACCGCATGCGAGCGATGAGCGCTCGCTCGACGACCC 416
Db 592 ATCTCGGGTTACTTCGTGACCGAGCGCGAGCGCCAGGAGCGCTTCGTGAGGATCC 647

RESULT 35
AR365988
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

AR365988
Sequence 115 from patent US 6328978.
AR365988
AR365988.1 GI:34598241
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 647)
Watson, J.D., Tan, P.L.J. and Prestidge, R.
Methods for the treatment of immunologically-mediated skin disorders
Patent: US 6328978-A 115 11-DEC-2001;
Genesis Research & Development Corp. Ltd.; Parnell;
NZX;

Location/Qualifiers
1..647
/organism="unknown"
/mol_type="genomic DNA"

Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 AAGACACGACGAGCTCGCGGTGACGCTAGCAGCAGCGACCGTTCTCGCCCGAGCG 60
Db 232 AAGAAGACCGACGAGCTCGCGGGCGAGCGCACACCGCCACCGTGTCTCGCTCAGGCT 291
Qy 61 CTGCTACGCGAGGCGCTCGGCAACGTCGCGCGCGTGCACACCGCATGCTCTCAAGCGC 120
Db 292 CTGGTTCGCGAAGGCTCGGCAACGTCGAGCGCGGCCCAACCGCTCGGCTCAAGCGT 351
Qy 121 GGCATCGAGAACGCGCTCGAGCGCGCTCTCCGCGCGCTCTGCTGAGCAGCGAGGATGTC 180
Db 352 GGCATCGAGAACGCGCTCGAGCGCGCTCTCCGCGCGCTCTGCTGAGTCCGCGAAGGATGTC 411
Qy 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCGCGCGCGACACCGCATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCGCGCGACACCGCATCGGC 471
Qy 241 GAGCTCATCGCGAGCGATGACAAAGTTCGCGAAGGAGGCTCATCACCGTTCGAGGAG 300
Db 472 GAGCTCATCGCGAGCGATGACAAAGTTCGCGAAGGAGGCTCATCACCGTTCGAGGAG 531
Qy 301 TCCAGACCTTCGCGTTCGAGCTCGAGCTCACCGAGGATGCTCGCTTCGACAAAGGCTAC 360
Db 532 TCGAACACCTTCGCGCTCGAGCTCGAGCTCACCGAGGATGCTCGCTTCGACAAAGGCTAC 591
Qy 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGTCGACGACCC 416
Db 592 ATCTCGGGTTACTTCGTGACCGAGCGCGAGCGCCAGGAGCGCTCTCGAGGATCC 647

RESULT 36
BD008541
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

BD008541
Compounds and methods for treatment and diagnosis of Mycobacterial infections.
BD008541
BD008541.1 GI:18635914
JP 2001503969-A/44.
unidentified

647 bp RNA linear PAT 31-JAN-2002

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

unidentified.
1 (bases 1 to 647)
Tan, P., Hiyaama, J., Visser, E.S., Skinner, M.A., Scott, L.M. and Prestidge, R.L.
Compounds and methods for treatment and diagnosis of Mycobacterial infections
Patent: JP 2001503969-A 44 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
OS Unidentified
PN JP 2001503969-A/44
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PI PAUL TAN, JUN HIYAMA, ELIZABETH S VISSER, MARGOT A SKINNER, PI LINDA M SCOTT.
PI ROSS L PRESTIDGE
PC A61K39/04, A61K35/74, C07K14/35, C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..647
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ORIGIN

Query Match 72.8%; Score 305.6; DB 6; Length 647;
Best Local Similarity 83.4%; Pred. No. 2.2e-23;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGAGCTCGCGGTGACGCTAGCAGCAGCGACCGTTCTCGCCCGAGCG 60
Db 232 AAGAAGACCGACGAGCTCGCGGGCGAGCGCACACCGCCACCGTGTCTCGCTCAGGCT 291
Qy 61 CTGCTACGCGAGGCGCTCGGCAACGTCGCGCGCGTGCACACCGCATGCTCTCAAGCGC 120
Db 292 CTGGTTCGCGAAGGCTCGGCAACGTCGAGCGCGGCCCAACCGCTCGGCTCAAGCGT 351
Qy 121 GGCATCGAGAACGCGCTCGAGCGCGCTCTCCGCGCGCTCTGCTGAGCAGCGAGGATGTC 180
Db 352 GGCATCGAGAACGCGCTCGAGCGCGCTCTCCGCGCGCTCTGCTGAGTCCGCGAAGGATGTC 411
Qy 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCGCGCGCGACACCGCATCGGC 240
Db 412 GAGACCAAGGAGCAGATTTCTGCCACCGCGCGGATTTCCGCGCGCGACACCGCATCGGC 471
Qy 241 GAGCTCATCGCGAGCGATGACAAAGTTCGCGAAGGAGGCTCATCACCGTTCGAGGAG 300
Db 472 GAGCTCATCGCGAGCGATGACAAAGTTCGCGAAGGAGGCTCATCACCGTTCGAGGAG 531
Qy 301 TCCAGACCTTCGCGTTCGAGCTCGAGCTCACCGAGGATGCTCGCTTCGACAAAGGCTAC 360
Db 532 TCGAACACCTTCGCGCTCGAGCTCGAGCTCACCGAGGATGCTCGCTTCGACAAAGGCTAC 591
Qy 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGTCGACGACCC 416
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RESULT 37
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WPCOMMENT

Sequence split into 61 fragments LOCUS AP006618 Accession AP006618

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AP006618_01 100001 210000
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Query Match 71.8%; Score 301.6; DB 1; Length 110000;
Best Local Similarity 82.4%; Pred. No. 1.1e-23;
Matches 346; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1 AAGAAAGCGGACGCTCGCGGTGACGCTGACGACCGGACCGGACCGCTTCGCGCCAGGCG 60
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QY 61 CTGCTAGCGGAGGCGCTGCGCAAGCTGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 77661 CTGCTAGCGGAGGCGCTGCGCAAGCTGCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 77602
QY 121 GGCATCGAGAGGCGCTGCGAGGCGCTTCGCGGCGCTTCGCGGAGCGAGGATGTC 180
Db 77601 GGCATCGAGAGGCGCTGCGAGGCGCTTCGCGGAGCGAGGATGTC 77542

181 GAGACCAAGGAGCAGATCGCTTCCAGGGCTCCATCTCGCGCGCGACACCCAGATCGGC 240
77541 GAGACCAAGGAGCAGATCGCTTCCAGGGCTCCATCTCGCGCGCGACCGCTCCATCGGT 77482
QY 241 GAGCTCATCGCGGAGCGATGACCAAGGTCGCAAGGAGGCGCTCATCACCGTCGAGGAG 300
Db 77481 GAGCTCATCGCGGAGCGATGACCAAGGTCGCAAGGAGGCGCTCATCACCGTCGAGGAG 77422
QY 301 TCCGAGACCTTCGCTCGAGCTCGAGCTCAGCGAGGCTATGGCTTCGACAGGCGCTAC 360
Db 77421 AGCAACACCTTCGCGCTCCAGCTCGAGCTGACCGAGGCGATCGCTTCGACAGGCGCTAC 77362
QY 361 ATCTCGGCGTACTTCGTCGACCGACATGAGGAGCGATGAGGCGCTCGACGACCGCTAC 420
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RESULT 38
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LOCUS Nocardia farcinica heat shock protein 60 (hsp60) gene, complete
DEFINITION
ACCESSION AF352577
VERSION AF352577.1 GI:13310798
KEYWORDS Nocardia farcinica
SOURCE Nocardia farcinica
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaaceae; Nocardia.
REFERENCE 1 (bases 1 to 1626)
AUTHORS Zimmermann, O.S. and Koechel, H.G.
TITLE Nocardia farcinica heat shock protein 60 (hsp60) gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1626)
AUTHORS Zimmermann, O.S. and Koechel, H.G.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2001) Virology, Univ. Goettingen, Kreuzberggring
57, Goettingen D-37075, Germany
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Query Match 71.4%; Score 300; DB 1; Length 1626;
Best Local Similarity 82.1%; Pred. No. 6.3e-23;
Matches 345; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 1 AAGAAAGCGGACGCTCGCGGTGACGCTGACGACCGGACCGGACCGCTTCGCGCCAGGCG 60
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ORIGIN					
Query Match	71.0%; Score 298.4; DB 1; Length 1648;				
Best Local Similarity	81.9%; Pred. No. 9.3e-23;				
Matches 344; Conservative	0; Mismatches 76; Indels 0; Gaps 0;				
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Dd	254	AAGAAGACCACACGTCGGCGGTGACGGCAGCAGACGGCCACCGTGTG	GCCCCAGCGC	313	
Qy	61	CTCGTAGCGCAGGGCCCTGCACAACGTCGCCCGCGGTGCCAACCCGAGT	GGCTCTCAAAGCGC	120	
Dd	314	CTGCTCAAGAGAGCCCTGCCACAGTTGCGCGCGGTGCCAACCCGCTCG	GTCTGAAGCGC	373	
Qy	121	GGCATCGAAGGCGCTCGAGGCGCTCTCCGGCGCCCTCTCTGGAGCAGG	CGAAGGATGTC	180	
Dd	374	GGCATCGAAGGCGCAGTGCAGAAAGTCAACGAGATCTCTCAAGTCGG	CCAAAGAGGTC	433	
Qy	181	GAGACCAAGAGCAGATCGCTTCCAGGCGCTCCATCTCCGCGCGCAC	CCCAGATCGGC	240	
Dd	434	GAGACCAAGAGCAGATCGCGGGCGACCGCAGCCATCTCCGCGCGCAC	CAGTCGATCGGC	493	
Qy	241	GAGCTCATCCCGAGGCGATGGAACAAGTCCGCAAGCAAGCGCTCAT	CACGTCGAGGAG	300	
Dd	494	GACCTGATCCCGAGGCGATGGACAAGTGGCAACGAGGGCGTCA	TCACCGTCGAGGAG	553	
Qy	301	TCCGAGACCTTCGGTCTFGAGCTTGAGCTCACCGAGGGTATGCGCT	TCGCAAGGGCTAC	360	
Dd	554	TCCAACACCTTCGGCTTCGAGCTCGAGCTCACCGAGGGGATGCGGT	TCGCAAGGGCTAC	613	
Qy	361	ATCTCGCGGTACTTCGCCACCGCATCGAGCGGATGCGAGCGTCGCT	CGACGCCCTTAC	420	
Dd	614	ATCTCGGGCTACTTTCGTCAACCGACCGCGCGCTCAGGAAGCGTCT	CGAGGCCCTTAC	673	
RESULT 41					
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DEFINITION	Mycobacterium marinum strain cyprinum CC240299 heat shock protein 65 (hsp65) gene, partial cds.				
ACCESSION	AF456469				
VERSION	AF456469.1				
KEYWORDS	GI:24571107				
SOURCE	Mycobacterium marinum				
ORGANISM	Mycobacterium marinum				
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
AUTHORS	Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and Knibb,W.R.				
TITLE	Strain Variation in Mycobacterium marinum Fish Isolates				
JOURNAL	Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)				

12406715
 2 (bases 1 to 1648)
 Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
 Knibb,W.R.
 Direct Submission
 Submitted (10-DEC-2001) Genetics, IOLR the National Center for
 Mariculture, P.O. Box 1212, Eilat 88112, Israel
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ORIGIN
 Query Match 71.0%; Score 298.4; DB 1; Length 1648;
 Best Local Similarity 81.9%; Pred. No. 9.3e-23;
 Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
 QY 1 AAGAAGCGGACGACGTCGCGGTGTGACGGTACGACCAACCGCGGATGCTCTCGGCCAGGCG 60
 DB 254 AAGAAGACCGACGACGTCGCGGTGTGACGGGACGACGACGCGCCACCGTCGTGCGCCAGGCG 313
 QY 61 CTGCTACGCGAGGCGCTGCGACAGCTGCGCGCGGTGCCAACCCCGATGGCTCTCAAGCGC 120
 DB 314 CTGGTCAAGGAAGGCTGCGGCAACGTTGCGGCGCGGTGCCAACCCCGTCGTCTGAAGCGC 373
 QY 121 GGCATCGAAGAGCCGTCGAGGCGGCTCTCGGCGCGCTCTGTCGAGCAGCGCAAGGATGTC 180
 DB 374 GGCATCGAGNAGGCAGTCTGAGAGGTACCGAGATCTCTGCTCAAGTCGCGCAAGAGGTC 433
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 DB 434 GAGACCAAGAGCAGATCGCGGACCGGACCGCATCTCCGCGCGCGACCAAGTCGATCGGC 493
 QY 241 GAGCTCATCGCCGAGGATGGACAGGTTCGCAAGAGGCGGTCTATCCCGTCGAGGAG 300
 DB 494 GACCTGATCGCCAGGCGATGGCAAGGTTGGGCAACGAGGCGGTCTATCACCGTCGAGGAG 553
 QY 301 TCCACAGACCTTCGCTCTGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACCAAGGCGTAC 360
 DB 554 TCCAACACCTTCGCGCTGCGCTCGAGCTCACCGAGGCGATGCGGTTTCGACAGGCGTAC 613
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RESULT 42
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LOCUS
DEFINITION Mycobacterium marinum strain ATCC 927 heat shock protein 65 (hsp65)
AP456470 1648 bp DNA linear BCT 05-NOV-2002
ACCESSION gene, partial cds.
VERSION AP456470
KEYWORDS AP456470.1 GI:24571110
SOURCE Mycobacterium marinum
ORGANISM Mycobacterium marinum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Ucko, M., Colorni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED 12406715
REFERENCE
AUTHORS Ucko, M., Colorni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2001) Genetics, IOLR the National Center for Mariculture, P.O. Box 1212, Eilat 88112, Israel
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Query Match 71.0%; Score 298.4; DB 1; Length 1648;
Best Local Similarity 81.9%; Pred. No. 9.3e-23;
Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCGTCCCGGTGACGCGTACGACCGACCGACCGTTCGCCCCAGGCG 60
DB 254 AAGAAGACGAGCGTCCCGGTGACGCGTACGACCGACCGACCGTTCGCCCCAGGCG 313
QY 61 CTCGTCAGCGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGC 120
DB 314 CTGGTCAGGAAGGCGCTCGCAACGTCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGC 373
QY 121 GGCATCGAGAGCGCGTGGAGCGCTCTCGCGCGCTCTCGCGCGCTCTGGACGCGCGAGATGTC 180
DB 374 GGCATCGAGAGCGCGTGGAGCGCTCTCGCGCGCTCTCGCGCGCTCTGGACGCGCGAGATGTC 433
QY 181 GAGACCAAGGAGCAGATGCTTTCACGGGCTCCATCTCGCGCGCGACACCGCATGCGC 240
DB 434 GAGACCAAGGAGCAGATGCTTTCACGGGCTCCATCTCGCGCGCGACACCGCATGCGC 493
QY 241 GAGCTCATGCGCGAGCGGATGCAACGTTGGCAAGGAGCGGTTCATCACCGTCGAGGAG 300

Db 494 GACCTGATCGCGAGCGCATGGAAGGTGGCAACGAGGGCGTTCATCACCGTCGAGGAG 553
QY 301 TCCCGAGACCTTCGGTCTCGAGCTCGAGCTCACCGAGGGTATCGCTTCGCAAGAGGCTAC 360
DB 554 TCCACACCTTCGGCTCGAGCTCGAGCTCACCGAGGGATCGGTTCCACAGGCTAC 613
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACACCGCTAC 420
DB 614 ATCTCGGCGTACTTCGTCACCGACCGCGATGAGGCGTCTCGAGGAGCGCTAC 673
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LOCUS Mycobacterium marinum strain hellenicum DL045 heat shock protein 65 (hsp65) gene, partial cds.
DEFINITION
ACCESSION AP456471
VERSION AP456471.1 GI:24571113
KEYWORDS
SOURCE Mycobacterium marinum
ORGANISM Mycobacterium marinum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Ucko, M., Colorni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED 12406715
REFERENCE
AUTHORS Ucko, M., Colorni, A., Kvitt, H., Diamant, A., Zlotkin, A. and Knibb, W.R.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2001) Genetics, IOLR the National Center for Mariculture, P.O. Box 1212, Eilat 88112, Israel
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Query Match 71.0%; Score 298.4; DB 1; Length 1648;
Best Local Similarity 81.9%; Pred. No. 9.3e-23;
Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCGTCCCGGTGACGCGTACGACCGACCGCGTTCGCCCCAGGCG 60

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Db 314 CTGGTCAAGAGAGCCCTGCGGACGCTGGCGCGGTGCCAACCGCTCGGTCTGAAGCGC 373
Qy 121 GGCATCGAGAGGCGCGTCTGAGGCGCGTCTCCGGCGCCCTGCTGGAGCAGGCGAAGAGGATGTC 180
Db 374 GGCATCGAGAGGCGCGTCTGAGGCGCGTCTCCGGCGCCCTGCTGGAGCAGGCGAAGAGGATGTC 433
Qy 181 GAGACCAAGAGAGGAGTCTGCTTCCAGCGCTCCATCTCCCGCGCGGACACCGAGATCGGC 240
Db 434 GAGACCAAGAGAGGAGTCTGCGGCGACCGGACCGCATCTCCCGCGCGGACACCGATCGGC 493
Qy 241 GAGCTCATCCCGAGGCGGATGAGCAAGGTGCGCAAGGCGCTCATCACCGTCTGAGGAG 300
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Db 614 ATCTCGGCGTACTTGGTCTGCGACCGCGCGGCGTCAAGGAGCGGTCTCTGGAGGACCGCTAC 673

RESULT 44
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LOCUS Mycobacterium ulcerans heat shock protein 65 (hsp65) gene, partial
DEFINITION cds.
VERSION AP456475.1 GI:24571125
KEYWORDS Mycobacterium ulcerans
SOURCE Mycobacterium ulcerans
ORGANISM Mycobacterium ulcerans
REFERENCE 1 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
AUTHORS Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
TITLE Strain Variation in Mycobacterium marinum Fish Isolates
JOURNAL Appl. Environ. Microbiol. 68 (11), 5281-5287 (2002)
PUBMED 12406715
REFERENCE 2 (bases 1 to 1648)
Ucko,M., Colorni,A., Kvitt,H., Diamant,A., Zlotkin,A. and
Knibb,W.R.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2001) Genetics, IOLR the National Center for
Mariculture, P.O. Box 1212, Eilat 88112, Israel
FEATURES
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ORIGIN
Query Match 71.0%; Score 298.4; DB 1; Length 1648;
Best Local Similarity 81.9%; Pred. No. 9.3e-23;
Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 1 AAGAAGACCGACGACGCTCGCGGTGACGTCAGCACCGACCGACCGTCTCGGCCGACGGCG 60
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RESULT 45
AY498743 667 bp DNA linear BCT 10-MAR-2005
LOCUS Mycobacterium abscessus 65 kDa heat shock protein gene, partial
DEFINITION cds.
VERSION AY498743.1 GI:45789952
KEYWORDS Mycobacterium abscessus
SOURCE Mycobacterium abscessus
ORGANISM Mycobacterium abscessus
REFERENCE 1 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
AUTHORS Selvaraju,S.B., Khan,I.U. and Yadav,J.S.
TITLE A new method for species identification and differentiation of
Mycobacterium chelonae complex based on amplified hsp65 restriction
analysis (AHSPPA)
JOURNAL Mol. Cell. Probes 19 (2), 93-99 (2005)
PUBMED 15680210
REFERENCE 2 (bases 1 to 667)
Selvaraju,S.B., Khan,I.U.H. and Yadav,J.S.
AUTHORS Direct Submission
TITLE Submitted (11-DEC-2003) Environmental Health, Molecular Toxicology
JOURNAL Division, University of Cincinnati, 3223 Eden Ave, Kettering
Laboratory, Cincinnati, OH 45267, USA
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Query Match 70.3%; Score 295.2; DB 1; Length 667;
Best Local Similarity 81.4%; Pred. No. 2.7e-22;
Matches 342; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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DB 350 GGCATCGAAGCGCTCGAGCGCTCTCGAGCGAGGTCACCGAGAGCTCTCTGAAGAGCGCCAGAGGTC 409
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACACCCAGATCGCG 240
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QY 241 GAGCTCATCGCGAGCGCATGGAACAAGGTGCGCAAGAAAGGCGTCAATCAACCGTCGAGGAG 300
DB 470 GACCTGATCGCGAGCGCATGGAACAAGGTGCGCAAGAGGTCATCAACCGTCGAGGAG 529
QY 301 TCCGAGACCTTGGCTCGAGCTGAGCTCACCGAGGATGCGGTTTCGACAAAGGCGTAC 360
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WPCOMMENT

Sequence split into 26 fragments LOCUS AE016822 Accession AE016822

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AE016822_03	300001	410000
AE016822_04	400001	510000
AE016822_05	500001	610000
AE016822_06	600001	710000
AE016822_07	700001	810000
AE016822_08	800001	910000
AE016822_09	900001	1010000
AE016822_10	1000001	1110000
AE016822_11	1100001	1210000
AE016822_12	1200001	1310000
AE016822_13	1300001	1410000
AE016822_14	1400001	1510000
AE016822_15	1500001	1610000
AE016822_16	1600001	1710000

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Query Match 70.3%; Score 295.2; DB 1; Length 110000;
Best Local Similarity 81.4%; Pred. No. 5.3e-23;
Matches 342; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCTAGCAGCACCGCGACCGTCTTCGCCCGAGCGG 60
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QY 361 ATCTCGGCGTACTTCCGCGCGCGATGAGCGCGATGAGCGCGTTCGACGACCGCGTAC 420
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RESULT 47

CQ816174

LOCUS

Sequence 3 from Patent WO2004041304.

DEFINITION

CQ816174

ACCESSION

CQ816174.1

VERSION

GI:48144533

KEYWORDS

Mycobacterium tuberculosis

ORGANISM

Mycobacterium tuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

tuberculosis complex.

REFERENCES

1 Coates, A.R.

Pain relief agents

Patent: WO 2004041304-A 3 21-MAY-2004;

Helpierby Therapeutics Limited (GB)

Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity

Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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RESULT 48
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DEFINITION Sequence 3 from patent US 6495347.
ACCESSION AR266836
VERSION AR266836.1 GI:29696202
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: US 6495347-A 3 17-DEC-2002;
Stressgen Biotechnologies Corporation; Victoria;
CAX;
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source Location/Qualifiers
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Query Match 69.9%; Score 293.6; DB 6; Length 1623;
Best Local Similarity 81.2%; Pred. No. 3e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
Qy 1 AAGAAGACCGATGACGTCGCGGTGACGCGACCAAGCGCCACCGTGTGCGCCAGGCG 60
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RESULT 49
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LOCUS AR655543 1623 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 23 from patent US 6892139.
ACCESSION AR655543
VERSION AR655543.1 GI:67587586
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Eisenberg, D., Rotstein, S.H. and Marcotte, E.M.
TITLE Determining the functions and interactions of proteins by
comparative analysis
JOURNAL Patent: US 6892139-A 23 10-MAY-2005;
The Regents of the University of California; Alameda, CA
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 1623;
Best Local Similarity 81.2%; Pred. No. 3e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
Qy 1 AAGAAGACCGATGACGTCGCGGTGACGCGACCAAGCGCGCTTCTCGCCAGGCG 60
Db 232 AAGAAGACCGATGACGTCGCGGTGACGCGACCAAGCGCGCTTCTCGCCAGGCG 291
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Qy 241 GAGCTCATCGCGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGCGATGGCTCTCAAGGAGG 300
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Qy 361 ATCTCGGCGTACTTCGCCACCGCATGCGAGCGGTGCGCGCGGTGCGCAACCGCGATGGCTCTCAAGGATGTC 420
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LOCUS AX073911 1623 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 3 from Patent WO0104344.
ACCESSION AX073911
VERSION AX073911.1 GI:12710171
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE Siegel, M., Chu, N.R. and Mizzen, L.A.
AUTHORS Induction of a th1-like response in vitro
TITLE Patent: WO 0104344-A 3 18-JAN-2001;
JOURNAL Stressgen Biotechnologies Corporation (CA)
FEATURES Location/Qualifiers
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Query Match 69.9%; Score 293.6; DB 6; Length 1623;
Best Local Similarity 81.2%; Pred. No. 3e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGNAGCGGACGAGCTCCCGGTGACGTCAGCACCGCGACCGTTCCTGCCCGCAGGG 60
DB 232 AAGNAGACCGATGACGTCCCGGTGACGTCAGCGCCACCGACCGCGCCAGGCG 291
QY 61 CTCGTACGCGAGGGCTCGCAACGCTCGCGCGCGTGCACCCCGATGCTCTCAAGCGC 120
DB 292 TTGGTTCGCGAGGGCTCGCAACGCTCGCGCGCGCGCCACCGCTCGGTCTCAACGC 351
QY 121 GGCATCGAGAAGCGCTCGAGCCGCTCTCCGCGCGCTCTCGAGCAGCGCGAAGGATGTC 180
DB 352 GGCATCGAAAAGCGCTCGAGAAGGTCCACGAGACCTGCTCAAGGGCGCCAGGAGTTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 412 GAGACCAAGGAGCAGATTCGCGCCACCGCAGCGATTCGCGCGGTGACACGATCCGCT 471
QY 241 GAGCTCATCGCGAGCGCATGCGCAAGCTCGCGAAGGAGGCGTATCATCCGTCGAGGAG 531
DB 472 GACCTGATCGCGAGCGCATGCGCAAGGTGGCGCAACGAGGGGCTATCATCCGTCGAGGAG 300
QY 301 TCCACAGACTTCGGTCTCGAGCTCGAGCTCACCGAGGCTATGCGCTTCGACAAAGGGCTAC 360
DB 532 TCCACACTTTGGCTCGAGCTCGAGCTCACCGAGGCTATGCGGTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGGCTCGCTCGACGACCCGCTAC 420
DB 592 ATCTCGGGGTACTTCGTGACCGACCGCGAGGCTCAGGAGGGGCTCTCGAGGAGCCCTTAC 651
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LOCUS AR266846 1920 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 16 from patent US 6495347.
ACCESSION AR266846
VERSION AR266846.1 GI:29696212
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 1920)
Siegel, M., Chu, N.R. and Mizzen, L.A.
Induction of a th1-like response in vitro
Patent: US 6495347-A 16 17-DEC-2002;
Stressgen Biotechnologies Corporation; Victoria;
CAX;
FEATURES Location/Qualifiers
source 1. .1920
/organism="unknown"
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ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 1920;
Best Local Similarity 81.2%; Pred. No. 2.8e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGNAGCGGACGAGCTCCCGGTGACGTCAGCACCGCGACCGTTCCTGCCCGCAGGG 60
DB 232 AAGNAGACCGATGACGTCCCGGTGACGTCAGCGCCACCGACCGCGCCAGGCG 291
QY 61 CTCGTACGCGAGGGCTCGCAACGCTCGCGCGCGTGCACCCCGATGCTCTCAAGCGC 120
DB 292 TTGGTTCGCGAGGGCTCGCAACGCTCGCGCGCGCGCCACCGCTCGGTCTCAACGC 351
QY 121 GGCATCGAGAAGCGCTCGAGCCGCTCTCCGCGCGCTCTCGAGCAGCGCGAAGGATGTC 180
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QY 241 GAGCTCATCGCGAGCGCATGCGCAAGCTCGCGAAGGAGGCGTATCATCCGTCGAGGAG 531
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QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGGCTCGCTCGACGACCCGCTAC 420
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RESULT 52
AX073924
LOCUS AX073924 1920 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 16 from Patent WO0104344.
ACCESSION AX073924
VERSION AX073924.1 GI:12710184
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
Siegel, M., Chu, N.R. and Mizzen, L.A.
Induction of a th1-like response in vitro
Patent: WO 0104344-A 16 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
FEATURES Location/Qualifiers
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 AEAMDVGNSGVITVRESNTFGLOLETEGMRFDKGYISGIFVTDPERQAVLEDPYI
 LTVSSKVTVDLPLLEKVGAGKPLLIIEADVEGEALSTLVNKRIRGTFFKSVAKA
 PGFGRKAMLOQMLITGGQVISEEVLITLENADISLLGKARKVVTVDKETTIVEGA
 GDTDAVAGVAQROETENSDDYDREKLOERLAKLAGGAVIKAGAAVELEKERRKH
 RIEDAVNRKAAVEEGIVAGGVTLQAPLDELKLEGEATGANIKVVALEAPLKO
 IAFNSGLEPGVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKTRSLQNAASIA
 GLFLTTEAVVADPEKEKASVPGGDMGDMFDHMGDPTLHMYMLDLPETTDLYCY
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 MGTGLIVCPICQKP"

ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 1920;
 Best Local Similarity 81.2%; Pred. No. 2.8e-22;
 Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGCGGCTTCGCGCCAGGCG 60
 DB 232 AAGAAGACGACGTCGCGGTGACGGTACGACACCGCGGCTTCGCGCCAGGCG 291
 QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGCGC 120
 DB 292 TTGGTTCGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGCGC 351
 QY 121 GGCATCAGAGAGCGCGTCGAGGCGGCTTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGCGC 180
 DB 352 GGCATCAGAGAGCGCGTCGAGGAGGTCACCGGAGGCGTTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGGAGGTC 411
 QY 181 GAGACCAAGGAGGACGATCGCTTCGCGCGGCTTCGCGCGGCGGACACCGGATCGGC 240
 DB 412 GAGACCAAGGAGGATGTCGCGGCGGTCGCGGCGGCGGATTCGCGCGGTCGCGGATCGGT 471
 QY 241 GAGCTCATCGCGAGGCGATGACCAAGGTCGCGGCGGTCGCGGCGGTCGCGGATCGGT 300
 DB 472 GACCTGATCGCGAGGCGATGACCAAGGTCGCGGCGGTCGCGGCGGTCGCGGATCGGT 531
 QY 301 TCCGAGACCTTCGCTCGAGCTGAGCTACCGAGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 360
 DB 532 TCCAAACACCTTTGGGCTGCGAGCTGAGCTACCGAGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 591
 QY 361 ATCTCGGCGTACTTCGCGCGGTCGCGGATGAGGCGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 420
 DB 592 ATCTCGGCGTACTTCGCGCGGTCGCGGATGAGGCGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 651

RESULT 53

AR266853
 LOCUS Sequence 28 from patent US 6495347. linear PAT 10-APR-2003
 DEFINITION
 ACCESSION AR266853
 VERSION AR266853.1 GI:29696219
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1947)
 AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
 TITLE Induction of a th1-like response in vitro
 JOURNAL Patent: US 6495347-A 28 17-DEC-2002;
 Stressgen Biotechnologies Corporation; Victoria;
 CAN;

FEATURES

source
 1. .1947
 /location="Qualifiers
 /mol_type="genomic DNA"

ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 1947;
 Best Local Similarity 81.2%; Pred. No. 2.8e-22;
 Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGCGGCTTCGCGCCAGGCG 60
 DB 556 AAGAAGACGACGTCGCGGTGACGGTACGACACCGCGGCTTCGCGCCAGGCG 615
 QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGCGC 120
 DB 616 TTGGTTCGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGCGC 675
 QY 121 GGCATCAGAGAGCGCGTCGAGGCGGCTTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGCGC 180
 DB 676 GGCATCAGAGAGCGCGTCGAGGAGGTCACCGGAGGCGTTCGCGCGCGGTGCGCAACCGGATGCGTCTCAAGGAGGTC 735
 QY 181 GAGACCAAGGAGGACGATCGCTTCGCGCGGCTTCGCGCGGCGGACACCGGATCGGC 240
 DB 736 GAGACCAAGGAGGATGTCGCGGCGGTCGCGGCGGCGGATTCGCGCGGTCGCGGATCGGT 795
 QY 241 GAGCTCATCGCGAGGCGATGACCAAGGTCGCGGCGGTCGCGGCGGTCGCGGATCGGT 300
 DB 796 GACCTGATCGCGAGGCGATGACCAAGGTCGCGGCGGTCGCGGCGGTCGCGGATCGGT 855
 QY 301 TCCGAGACCTTCGCTCGAGCTGAGCTACCGAGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 360
 DB 856 TCCAAACACCTTTGGGCTGCGAGCTGAGCTACCGAGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 915
 QY 361 ATCTCGGCGTACTTCGCGCGGTCGCGGATGAGGCGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 420
 DB 916 ATCTCGGCGTACTTCGCGCGGTCGCGGATGAGGCGGTCGCGGTCGCGGATCGGTTCGCAAGGCGTAC 975

RESULT 54

AR2673936
 LOCUS Sequence 28 from Patent WO0104344. linear PAT 06-FEB-2001
 DEFINITION
 ACCESSION AR2673936
 VERSION AR2673936.1 GI:12710196
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
 TITLE Induction of a th1-like response in vitro
 JOURNAL Patent: WO 0104344-A 28 18-JAN-2001;
 Stressgen Biotechnologies Corporation (CA)
 FEATURES
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 1. .1947
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="fusion sequence"
 1. .1947
 /note="unnamed protein product"
 /codon_start=1
 /transl_table=11
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 /db_xref="GI:12710197"
 /translation="MDGDTFLHEYMLDLPETTDLYCYEQLNDSSEEDIEDGPAQ
 GEPDRAHYNIVTFCCKCDSTLRCLVQSTHVDIETLEDLMTGLIVCPICQKP
 GGGSHMAKTIAYDEARRGLERGLNALADAVKVTGLGPKNRNVLEKKGAPITINDG
 VSIKIEIELEDPEYKIGAEVLKEVAKKTDVAGDGTATVLAQALVREGLRNVAAGA
 NPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIATAISALDSIGDILAEAMDVKG
 NEGIVTESNTFGLOLETEGMRFDKGYISGIFVTDPERQAVLEDPYIILVSSKVS
 TVKDLPLLEKVGAGKPLLIIEADVEGEALSTLVNKRIRGTFFKSVAKVAGGDRRK
 AMQMDLITGGQVISEEVLITLENADISLLGKARKVVTVDKETTIVEGAGTDAIAG
 RVAQIROETENSDDYDREKLOERLAKLAGGAVIKAGAAVELEKERRKHRIEDAVRN
 AKAAVEEGIVAGGVTLQAPLDELKLEGEATGANIKVVALEAPLKOIAFNSGLE
 PGVAAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKTRSLQNAASIALGLFLTEA
 VVADKEPEKEKASVPGGDMGDMFDHMGDPTLHMYMLDLPETTDLYCYEQLNDSSEEDIEDGPAQ
 GEPDRAHYNIVTFCCKCDSTLRCLVQSTHVDIETLEDLMTGLIVCPICQKP"

CDS

Query Match 69.9%; Score 293.6; DB 6; Length 1947;
 Best Local Similarity 81.2%; Pred. No. 2.8e-22;
 Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGCTGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCCGAGGCG 60
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Db 556 AAGAAGACCGATGACGCTGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCCGAGGCG 615
|||||
QY 61 CTGCTACGCGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
|||||
Db 616 TTGGTTGCGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 675
|||||
QY 121 GGCATCGAAGGCGCTGCGAGGCGCTCTCGCGCGCGCTGCTGAGCAGGCGAAGGATGTC 180
|||||
Db 676 GGCATCGAAGGCGCTGCGAGGCGCTCACCGAGAGCTGCTCAAGGCGCGCAAGGAGTTC 735
|||||
QY 181 GAGACCAAGGAGCAGATGCTTCCAGCGCTTCCATCTCGCGCGCGCACCAACCGATCGGC 240
|||||
Db 736 GAGACCAAGGAGCAGATGCGCGCACCGCAGCGATTTGCGCGCGGTGACCGATCCATCGT 795
|||||
QY 241 GAGCTATCGCCAGGCGATGGACAGGTGCGCAAGGAGCGTATCAACCGTCGAGGAG 300
|||||
Db 796 GACCTATCGCCAGGCGATGGACAGGTGCGCAAGGAGCGTATCAACCGTCGAGGAG 855
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QY 301 TCCACAGCTTCGCTGCGAGCTGGAGCTCACCGAGGCTATGCGTTCCGACAGGCGCTAC 360
|||||
Db 856 TCCACAGCTTCGCTGCGAGCTGGAGCTCACCGAGGCTATGCGTTCCGACAGGCGCTAC 915
|||||
QY 361 ATCTCGCGTACTTCGCGCGACCGACATGCGAGCGGATGCGGCTCGACGACCGCGTAC 420
|||||
Db 916 ATCTCGCGTACTTCGCGCGACCGACCGAGCGGTGCGAGGCGGCTCGCTCGAGGACCGCTAC 975
|||||

RESULT 55
MSGBCG 2431 bp DNA linear BCT 26-APR-1993
LOCUS M.bovis BCG gene encoding antigen A (MbaA), complete cds.
DEFINITION M17705
ACCESSION M17705
VERSION M17705.1 GI:149933
KEYWORDS antigen.
SOURCE Mycobacterium bovis
ORGANISM Mycobacterium bovis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE 1 (bases 1 to 2431)
Thole, J.E., Keulen, W.J., De Bruyn, J., Kolk, A.H., Groothuis, D.G.,
Berwald, L.G., Tiesjema, R.H. and van Embden, J.D.
Characterization, sequence determination, and immunogenicity of a
64-kilodalton protein of Mycobacterium bovis BCG expressed in
Escherichia coli K-12
Infect. Immun. 55 (6), 1466-1475 (1987)
3553003
Original source text: M.bovis (strain BCG P3) DNA, clones
PRIB10[2-3].

FEATURES
source
1..2431
/organism="Mycobacterium bovis"
/mol_type="genomic DNA"
/db_xref="taxon:1765"
576..2198
/note="antigen A"
/codon_start=1
/transl_table=11
/protein_id="AAA25358.1"
/db_xref="GI:149934"

CDS
translation="NAKTIAYDEARRGLERGLNALADAVKVTLPKGRNVLEKKWG
APTINDGVSIAKEIELEDPYKIGALVEKVAKTDDVAGDGTITATVLAQALVREG
LRNAAAGNPLGKRGIEKAEKVTETLLKGAKEVETKEQIAATAAISAGDSIGDLI
AEAMDKNVGVITVEESNTFGLQLETEGMRPKGYISGVPVDPERQEAFLVEDPYI
LIVSKSVTLPLLEKVIAGKPLLI IAEDEVGEALSTLVNKNKRGTFKSVAKA
PGFDRRAMLDQMAILTGGOVI SEEVGLTLENADLSLIGKARKVWVTKDETTIVEGA
GPTDAIAGRAIQROEINSDSDYDREKLOERLAKAGGAVIKAGATVELEKREH
RIEDAVRNKAAVEGIVAGGVTLQAAPTLDLKLGDDEATGANIVKVALEAPLKQ
IAFNSGLPVGVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTSLRSLQNAASIA
GLFLTFEAVADKPEKESVPGGDMGMDP"

ORIGIN 2 bp upstream of MluI site.

Query Match 69.9%; Score 293.6; DB 1; Length 2431;
Best Local Similarity 81.2%; Pred. No. 2.6e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGCTGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCCGAGGCG 60
807 AAGAAGACCGATGACGCTGCGCGGTGACGGTACGACCAACCGCGCGCTGCTCGCCCGAGGCG 866
61 CTGCTACGCGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
867 TTGGTTGCGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGCTCGGTCTCTCAAGCGC 926
121 GCATCTGAGAGGCGCTGAGGCGCGCTCTCGCGCGCGCTGCTGAGCAGGCGAAGGATGTC 180
927 GGCATCGAAGGCGCTGAGGAGGTCACCGAGACCTCTGCTCAAGGCGCGCAAGGAGGTC 986
181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCTCGCGCGCGCACCAACCGATCGGC 240
987 GAGACCAAGGAGCAGATTCGCGCGCACCGCAGCGATTCGCGCGGTGACCGATCCATCGGT 1046
241 GAGCTATCTCGCGAGCGGATGGAAGAAGTGGCGCAAGAGGCGTCAATCAACGTCGAGGAG 300
1047 GACCTGATCGCGAGGCGGATGGAAGAAGTGGCGCAACGAGGCGGTCAATCAACCGTCGAGGAG 1106
301 TCCACAGCTTCGCTGCGAGCTGGAGCTCACCGAGGCTATGCGTTCCGACAGGCGCTAC 360
1107 TCCACAGCTTCGCTGCGAGCTGGAGCTCACCGAGGCTATGCGTTCCGACAGGCGCTAC 1166
361 ATCTCGCGTACTTCGCGCGACCGACATGCGAGCGGATGGAGGCGTCTGCTCGACGACCGCTAC 420
1167 ATCTCGCGTACTTCGCGCGACCGACCGAGCGTCAAGGCGGTCTCTCGAGGACCGCTAC 1226

RESULT 56
CQ860158 2585 bp DNA linear PAT 10-SBP-2004
LOCUS Sequence 1 from Patent WO2004071387.
DEFINITION CQ860158
ACCESSION CQ860158
VERSION CQ860158.1 GI:51982035
KEYWORDS

SOURCE Arthrobacter sp.
ORGANISM Arthrobacter sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococciaceae; Micrococcaceae; Arthrobacter.

REFERENCE 1
Griffiths, S.G., Ritchie, R.J. and Simard, N.C.
Hsp60 from arthrobacter
Patent: WO 2004071387-A 1 26-AUG-2004;
Novartis AG (CH); Novartis Pharma GmbH (AT)

FEATURES
source
1..2585
/organism="Arthrobacter sp."
/mol_type="unassigned DNA"
/db_xref="taxon:1667"

ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 2585;
Best Local Similarity 81.2%; Pred. No. 2.6e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGCTGCGCGGTGACGGTACGACCAACCGCGACCGTTCTCGCCCGAGGCG 60
1184 AAGAAGACGACGAGTGGCGCGGACCGTACCGACCGCTTACCGTTTGGCCCGAGGCG 1243
61 CTGCTACGCGAGGCGCTCGCAACCGTCCCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
1244 CTGGTTCCGAGAGCGCTCGCAACCGTCCGACGCGCGGTGATCCGCTGAGCTCAAGCGC 1303
121 GGCATCGAAGGCGCGTCTGAGCGCGCTCTCGCGCGCGCTGCTGAGAGCAGCGGAGGATGTC 180
1304 GGCATCGAAGGCGTCTCGCGCGGTGACCGAGGAGCTGCTGGCTTCCGCGCAAGGAGTTC 1363

QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCCCTCCATCTCCCGCGCGACACCCAGATCGGC 240
Db 1364 GAGACCAAGGAGATCGCGGCCATCTGCTTCCATCTCGCGCGCGACACCCAGATCGGC 1423
QY 241 GAGCTCATCCCGAGGCGATGAGCAAGGTTCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 300
Db 1424 GCGTTGATCCCGAGGCGATGAGCAAGGTTCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 1483
QY 301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGATCGCTTCGCAAGGAGGCTAC 360
Db 1484 TCCAAACACCTTCGCTTCGAGCTGGAGCTCACCGAGGAGGATGATCGCTTCGCAAGGAGGCTAC 1543
QY 361 ATCTCGGCTACTTCGCGCCAGCATGAGGAGGATGAGGAGGCTTCGCTCGAGGAGGCTAC 420
Db 1544 ATCTCGGCTACTTCGCTCACCGAGGCGGAGGAGGAGGCTTCGCTCGAGGAGGCTAC 1603

RESULT 57
AR266848
LOCUS AR266848 2847 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 20 from patent US 6495347.
ACCESSION AR266848
VERSION AR266848.1 GI:29696214
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2847)
AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: US 6495347-A 20 17-DEC-2002;
Stressgen Biotechnologies Corporation; Victoria;
CA;

FEATURES
source
1. .2847
/location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 69.9%; Score 293.6; DB 6; Length 2847;
Best Local Similarity 81.2%; Pred. No. 2.5e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGAACGAGCAGCAGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCGAGGCG 60
Db 292 AAGAACGAGCAGCAGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCGAGGCG 351
QY 61 CTGTTACGCGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
Db 352 TTGGTTCCGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 411
QY 121 GGATTCGAGAGGCGCTCGAGGCGCTTCCCGCGCCCTTCGCGCGCGGACGCGGATGTC 180
Db 412 GGCATCGAAAGGCGCTCGAGAGGTCACCGAGACCGCTCTCAAGGCGCGCAAGGAGTC 471
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTTCATCTCCCGCGCGACACCCAGATCGGC 240
Db 472 GAGACCAAGGAGCAGATTCGCGGCCACCGAGCGGATTCGCGCGGTGACCAAGTCCATCGGT 531
QY 241 GAGCTCATCCCGAGGCGATGAGCAAGGTTCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 300
Db 532 GACCTGATCCCGAGGCGATGAGCAAGGTTCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 591
QY 301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGATCGCTTCGCAAGGAGGCTAC 360
Db 592 TCCAAACACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGATCGCTTCGCAAGGAGGCTAC 651
QY 361 ATCTCGGCTACTTCGCGCCAGCATGAGGAGGATGAGGAGGCTTCGCTCGAGGAGGCTAC 420
Db 652 ATCTCGGCTACTTCGCTCACCGAGGCGGAGGAGGAGGCTTCGCTCGAGGAGGCTAC 711

RESULT 58

AX073928
LOCUS AX073928 2847 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 20 from Patent WO0104344.
ACCESSION AX073928
VERSION AX073928.1 GI:12710188
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.
TITLE Induction of a Th1-like response in vitro
JOURNAL Patent: WO 0104344-A 20 18-JAN-2001;
Stressgen Biotechnologies Corporation (CA)
FEATURES
source
1. .2847
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="fusion sequence"
1. .2847
/notes="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="Cac28424.1"
/db_xref="GI:12710189"

CDS

translation="MGSSHHHHHSSGLVPRGSHMAKTYAYDEARRGLERGLNALAD
AVKVTLPGRNVLKRWGAPTTINDGVSIAKRIELEDPEYKIGABLKVKEVAKTDD
VAGDGTATVLAQVLRGLNVAAGNPGLKRGIEKAEKVTETLLKGAKEVETK
EOLATAAISAGDSIGDLIAEMDKVNEGVTVEESNTFGLQLELTGMRFDKGYI
SGYFTDPERQEAILEDVYLLAVSSKVTVDLLPLEKIVIGAKPLLLIAEDVEGEA
LSTLVNKRIGTFKSAVAKAPGFRKRLQDMALITGQVISEVGLTLENADLSL
LGKARKVVTDETTIVEGADTDAIGRAVAQIRQIENSDDSDREKLOERLAKLAG
GVAVIKAGAEATELKERHRIEDAVRNAKAAVEGIVAGGVVTLQNAATLDLEKLE
GDEATGANIVKVALEAPLQIAFNSGLEPVAEKVRNLPAGHGLNAQTGVTEDLLAA
GVADPVKTRSLQNAASITAGLPLTTEAVADPEKEKASVPGGDMGMDFASMGSI
GAASMEFCDFVEKELKVHANENIFVCPAIIISALAMVYLGAQDSTRTOINKVVRPDK
LPGFGDSIEAQCGTISVNHSSLRDLNQITKENDVYSFSLASRLYAEERYPIPLVEYLQ
CVKELYRGLEDFINFQADQARELINSWESQTINGIIRNVLPSSVSDSQTAMVLVA
IVFGKLEMTFKEDTQAMPFRVTEQSPQVMYQIGLFRVASWASERKMLLELPPA
SGTMSMLVLLPDEVSLEQLESIINPEKLTQMTSSNMVEERKI KVLPRMQWEEKYNL
TSVLAMAGITDVFSSSANTLSSIAESLKI SQAVHAHAHAEINEAGREVVSABAGVDA
ASVSEFRADHPFLFCIKHIAITNAVILFFRCVGS"

ORIGIN

Query Match 69.9%; Score 293.6; DB 6; Length 2847;
Best Local Similarity 81.2%; Pred. No. 2.5e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1 AAGAACGAGCAGCAGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCGAGGCG 60
Db 292 AAGAACGAGCAGCAGCTCGCGGTGACGTTACGACACCGGACCGCTTCTCGCCCGAGGCG 351
QY 61 CTGTTACGCGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
Db 352 TTGGTTCCGAGGCGCTCGCGCAACGTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 411
QY 121 GGATTCGAGAGGCGCTCGAGGCGCTTCCCGCGCCCTTCGCGCGCGGACGCGGATGTC 180
Db 412 GGCATCGAAAGGCGCTCGAGAGGTCACCGAGACCGCTCTCAAGGCGCGCAAGGAGTC 471
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTTCATCTCCCGCGCGACACCCAGATCGGC 240
Db 472 GAGACCAAGGAGCAGATTCGCGGCCACCGAGCGGATTCGCGCGGTGACCAAGTCCATCGGT 531
QY 241 GAGCTCATCCCGAGGCGATGAGCAAGGTTCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 300
Db 532 GACCTGATCCCGAGGCGATGAGCAAGGTTCGCAAGGAGGAGGCTCATCACCGTCGAGGAG 591
QY 301 TCCAGACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGATCGCTTCGCAAGGAGGCTAC 360
Db 592 TCCAAACACCTTCGCTTCGAGCTGGAGCTCACCGAGGATGATCGCTTCGCAAGGAGGCTAC 651

Qy 361 ATCTCGCGTACTTGGCCACCGCATGAGCGGATGAGCGTGGCTCGACGACCCGTAC 420
|||||
Db 652 ATCTCGGGGTACTTGGTACCGACCGCCCGGAGCGTCAAGGAGCGGTCTCGGAGGACCCCTAC 711
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RESULT 59
MSGTCWPA 4380 bp DNA linear BCT 14-FEB-1996
LOCUS M.tuberculosis 65 kDa antigen (cell wall protein a) gene.
DEFINITION M15467
ACCESSION M15467.1 GI:149999
VERSION antigen; cell wall protein.
KEYWORDS Mycobacterium tuberculosis
SOURCE Mycobacterium tuberculosis
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
1 (bases 1 to 4380)
Shinnick, T.M.
AUTHORS The 65-kilodalton antigen of Mycobacterium tuberculosis
TITLE J. Bacteriol. 169 (3), 1080-1088 (1987)
JOURNAL 3029018
PUBMED
COMMENT Original source text: Mycobacterium tuberculosis (strain Erdman)
DNA.
Draft entry and clean copy of sequence in [1] were kindly provided
by T.M.Shinnick, 04-MAY-1987.
Location/Qualifiers
1. .4380
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/strain="Erdman"
/db_xref="taxon:1773"
complement(242..769)
/note="ORF F175; putative"
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/protein_id="AAA88231.1"
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RAPISYSGSSSISLAMDTPSLVIGAPHFPSRTLRPLPGNVITFASARAPKPSRP
REASSVAIVAIK"
252..1874
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/protein_id="AAA88232.1"
/db_xref="GI:150000"
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LVVSKVSTKDLLPPEKVIKAGKPLLIADDEVEALSTLVNKKIRGTGPKSAVKA
PFGDRKAMQLMDAILTGQVYSEEVGLTIADENADLSLIGKARKVVTVDKETTIVEGA
GDTDAVRKAQIOIEKNSDSDYDREKLQERLAKLAGVAVIKAGAAATEVELEKPKH
RIEDAVRNAKAAVEGIVAGGVVTLQAAPTLDLKLKSGDEATGANIVKVALEAPLQK
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complement(1194..1670)
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/translation="WASRQVAHLGHARLQFVGEDLLQRLQRLHLDVAGRLVAF
ELQLVQGRQLQORHTPGDDALLDGLGIANRILDVALLLEDFLGGTGLDHRDTT
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LOCUS
DEFINITION Sequence 5 from Patent WO 8805823.
ACCESSION I08847
VERSION I08847.1 GI:588446
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4380)
Hudson, R.N., Young, Richard A. and Shinnick, T.M.
TITLE MYCOBACTERIUM TUBERCULOSIS GENES ENCODING PROTEIN ANTIGENS
JOURNAL Patent: WO 8805823-A 5 11-AUG-1988;
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Best Local Similarity 81.2%; Pred. No. 2.2e-22;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
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Qy 361 ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGCGGTCTCGACGACCCGTAC 420
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Search completed: April 1, 2006, 23:37:24
Job time : 2961.29 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 21:55:10 ; Search time 853.578 Seconds
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3279.340 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4966997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

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- 1: Geneseq1980s.*
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- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
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- 11: Geneseq2003ds.*
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- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	412	98.1	420	14	ADV99178
4	396	94.3	420	14	ADV99167
5	396	94.3	420	14	ADV99168
6	394.4	93.9	420	14	ADV99123
7	394.4	93.9	420	14	ADV99131
8	394.4	93.9	420	14	ADV99140
9	394.4	93.9	420	14	ADV99129
10	392.8	93.5	420	14	ADV99143
11	392.8	93.5	420	14	ADV99135
12	392.8	93.5	420	14	ADV99175
13	391.2	93.1	420	14	ADV99136
14	391.2	93.1	420	14	ADV99126
15	391.2	93.1	420	14	ADV99142
16	388	92.4	420	14	ADV99156
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18	388	92.4	420	14	ADV99144
19	386.4	92.0	420	14	ADV99158

20	386.4	92.0	420	14	ADV99166	ADV99166 groEL2 ge
21	386.4	92.0	420	14	ADV99154	ADV99154 groEL2 ge
22	386.4	92.0	420	14	ADV99169	ADV99169 groEL2 ge
23	386.4	92.0	420	14	ADV99152	ADV99152 groEL2 ge
24	386.4	92.0	420	14	ADV99177	ADV99177 groEL2 ge
25	386.4	92.0	420	14	ADV99137	ADV99137 groEL2 ge
26	386.4	92.0	420	14	ADV99160	ADV99160 groEL2 ge
27	386.4	92.0	422	14	ADV99138	ADV99138 groEL2 ge
28	384.8	91.6	420	14	ADV99151	ADV99151 groEL2 ge
29	384.8	91.6	420	14	ADV99155	ADV99155 groEL2 ge
30	384.8	91.6	420	14	ADV99128	ADV99128 groEL2 ge
31	383.2	91.2	420	14	ADV99139	ADV99139 groEL2 ge
32	383.2	91.2	420	14	ADV99157	ADV99157 groEL2 ge
33	383.2	91.2	420	14	ADV99133	ADV99133 groEL2 ge
34	383.2	91.2	420	14	ADV99146	ADV99146 groEL2 ge
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51	370.2	88.1	423	14	ADV99127	ADV99127 groEL2 ge
52	368.6	87.8	423	14	ADV99150	ADV99150 groEL2 ge
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54	362.4	86.3	420	14	ADV99153	ADV99153 groEL2 ge
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ALIGNMENTS

RESULT 1
ID ADV99163 standard; DNA; 420 BP.
XX AC ADV99163;
XX XX

DT 24-MAR-2005 (first entry)
XX groEL2 gene fragment, SEQ ID 43.
XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX Streptomyces scabiei.
OS US2004265873-A1.
PN 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
PI

```
XX DR WPI; 2005-089568/10.
XX PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PT species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 4; SEQ ID NO 43; 34pp; English.
XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 82 A; 141 C; 139 G; 58 T; 0 U; 0 Other;

Query Match 100.0%; Score 420; DB 14; Length 420;
Best Local Similarity 100.0%; Pred. No. 7.8e-61;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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ID ADV99165 standard; DNA; 420 BP.
XX AC ADV99165;
XX AC ADV99165;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 45.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces scabiei.
XX PN US2004265873-A1.
XX XX
XX PD 30-DEC-2004.
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XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PT species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 4; SEQ ID NO 45; 34pp; English.
XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 82 A; 141 C; 139 G; 58 T; 0 U; 0 Other;

Query Match 100.0%; Score 420; DB 14; Length 420;
Best Local Similarity 100.0%; Pred. No. 7.8e-61;
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGGACCGGTCGCGCCAGGGC 60
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DB 241 GAGCTCATCGCGAGGCGATGGACAGGTGCGCAAGGCGCTCATCCCGCTCGAGGAG 300
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DB 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTCGACAGGGCTAC 360
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DB 361 ATCTCGGCGTACTTCGCGCACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCGGTAC 420

RESULT 3
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XX AC ADV99178;
XX AC ADV99178;
XX DT 24-MAR-2005 (first entry)
XX XX
XX DE groEL2 gene fragment, SEQ ID 58.
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Db 61 CTCGTACGCGAGGCGCTTGCACACGTCGCCCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAGGCGCTTGCAGGCGCTTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCGAGAGGCGCTTGCAGGCGCTTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTTCACGGCTTCCATCTTCGCGCGCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTTCACGGCTTCCATCTTCGCGCGCCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGACAAGGTTCGCAAGGCGTTCATCAACCGTCGAGGAG 300
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Qy 301 TCCGAGACCTTCGCTTGGAGCTGGAGCTCACCGAGGATGGCTTTCGACAAAGGCTTAC 360
Db 301 TCCGAGACCTTCGCTTGGAGCTGGAGCTCACCGAGGATGGCTTTCGACAAAGGCTTAC 360
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Db 361 ATCTCGCGGTACTTCCGACCGACATGGAGCGGATGGAGCGCTCGCTTCGACGACCCGTTAC 420

RESULT 7

ADV99131
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AC ADV99131;
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DE groEL2 gene fragment, SEQ ID 11.
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KW potato scab; gene; db.
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OS Streptomyces ambofaciens.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
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PR 18-APR-2003; 2003KR-00024656.
XX
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX
WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.

XX Claim 3; SEQ ID NO 11; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX

SQ Sequence 420 BP; 84 A; 144 C; 137 G; 55 T; 0 U; 0 Other;
Query Match 93.9%; Score 394.4; DB 14; Length 420;
Best Local Similarity 96.2%; Pred. No. 1.3e-56;
Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCAGCGTCGCCGTTGACCGGTACGACCAACCGGACCGTTCTCGCCCGAGGCC 60
Db 1 AAGAAGACGAGCAGCGTCGCCGTTGACCGGTACGACCAACCGGACCGTTCTCGCCCGAGGCC 60
Qy 61 CTCGTACGCGAGGCGCTTGCACACGTCGCCCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTCGTACGCGAGGCGCTTGCACACGTCGCCCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAGGCGCTTGCAGGCGCTTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCGAGAGGCGCTTGCAGGCGCTTCTCGGCGCCCTGCTGAGCAGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTTCACGGCTTCCATCTTCGCGCGCCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTTCACGGCTTCCATCTTCGCGCGCCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGACAAGGTTCGCAAGGCGTTCATCAACCGTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGACAAGGTTCGCAAGGCGTTCATCAACCGTCGAGGAG 300
Qy 301 TCCGAGACCTTCGCTTGGAGCTGGAGCTCACCGAGGATGGCTTTCGACAAAGGCTTAC 360
Db 301 TCCGAGACCTTCGCTTGGAGCTGGAGCTCACCGAGGATGGCTTTCGACAAAGGCTTAC 360
Qy 361 ATCTCGCGGTACTTCCGACCGACATGGAGCGGATGGAGCGCTCGCTTCGACGACCCGTTAC 420
Db 361 ATCTCGCGGTACTTCCGACCGACATGGAGCGGATGGAGCGCTCGCTTCGACGACCCGTTAC 420

RESULT 8

ADV99140
ID ADV99140 standard; DNA; 420 BP.
XX
AC ADV99140;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 20.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; db.
XX
OS Streptomyces chartreusis.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
XX
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX
WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.

XX Claim 3; SEQ ID NO 20; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and

CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 82 A; 144 C; 136 G; 58 T; 0 U; 0 Other;

Query Match 93.9%; Score 394.4; DB 14; Length 420;
Best Local Similarity 96.2%; Pred. No. 1.3e-56;
Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGACGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 60
DB 1 AAGAAGACGAGACGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 60

QY 61 CTCTGACGCGAGGCGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 120
DB 61 CTCTGACGCGAGGCGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 120

QY 121 GGCAATCGAAGAGGCGCTCGAGGCGCTCTCGCGGCGCTCTGAGAGCAGGCGAAGGATGTC 180
DB 121 GGTAATCGAGGCGCTCGAGGCGCTCTCGCGGCGCTCTGAGAGCAGGCGAAGGATGTC 180

QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240

QY 241 GAGCTCATCGCGAGGCGATGGACCAAGGTGCGGAGAGGAGGCGTATCATCGATCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGGACCAAGGTGCGGAGAGGAGGCGTATCATCGATCGAGGAG 300

QY 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCACCAGGAGTATGCGCTTCGACAGGGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCACCAGGAGTATGCGCTTCGACAGGGGCTAC 360

QY 361 ATCTCGCGCTACTTCGCGCACCGACATCGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420
DB 361 ATCTCGCGCTACTTCGCGCACCGACATCGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420

RESULT 9
ADV99129
ID ADV99129 standard; DNA; 420 BP.
XX
AC ADV99129;
XX
XX
DT 24-MAR-2005 (first entry)
DE groEL2 gene fragment, SEQ ID 9.
XX
XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces alboniger.
XX
XX US2004265873-A1.
XX
XX 30-DEC-2004.
XX
XX 15-APR-2004; 2004US-00824527.
XX
XX 18-APR-2003; 2003KR-00024656.
XX
XX 14-NOV-2003; 2003KR-00080580.
XX
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX
XX

DR WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
XX or purifying natural products using such microorganisms.
XX
XX Claim 3; SEQ ID NO 9; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
XX STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX Potato scab is a pathogenic disease caused by certain Streptomyces
XX species. Primers ADV99121 and ADV99122 are useful in a method for
XX identifying Streptomyces species, comprising amplifying groEL2 gene
XX fragment of target strain, analyzing the nucleotide sequence of groEL2
XX gene fragment amplified, and comparing the nucleotide sequence obtained
XX with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 81 A; 141 C; 140 G; 58 T; 0 U; 0 Other;

Query Match 93.9%; Score 394.4; DB 14; Length 420;
Best Local Similarity 96.2%; Pred. No. 1.3e-56;
Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGACGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 60
DB 1 AAGAAGACGAGACGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 60

QY 61 CTCTGACGCGAGGCGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 120
DB 61 CTCTGACGCGAGGCGCTCGCGGTGACGGTACGACCAACCGGCTCTCTCAAGCGC 120

QY 121 GGCAATCGAAGAGGCGCTCGAGGCGCTCTCGCGGCGCTCTGAGAGCAGGCGAAGGATGTC 180
DB 121 GGTAATCGAGGCGCTCGAGGCGCTCTCGCGGCGCTCTGAGAGCAGGCGAAGGATGTC 180

QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240

QY 241 GAGCTCATCGCGAGGCGATGGACCAAGGTGCGGAGAGGAGGCGTATCATCGATCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGGACCAAGGTGCGGAGAGGAGGCGTATCATCGATCGAGGAG 300

QY 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCACCAGGAGTATGCGCTTCGACAGGGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGAGCTGAGCTCACCAGGAGTATGCGCTTCGACAGGGGCTAC 360

QY 361 ATCTCGCGCTACTTCGCGCACCGACATCGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420
DB 361 ATCTCGCGCTACTTCGCGCACCGACATCGAGCGGATGAGGCGTCTCGACGACCCCGTAC 420

RESULT 10
ADV99143
ID ADV99143 standard; DNA; 420 BP.
XX
XX ADV99143;
XX
XX 24-MAR-2005 (first entry)
XX
XX groEL2 gene fragment, SEQ ID 23.
XX
XX Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
XX Streptomyces cinereoruber.
XX
XX US2004265873-A1.
XX
XX 30-DEC-2004.
XX

QY 181 GAGACCAAGGAGCAGATCGTTCCACGGGCTTCATCTCCGCGCCGACACCCAGATCGGC 240
 DB 181 GAGACCAAGGAGCAGATCGTTCCACGGGCTTCATCTCCGCGCCGACACCCAGATCGGC 240
 QY 241 GAGCTCATCGCCGAGGCGATGACAAAGGTCCGCAAGGAGGCGTCAACCCGTCGAGGAG 300
 DB 241 GAGCTCATCGCCGAGGCGATGACAAAGGTCCGCAAGGAGGCGTCAACCCGTCGAGGAG 300
 QY 301 TCCACAGCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
 DB 301 TCCACAGCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCGTCTCTGACGACCGGTAC 420
 DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCGTCTCTGACGACCGGTAC 420

RESULT 14

ADV99126
 ID ADV99126 standard; DNA; 420 BP.

XX AC ADV99126;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 6.

XX KW Microorganism identification; microorganism detection; groEL2;

XX KW potato scab; gene; ds.

XX OS Streptomyces albireticuli.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX DR WPI; 2005-089568/10.

XX PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.

XX PS Claim 3; SEQ ID NO 6; 34pp; English.

XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.

XX SQ Sequence 420 BP; 81 A; 144 C; 139 G; 56 T; 0 U; 0 Other;

Query Match 93.1%; Score 391.2; DB 14; Length 420;

Best Local Similarity 95.7%; Pred. No. 4.6e-56;

Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCAGCTGCCCGTACCGTACGACACCGGACCGTCTCGCCGAGCG 60

DB 1 AAGAGACGAGCAGCTGCCCGTACCGTACGACACCGGACCGTCTCGCCGAGCG 60

QY 61 CTCTGATCGGAGGCGCTCGCAACGTCGCGCGGTGCAACCCGATGCTCTCAAGCGC 120
 DB 61 CTCTGATCGGAGGCGCTCGCAACGTCGCGCGGTGCAACCCGATGCTCTCAAGCGC 120
 QY 121 GGCATCGAAGAGCGCTCGAGCCGCTTCGCGCGCCCTGCTGGAGCGCGAAGATGTC 180
 DB 121 GGCATCGAAGAGCGCTCGAGCCGCTTCGCGCGCCCTGCTGGAGCGCGAAGATGTC 180
 QY 181 GAGACCAAGGAGCAGATCGTTCCACGGGCTTCATCTCCGCGCCGACACCCAGATCGGC 240
 DB 181 GAGACCAAGGAGCAGATCGTTCCACGGGCTTCATCTCCGCGCCGACACCCAGATCGGC 240
 QY 241 GAGCTCATCGCCGAGGCGATGACAAAGGTCCGCAAGGAGGCGTCAACCCGTCGAGGAG 300
 DB 241 GAGCTCATCGCCGAGGCGATGACAAAGGTCCGCAAGGAGGCGTCAACCCGTCGAGGAG 300
 QY 301 TCCACAGCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
 DB 301 TCCACAGCTTCGGTCTGGAGCTGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCGTCTCTGACGACCGGTAC 420
 DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGCGTCTCTGACGACCGGTAC 420

RESULT 15

ADV99142

ID ADV99142 standard; DNA; 420 BP.

XX AC ADV99142;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 22.

XX KW Microorganism identification; microorganism detection; groEL2;

XX KW potato scab; gene; ds.

XX OS Streptomyces cinnamonensis.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX DR WPI; 2005-089568/10.

XX PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.

XX PS Claim 3; SEQ ID NO 22; 34pp; English.

XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.

XX

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SQ Sequence 420 BP; 80 A; 150 C; 132 G; 58 T; 0 U; 0 Other;
Query Match 93.1%; Score 391.2; DB 14; Length 420;
Best Local Similarity 95.7%; Pred. No. 4.6e-56;
Matches 402; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACCAACCGCCGCTTCGCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGCGGTGACGACCAACCGCCGCTTCGCGCCAGGCG 60
QY 61 CTCGTACGAGGCGCTGCGCAACGTCGCCCGCGTGCACACCGCATGGCTCTCAAGCGC 120
DB 61 CTCGTCCGAGGCGCTGCGCAACGTCGCCCGCGTGCACACCGCATGGCTCTCAAGCGT 120
QY 121 GGCATCGAAGGCGCTGCGAGGCGCTTCGCGCGCGTTCGCGCGCGTTCGCGCGCGTTC 180
DB 121 GGTATCGAAGGCGCTGCGAGGCGCTTCGCGCGCGTTCGCGCGCGTTCGCGCGCGTTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCCGCGCGCGTTCGCGCGCGTTC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCACGCGCTTCATCTCCGCGCGCGTTCGCGCGCGTTC 240
QY 241 GAGCTCATCGCGAGGCGATGGAAGGTGCGCAAGGTGCGCAAGGCGTTCATCACCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGGAAGGTGCGCAAGGTGCGCAAGGCGTTCATCACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTCGAGGCTGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
DB 301 TCCGAGACCTTCGCTCGAGGCTGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCGCCACGACATGAGCGGATGAGGCGTTCGCTCGACGACCGCGTAC 420
DB 361 ATCTCGGCGTACTTCGCGCCACGACATGAGCGGATGAGGCGTTCGCTCGACGACCGCGTAC 420

RESULT 17
ADV99181
ID ADV99181 standard; DNA; 420 BP.
XX AC ADV99181;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 61.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces acidiscabies.
XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX DR

New primer specifically amplifying groEL2 gene fragment of Streptomyces
species, useful in identifying the genus Streptomyces, and for isolating
or purifying natural products using such microorganisms.
Claim 3; SEQ ID NO 36; 34pp; English.
The present invention relates to novel primers STGROF1 (ADV99121) and
STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
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KW potato scab; gene; ds.
XX Streptomyces minutisclerototicus.
OS
XX US2004265873-A1.
PN
XX 30-DEC-2004.
PD
XX
XX 15-APR-2004; 2004US-00824527.
PF
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
PR
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
XX Claim 3; SEQ ID NO 38; 34pp; English.
PS
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
XX Sequence 420 BP; 80 A; 143 C; 141 G; 56 T; 0 U; 0 Other;
SQ
Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGCGTCTCTCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGCGTCTCTCGCCAGGCG 60
QY 61 CTGTATCGGAGGCGCTCGCGCAACGTCGCGCGCGCGTCCAAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGTATCGGAGGCGCTCGCGCAACGTCGCGCGCGCGTCCAAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGCGCGTTCGAGGCGGCTCTCGGCGCGCTCTGTCGAGGCGGAGGATGTC 180
DB 121 GGCATCGAGAAGCGCGTTCGAGGCGGCTCTCGGCGCGCTCTGTCGAGGCGGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCTCGCGAGGCGTTCGAGGCGGCTTCATCAGGAGGCGTTCATCAGGAGGCGTAC 300
DB 241 GAGCTCATCTCGCGAGGCGTTCGAGGCGGCTTCATCAGGAGGCGTTCATCAGGAGGCGTAC 300
QY 301 TCCAGACCTTTCGCTTGGAGCTGAGCTACCGAGGGGTATGCGCTTTCGACAGAGGGGTAC 360
DB 301 TCCAGACCTTTCGCTTGGAGCTGAGCTACCGAGGGGTATGCGCTTTCGACAGAGGGGTAC 360
QY 361 ATCTCGCGGTACTTTCGCGCACCGCATGAGCGGATGAGGCGTCTGCTCGACGACCGCTAC 420
DB 361 ATCTCGCGGTACTTTCGCGCACCGCATGAGCGGATGAGGCGTCTGCTCGACGACCGCTAC 420
RESULT 20
ADV99166

ADV99166 standard; DNA; 420 BP.
XX
AC ADV99166;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 46.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces scabiei.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
XX 15-APR-2004; 2004US-00824527.
XX
XX 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
XX Claim 4; SEQ ID NO 46; 34pp; English.
PS
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
XX Sequence 420 BP; 84 A; 142 C; 135 G; 59 T; 0 U; 0 Other;
SQ
Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGCGTCTCTCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGCGGTGACGTTACGACACCGCGCGTCTCTCGCCAGGCG 60
QY 61 CTGTATCGGAGGCGCTTCGCGCAACGTCGCGCGCGGTCCAAACCGGATGGCTCTCAAGCGC 120
DB 61 CTGTATCGGAGGCGCTTCGCGCAACGTCGCGCGCGGTCCAAACCGGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGCGCGTTCGAGGCGGCTCTCGGCGCGCTCTGTCGAGGCGGAGGATGTC 180
DB 121 GGCATCGAGAAGCGCGTTCGAGGCGGCTCTCGGCGCGCTCTGTCGAGGCGGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCTCGCGAGGCGTTCGAGGCGGCTTCATCAGGAGGCGTTCATCAGGAGGCGTAC 300
DB 241 GAGCTCATCTCGCGAGGCGTTCGAGGCGGCTTCATCAGGAGGCGTTCATCAGGAGGCGTAC 300
QY 301 TCCAGACCTTTCGCTTGGAGCTGAGCTACCGAGGGGTATGCGCTTTCGACAGAGGGGTAC 360
DB 301 TCCAGACCTTTCGCTTGGAGCTGAGCTACCGAGGGGTATGCGCTTTCGACAGAGGGGTAC 360
QY 361 ATCTCGCGGTACTTTCGCGCACCGCATGAGCGGATGAGGCGTCTGCTCGACGACCGCTAC 420
DB 361 ATCTCGCGGTACTTTCGCGCACCGCATGAGCGGATGAGGCGTCTGCTCGACGACCGCTAC 420
RESULT 20
ADV99166

Db 301 TCCACGACCTTCGGTCTGGAGCTGGAACCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
Qy 361 ATCTCGGCGTACTTCGCGCAACGATGAGACCGGATGAGCGGTCGCTCGACGACCCGTTAC 420
Db 361 ATCTCGGCGTACTTCGCGCAACGATGAGACCGGATGAGACCGGTCGCTTCGACGACCCGTTAC 420

RESULT 21
ADV99154
ID ADV99154 standard; DNA; 420 BP.
XX
AC ADV99154;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 34.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces griseolus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 34; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 84 A; 142 C; 135 G; 59 T; 0 U; 0 Other;
Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGACGTCGCCGGTACGATGACACCGGACCGTTCGCCGACGCG 60
Db 1 AAGAAGACGACGACGTCGCCGGTACGATGACACCGGACCGTTCGCCGACGCG 60

Qy 61 CTCGTACCGGAGGCTCGGCAACCTCGCGCGGTCGCAACCCGATGCTCTCAAGCGC 120
Db 61 CTCGTACCGGAGGCTCGGCAACCTCGCGCGGTCGCAACCCGATGCTCTCAAGCGT 120

Qy 121 GGCATCGAAGAGCGCTCGAGGCGCTCTCCGGCGCTCTGTCGAGCAGCGAAGGATGTC 180
Db 121 GGCATCGAAGAGCGCTCGAGGCGCTCTCCGGCGCTCTGTCGAGCAGCGAAGGATGTC 180

Qy 181 GAGACCAAGGACGATCGCTTCCACGGGCTCCATCTCCGCGCGGACACCCAGATCGGC 240

Db 181 GAGACCAAGGACGATCGCTTCGACCGGCTCATCTCCGCGCGGACACCCGAGATCGGC 240
Qy 241 GAGCTCATCGCGGCGGATGACCAAGGTCGCAAGGAGGCGTCAATACCGCTCGAGGAG 300
Db 241 GCCAAGATCGCCGAGCGGATGACCAAGGTCGCAAGGAGGCGTCAATACCGCTCGAGGAG 300

Qy 301 TCCACGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360
Db 301 TCCACGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGATATGCGCTTCGACAAAGGCGTAC 360

Qy 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGCGGTCGCTCGACGACCCGTTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGCGGTCGCTTCGACGACCCGTTAC 420

RESULT 22
ADV99169
ID ADV99169 standard; DNA; 420 BP.
XX
AC ADV99169;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 49.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces scabiei.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 4; SEQ ID NO 49; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 83 A; 137 C; 140 G; 60 T; 0 U; 0 Other;

Query Match 92.0%; Score 386.4; DB 14; Length 420;
Best Local Similarity 95.0%; Pred. No. 2.8e-55;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGACGTCGCCGGTACGATGACACCGGACCGTTCGCCGACGCG 60
Db 1 AAGAAGACGACGACGTCGCCGGTACGATGACACCGGACCGTTCGCCGACGCG 60


```
XX AC ADV99151;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 31.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces fulvissimus.
XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WI WPI; 2005-089568/10.
XX DE New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PT species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 3; SEQ ID NO 31; 34pp; English.
XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 84 A; 146 C; 137 G; 53 T; 0 U; 0 Other;
Query Match 91.6%; Score 384.8; DB 14; Length 420;
Best Local Similarity 94.8%; Pred. No. 5.2e-55;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCAGCTCGCCGGTGACGGTACGACACCGACCGACCGTTCGCCCGAGGCG 60
DB 1 AAGAAGACGAGCAGCTCGCCGGTGACGGTACGACACCGACCGACCGTTCGCCCGAGGCG 60
QY 61 CTCGTACGGCAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
DB 61 CTCGTACGAGGAAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
QY 121 GGCATCGAGAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 180
DB 121 GGCATCGAGAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGACACCGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGACACCGATCGGC 240
QY 241 GAGCTCATCGCAGGCGATGACCAAGTTCGCGCAAGGAGGCTCATCACGTCGAGGAG 300
DB 241 GAGCTCATCGCAGGCGATGACCAAGTTCGCGCAAGGAGGCTCATCACGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 360
DB 301 TCCGAGACCTTCGGTCTGGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAAGGCTAC 360
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QY 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGATGAGGGCGTCTCGACGACCGGTAC 420
DB 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGATGAGGGCGTCTCGACGACCGGTAC 420

RESULT 29
ADV99155
ID ADV99155 standard; DNA; 420 BP.
XX AC ADV99155;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 35.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces griseoviridis.
XX PN US2004265873-A1.
XX PD 30-DEC-2004.
XX PF 15-APR-2004; 2004US-00824527.
XX PR 18-APR-2003; 2003KR-00024656.
XX PR 14-NOV-2003; 2003KR-00080580.
XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WI WPI; 2005-089568/10.
XX DE New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PT species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 3; SEQ ID NO 35; 34pp; English.
XX CC The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 84 A; 142 C; 138 G; 56 T; 0 U; 0 Other;
Query Match 91.6%; Score 384.8; DB 14; Length 420;
Best Local Similarity 94.8%; Pred. No. 5.2e-55;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCAGCTCGCCGGTGACGGTACGACACCGACCGACCGTTCGCCCGAGGCG 60
DB 1 AAGAAGACGAGCAGCTCGCCGGTGACGGTACGACACCGACCGACCGTTCGCCCGAGGCG 60
QY 61 CTCGTACGGCAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
DB 61 CTCGTACGAGGAAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
QY 121 GGCATCGAGAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 180
DB 121 GGCATCGAGAGGCGCTGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGACACCGATCGGC 240
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Db 181 GAGACCAAGGAGCAGATCGCTCCACGGCTCCATCTCCGCCGCGACACCCAGATCGGC 240
QY 241 GAGCTATCCCGAGGCGATGACAGAGTCCGCAAGGAAGGCGTTCATCACCGTTCGAGGAG 300
Db 241 GAGCTGATCCCGAGGCGCATGGAACAAGGTCCGCAAGGAAGGCGTTCATCACCGTTCGAGGAG 300
QY 301 TCCACAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAGGGCTAC 360
Db 301 TCCACAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAGGGCTAC 360
QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTGCTCGACGACCCGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTGCTCGACGACCCGTAC 420

RESULT 30
ADV99128
ID ADV99128 standard; DNA; 420 BP.
XX
AC ADV99128;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 8.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces albobroiseolus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 8; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 83 A; 144 C; 137 G; 56 T; 0 U; 0 Other;

Query Match 91.6%; Score 384.8; DB 14; Length 420;
Best Local Similarity 94.8%; Pred. No. 5.2e-55;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGTTCGCGCCAGGCG 60
QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGGTGCCAACCGATGGCTCTCAAGCGC 120
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Db 61 CTGGTCAAGGAGGCGCTGCGCAACGTCGCGCGCGGCCAACCCGATGGCCCTGAAGCGC 120
QY 121 GGCATCGACAAGCGCGTCGAGGCGGCTCTCCGGGCGCCCTCTGGAGCAGCGGAGGATGTC 180
Db 121 GGTATCGAAGAGGCGCGTCGAGGCGGCTCTCCGGGCGCCCTCTGGAGCAGCGGAGGACGTG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGCCGCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCCCGAGGCGATGGAACAAGTTCGCAAGGAAGGCGTTCATCACCGTTCGAGGAG 300
Db 241 GAGCTCATCCCGAGGCGATGGAACAAGTTCGCAAGGAAGGCGTTCATCACCGTTCGAGGAG 300
QY 301 TCCACAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAGGGCTAC 360
Db 301 TCCACAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAGGGCTAC 360
QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTGCTCGACGACCCGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGATGAGCGGCTGCTCGACGACCCGTAC 420

RESULT 31
ADV99139
ID ADV99139 standard; DNA; 420 BP.
XX
AC ADV99139;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 19.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces cellulosa.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 19; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 82 A; 140 C; 141 G; 57 T; 0 U; 0 Other;
```


Query Match 91.2%; Score 383.2; DB 14; Length 420;
Best Local Similarity 94.5%; Pred. No. 9.6e-55;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCAGCTCGCGGTGACGCTACGACACCGCGCGGCTTCGCGCCAGGCG 60
DB 1 AAGAAGACGAGCAGCTCGCGGTGACGCTACGACACCGCGCGGCTTCGCGCCAGGCG 60
QY 61 CTCGTACGCGAGGCGCTCGCGCAACGTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
DB 61 CTGGTCAAGGAGGCGCTCGCGCAACGTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAGCGAGGATGTC 180
DB 121 GGTATCGAGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAGCGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCACGCGCTCGCGCGGTGCCAACCCGATGGCT 240
DB 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCACGCGCTCGCGCGGTGCCAACCCGATGGCT 240
QY 241 GAGCTCATCGCGAGCGGATGACAAAGGTGCGCAAGGAGGCGTCATCACCGCTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGGATGACAAAGGTGCGCAAGGAGGCGTCATCACCGCTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGCTTCGACAAAGGCTTAC 360
DB 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGCTTCGACAAAGGCTTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGACGACCGCTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGACGACCGCTAC 420

RESULT 32
ADV99157
ID ADV99157 standard; DNA; 420 BP.
XX
AC ADV99157;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 37.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces hygroscopicus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 37; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).

CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 80 A; 146 C; 137 G; 57 T; 0 U; 0 Other;
Query Match 91.2%; Score 383.2; DB 14; Length 420;
Best Local Similarity 94.5%; Pred. No. 9.6e-55;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGACGAGCAGCTCGCGGTGACGCTACGACACCGCGCGGCTTCGCGCCAGGCG 60
DB 1 AAGAAGACGAGCAGCTCGCGGTGACGCTACGACACCGCGCGGCTTCGCGCCAGGCG 60
QY 61 CTCGTACGCGAGGCGCTCGCGCAACGTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
DB 61 CTGGTCCGAGGCGCTCGCGCAACGTCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAGGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAGCGAGGATGTC 180
DB 121 GGTATCGAGCGCTCGAGCGCTCTCGCGCGCTCTCGCGCGCTCTCGAGCGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCACGCGCTCGCGCGGTGCCAACCCGATGGCT 240
DB 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCACGCGCTCGCGCGGTGCCAACCCGATGGCT 240
QY 241 GAGCTCATCGCGAGCGGATGACAAAGGTGCGCAAGGAGGCGTCATCACCGCTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGGATGACAAAGGTGCGCAAGGAGGCGTCATCACCGCTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGCTTCGACAAAGGCTTAC 360
DB 301 TCCGAGACCTTCGCTCGAGCTGAGCTCACGAGGATGCGCTTCGACAAAGGCTTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGACGACCGCTAC 420
DB 361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGGTCTCGACGACCGCTAC 420

RESULT 33
ADV99133
ID ADV99133 standard; DNA; 420 BP.
XX
AC ADV99133;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 13.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces anandii.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 37; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGRO2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).


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OS Streptomyces diastaticus.
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 28; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence of groEL2
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 81 A; 146 C; 137 G; 56 T; 0 U; 0 Other;

Query Match 90.9%; Score 381.6; DB 14; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.8e-54;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGTCCCGGTGACGTACGACACCGCGGTCACCGATGCTCTCAAGCGC 60
DB 1 AAGAAGACGAGCAGTCCCGGTGACGTACGACACCGCGGTCACCGATGCTCTCAAGCGC 60
QY 61 CTCGTACGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCGAGCGAAGGATGTC 180
DB 121 GGCATCGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCGAGCGAAGGATGTC 180
QY 121 GGCATCGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCGAGCGAAGGATGTC 180
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGAACCAGATCGGC 240
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGAACCAGATCGGC 240
DB 241 GAGCTCATCGCGAGGCGATGACAAGGTGCGCAAGGAGCGTCAACCGTCTGAGGAG 300
QY 241 GAGCTCATCGCGAGGCGATGACAAGGTGCGCAAGGAGCGTCAACCGTCTGAGGAG 300
DB 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTGAGGAGGATGCGGTTTCGACCAAGGGCTAC 360
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTGAGGAGGATGCGGTTTCGACCAAGGGCTAC 360
DB 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGTATGAGGGCGTCCCTGAGACCGCTAC 420
QY 361 ATCTCGGCGTACTTCCGCCACCGACATGAGCGGTATGAGGGCGTCCCTGAGACCGCTAC 420

RESULT 36
ADV99180
ID ADV99180 standard; DNA; 420 BP.
XX
```

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AC ADV99180;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 60.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces acidiscabies.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 4; SEQ ID NO 60; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence of groEL2
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 83 A; 147 C; 139 G; 51 T; 0 U; 0 Other;

Query Match 90.9%; Score 381.6; DB 14; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.8e-54;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGTCCCGGTGACGTACGACACCGCGGTCACCGATGCTCTCAAGCGC 60
DB 1 AAGAAGACGAGCAGTCCCGGTGACGTACGACACCGCGGTCACCGATGCTCTCAAGCGC 60
QY 61 CTCGTACGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCGAGCGAAGGATGTC 120
DB 61 CTCGTACGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCGAGCGAAGGATGTC 120
QY 121 GGCATCGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCGAGCGAAGGATGTC 180
DB 121 GGCATCGAGAGGCGGTGCGCAACGTCGCGCGCCCTGCTGGAGCGAGCGAAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGAACCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGAACCAGATCGGC 240
QY 241 GAGCTCATCGCGAGGCGATGACAAGGTGCGCAAGGAGCGTCAACCGTCTGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGACAAGGTGCGCAAGGAGCGTCAACCGTCTGAGGAG 300
QY 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTGAGGAGGATGCGGTTTCGACCAAGGGCTAC 360
DB 301 TCCAGACCTTCGGTCTGGAGCTGAGGCTGAGGAGGATGCGGTTTCGACCAAGGGCTAC 360
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QY 361 ATCTCGCGTACTTCCGACCGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
 |||||
 Db 361 ATCTCGCGTACTTCCGACCGACATGAGCGTATGAGGCGTCTCGACGACCCGCTAC 420
 |||||

RESULT 37
 ADV99145
 ID ADV99145 standard; DNA; 420 BP.
 XX
 AC ADV99145;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE groEL2 gene fragment, SEQ ID 25.
 XX
 KW Microorganism identification; microorganism detection; groEL2;
 KW potato scab; gene; ds.
 XX
 OS Streptomyces coeruleorubidus.
 XX
 PN US2004265873-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 15-APR-2004; 2004US-00824527.
 XX
 PR 18-APR-2003; 2003KR-00024656.
 PR 14-NOV-2003; 2003KR-00080580.
 XX
 PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 XX
 PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
 XX WPI; 2005-089568/10.
 DR
 XX
 XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.
 XX
 PS Claim 3; SEQ ID NO 25; 34pp; English.
 CC
 CC The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.
 XX
 SQ Sequence 420 BP; 83 A; 145 C; 136 G; 56 T; 0 U; 0 Other;
 Query Match 90.9%; Score 381.6; DB 14; Length 420;
 Best Local Similarity 94.3%; Pred. No. 1.8e-54;
 Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 60
 |||||
 Db 1 AAGAAGACGACGACGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 60
 |||||

QY 61 CTGCTACGCGAGGCGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 120
 |||||
 Db 61 CTGCTACGCGAGGCGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 120
 |||||

QY 121 GGCATCAGAGAGCGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 180
 |||||
 Db 121 GGCATCAGAGAGCGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 180
 |||||

QY 181 GAGACCAAGGACGATCGCTCTCCACGCGCTTCCATCTCCCGCGCGACCCGATCGGC 240
 |||||
 Db 181 GAGACCAAGGACGATCGCTCTCCACGCGCTTCCATCTCCCGCGCGACCCGATCGGC 240
 |||||

QY 241 GAGCTCATCCGAGGCGATGCAAGGTCCGCAAGGAAGGGGTATCATCCCGTCGAGGAG 300
 |||||
 Db 241 GAGCTCATCCGAGGCGATGCAAGGTCCGCAAGGAAGGGGTATCATCCCGTCGAGGAG 300
 |||||

QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTTCCAGGGGTATGGCTTCCAGAGGCGTAC 360
 |||||
 Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTTCCAGGGGTATGGCTTCCAGAGGCGTAC 360
 |||||

QY 361 ATCTCGCGTACTTCCGACCGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
 |||||
 Db 361 ATCTCGCGTACTTCCGACCGACATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
 |||||

RESULT 38
 ADV99149
 ID ADV99149 standard; DNA; 420 BP.
 XX
 AC ADV99149;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE groEL2 gene fragment, SEQ ID 29.
 XX
 KW Microorganism identification; microorganism detection; groEL2;
 KW potato scab; gene; ds.
 XX
 OS Streptomyces djakartensis.
 XX
 PN US2004265873-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 15-APR-2004; 2004US-00824527.
 XX
 PR 18-APR-2003; 2003KR-00024656.
 PR 14-NOV-2003; 2003KR-00080580.
 XX
 PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 XX
 PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
 XX WPI; 2005-089568/10.
 DR
 XX
 XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
 PT species, useful in identifying the genus Streptomyces, and for isolating
 PT or purifying natural products using such microorganisms.
 XX
 PS Claim 3; SEQ ID NO 29; 34pp; English.
 CC
 CC The present invention relates to novel primers STGROF1 (ADV99121) and
 CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
 CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
 CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
 CC Potato scab is a pathogenic disease caused by certain Streptomyces
 CC species. Primers ADV99121 and ADV99122 are useful in a method for
 CC identifying Streptomyces species, comprising amplifying groEL2 gene
 CC fragment of target strain, analyzing the nucleotide sequence of groEL2
 CC gene fragment amplified, and comparing the nucleotide sequence obtained
 CC with that of groEL2 gene fragment of a reference strain.
 XX
 SQ Sequence 420 BP; 82 A; 148 C; 135 G; 55 T; 0 U; 0 Other;
 Query Match 90.9%; Score 381.6; DB 14; Length 420;
 Best Local Similarity 94.3%; Pred. No. 1.8e-54;
 Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 60
 |||||
 Db 1 AAGAAGACGACGACGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 60
 |||||

QY 61 CTGCTACGCGAGGCGCTCGCGGTACGATACGACACCGCGCTCTCGCCAGGCG 120
 |||||

Db 61 CTGGTCAAGAGGCGCTGCGCAAGCTGCGCGCGCGCGCGCAACCCGATGGCCCTGGAAGCGC 120
QY 121 GGCATCGAGAGGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 180
Db 121 GGTATCGAGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 180
QY 181 GAGACCAAGAGGAGGAGTGTTCAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 240
Db 181 GAGACCAAGAGGAGGAGTGTTCAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 240
QY 241 GAGCTCATCGCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 300
Db 241 GAGCTCATCGCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 300
QY 301 TCCAGACCTTCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 360
Db 301 TCCAGACCTTCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 360
QY 361 ATCTCGGCGTACTTCCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 420
Db 361 ATCTCGGCGTACTTCCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 420

RESULT 39

ADV99141

ID ADV99141 standard; DNA; 420 BP.

XX ADV99141;

DT 24-MAR-2005 (first entry)

DE groEL2 gene fragment, SEQ ID 21.

XX Microorganism identification; microorganism detection; groEL2;

KW potato scab; gene; ds.

XX Streptomyces chattanoogensis.

XX US2004265873-A1.

XX 30-DEC-2004.

PF 15-APR-2004; 2004US-00824527.

XX 18-APR-2003; 2003KR-00024656.

PR 14-NOV-2003; 2003KR-00080580.

XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces species, useful in identifying the genus Streptomyces, and for isolating or purifying natural products using such microorganisms.

PS Claim 3; SEQ ID NO 21; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment derived from a potato scab pathogenic microorganism (ADV99163-ADV99181). CC Potato scab is a pathogenic disease caused by certain Streptomyces CC species. Primers ADV99121 and ADV99122 are useful in a method for CC identifying Streptomyces species, comprising amplifying groEL2 gene CC fragment of target strain, analyzing the nucleotide sequence of groEL2 CC gene fragment amplified, and comparing the nucleotide sequence obtained CC with that of groEL2 gene fragment of a reference strain.

SQ Sequence 420 BP; 81 A; 139 C; 139 G; 61 T; 0 U; 0 Other;

Query Match 90.9%; Score 381.6; DB 14; Length 420;

Best Local Similarity 94.3%; Pred. No. 1.8e-54;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 AAGAGAGCGAGCGAGCTGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTCTCCGCGCGCGCG 60

Db 1 AAGAGAGCGAGCGAGCTGAGGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTCTCCGCGCGCGCG 60

QY 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGCTGCGCAACCGATGGCTCTCAAGCGC 120

Db 61 CTGGTCCGCGAGGCGCTGCGCAACGTCGCGCGCGCTGCGCAACCGATGGCTCTCAAGCGC 120

QY 121 GGCATCGAGAGGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 180

Db 121 GGTATCGAGAGGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 180

QY 181 GAGACCAAGAGGAGGAGTGTTCAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 240

Db 181 GAGACCAAGAGGAGGAGTGTTCAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 240

QY 241 GAGCTCATCGCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 300

Db 241 GAGCTCATCGCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 300

QY 301 TCCAGACCTTCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 360

Db 301 TCCAGACCTTCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 360

QY 361 ATCTCGGCGTACTTCCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 420

Db 361 ATCTCGGCGTACTTCCGCGCGCGCTGAGGCGCGCTCTCCGCGCGCGCTGCTGAGCAGGCGAGGAGTGTTC 420

RESULT 40

ADV99134

ID ADV99134 standard; DNA; 420 BP.

XX ADV99134;

DT 24-MAR-2005 (first entry)

DE groEL2 gene fragment, SEQ ID 14.

XX Microorganism identification; microorganism detection; groEL2;

KW potato scab; gene; ds.

XX Streptomyces argenteolus.

XX US2004265873-A1.

XX 30-DEC-2004.

PF 15-APR-2004; 2004US-00824527.

PR 18-APR-2003; 2003KR-00024656.

PR 14-NOV-2003; 2003KR-00080580.

XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces species, useful in identifying the genus Streptomyces, and for isolating or purifying natural products using such microorganisms.

PS Claim 3; SEQ ID NO 14; 34pp; English.

XX The present invention relates to novel primers STGROF1 (ADV99121) and STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment derived from a potato scab pathogenic microorganism (ADV99163-ADV99181). CC Potato scab is a pathogenic disease caused by certain Streptomyces


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XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX PD WPI; 2005-089568/10.
XX PF New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX PR species, useful in identifying the genus Streptomyces, and for isolating
XX PT or purifying natural products using such microorganisms.
XX PS Claim 4; SEQ ID NO 52; 34pp; English.
XX PS The present invention relates to novel primers STGROF1 (ADV99121) and
XX CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX CC Potato scab is a pathogenic disease caused by certain Streptomyces
XX CC species. Primers ADV99121 and ADV99122 are useful in a method for
XX CC identifying Streptomyces species, comprising amplifying groEL2 gene
XX CC fragment of target strain, analyzing the nucleotide sequence of groEL2
XX CC gene fragment amplified, and comparing the nucleotide sequence obtained
XX CC with that of groEL2 gene fragment of a reference strain.
XX SQ Sequence 420 BP; 83 A; 135 C; 147 G; 55 T; 0 U; 0 Other;

Query Match 90.1%; Score 378.4; DB 14; Length 420;
Best Local Similarity 93.8%; Pred. No. 6e-54;
Matches 394; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 AAGAGACGAGGAGCGTCCGGTACCGTACGACCGGCGGTCGCAACCGATGGCTCTCAAGCGC 60
DB 1 AAGAGACGAGGAGCGTCCGGTACCGTACGACCGGCGGTCGCAACCGATGGCTCTCAAGCGC 60
QY 61 CTGCTACGAGAGCGGCTTCGAGCGCTCTCCGCGCCCTCTCGAGCGAGGCGTATCGATGTC 180
DB 121 GGCATCGAGAGAGCGGCTTCGAGCGCTCTCCGCGCCCTCTCGAGCGAGGCGTATCGATGTC 180
QY 121 GGCATCGAGAGAGCGGCTTCGAGCGCTCTCCGCGCCCTCTCGAGCGAGGCGTATCGATGTC 180
DB 181 GAGACCAAGGAGGAGCGTTCGAGCGCTTCGAGCGCTTCGAGCGAGGCGTATCGATGTC 240
DB 181 GAGACCAAGGAGGAGCGTTCGAGCGCTTCGAGCGCTTCGAGCGAGGCGTATCGATGTC 240
QY 241 GAGCTCATCGCGAGGCGGATGGAACAAGTGGCAAGGAGGCGTATCGATGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGGATGGAACAAGTGGCAAGGAGGCGTATCGATGTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTTCGAGCGTTCGAGCGCTTCGAGCGCTTCGAGCGAGGCGTATCG 360
DB 301 TCCGAGACCTTCGCTTCGAGCGTTCGAGCGCTTCGAGCGCTTCGAGCGAGGCGTATCG 360
QY 361 ATCTCGGCGTACTTCGCGACCGGATGAGGCGTTCGAGCGCTTCGAGCGAGGCGTATCG 420
DB 361 ATCTCGGCGTACTTCGCGACCGGATGAGGCGTTCGAGCGCTTCGAGCGAGGCGTATCG 420

RESULT 43
ADV99173
ID ADV99173 standard; DNA; 420 BP.
XX AC ADV99173;
XX DT 24-MAR-2005 (first entry)
XX DE groEL2 gene fragment, SEQ ID 53.
XX KW Microorganism identification; microorganism detection; groEL2;
XX KW potato scab; gene; ds.
XX OS Streptomyces turgidiscabies.
```



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QY 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
DB 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGTTTCGACAAGGCGTAC 360
DB 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGTTTCGACAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCGCCAGCATGGAGCGGATGGAGCGGTCGTCGACGACCCGTTAC 420
DB 361 ATCTCGGCGTACTTCGCGCCAGCATGGAGCGGATGGAGCGGTCGTCGACGACCCGTTAC 420

RESULT 46
ADV99176
ID ADV99176 standard; DNA; 420 BP.
XX
AC ADV99176;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 56.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces diastatochromogenes.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KOR-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 4; SEQ ID NO 56; 34pp; English.
XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 85 A; 142 C; 138 G; 55 T; 0 U; 0 Other;

Query Match 88.6%; Score 372; DB 14; Length 420;
Best Local Similarity 92.9%; Pred. No. 6.8e-53;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGCGTACGACACCGGACCGGTTCTCGCCGAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGCGTACGACACCGGACCGGTTCTCGCCGAGGCG 60
QY 61 CTCGTCACGAGGCGGCTCGGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGGCG 120
DB 61 CTGGGTCAAGGAAGGCGCTGCGCAACGTCAGCCGCGGCGCCCAACCCGATGGCCCTCAAGGCG 120
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QY 121 GGCATCGAGAAGCCGTCGAGGCCGTCCTCCGCGCCCTCTCGAGCCGAGGATGTC 180
DB 121 GGCATCGAGAAGCCGTCGAGGCCGTCCTCCGCGCCCTCTCGAGCCGAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCGACGGCTTCATCTCCGCGCCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCGACGGCTTCATCTCCGCGCCGCGACACCCAGATCGGC 240
QY 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
DB 241 GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAGGCGTCATCACCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGTTTCGACAAGGCGTAC 360
DB 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGTTTCGACAAGGCGTAC 360
QY 361 ATCTCGGCGTACTTCGCGCCAGCATGGAGCGGATGGAGCGGTCGTCGACGACCCGTTAC 420
DB 361 ATCTCGGCGTACTTCGCGCCAGCATGGAGCGGATGGAGCGGTCGTCGACGACCCGTTAC 420
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RESULT 47

ADV99179
ID ADV99179 standard; DNA; 420 BP.

XX
AC ADV99179;

XX
DT 24-MAR-2005 (first entry)

XX
DE groEL2 gene fragment, SEQ ID 59.

XX
KW Microorganism identification; microorganism detection; groEL2;

XX
KW potato scab; gene; ds.

XX
OS Streptomyces scabiei.

XX
PN US2004265873-A1.

XX
PD 30-DEC-2004.

XX
PF 15-APR-2004; 2004US-00824527.

XX
PR 18-APR-2003; 2003KR-00024656.

XX
PR 14-NOV-2003; 2003KR-00080580.

XX
PA (KOR-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX
WPI; 2005-089568/10.

XX
PT New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.

XX
PS Claim 4; SEQ ID NO 59; 34pp; English.

XX
CC The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

SQ Sequence 420 BP; 83 A; 142 C; 141 G; 54 T; 0 U; 0 Other;

Query Match 88.6%; Score 372; DB 14; Length 420;
Best Local Similarity 92.9%; Pred. No. 6.8e-53;


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PN US2004265873-A1.
XX 30-DEC-2004.
XX 15-APR-2004; 2004US-00824527.
XX 18-APR-2003; 2003KR-00024656.
XX 14-NOV-2003; 2003KR-00080580.
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
XX or purifying natural products using such microorganisms.
XX Claim 3; SEQ ID NO 7; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
XX STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
XX Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
XX derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
XX Potato scab is a pathogenic disease caused by certain Streptomyces
XX species. Primers ADV99121 and ADV99122 are useful in a method for
XX identifying Streptomyces species, comprising amplifying groEL2 gene
XX fragment of target strain, analyzing the nucleotide sequence of groEL2
XX gene fragment amplified, and comparing the nucleotide sequence obtained
XX with that of groEL2 gene fragment of a reference strain.
XX Sequence 423 BP; 82 A; 149 C; 138 G; 54 T; 0 U; 0 Other;
XX
XX Query Match 88.1%; Score 370.2; DB 14; Length 423;
XX Best Local Similarity 93.9%; Pred. No. 1.4e-52;
XX Matches 397; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
XX
QY 1 AAGNAGACGACGACGTCGCGGTGACGGTACGACACCGCGGACCGTCTCGCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGCGGACCGTCTCGCCAGGCG 60
QY 61 CTGCT---ACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 117
DB 61 CTGCTACAGCGGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 120
QY 118 CGCGGATCGAGAGGCGCGTTCGAGGCGGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 177
DB 121 CGCGGTATCGAGAGGCGCGTTCGAGGCGGTCGCGCGCGGTGCCAACCGATGGCTCTCAAG 180
QY 178 GTGAGACGACGACGATCGCTTCCACCGCTTCCACCGCGCGGTGCCAACCGATGGCTCTCAAG 237
DB 181 GTGAGACGACGACGATCGCTTCCACCGCTTCCACCGCGCGGTGCCAACCGATGGCTCTCAAG 240
QY 238 GCGAGCTCATCGCCGAGGCGGATGGAACAAGTCCGCAAGGAGCGCTCATCAGCTCGAG 297
DB 241 GCGAGCTCATCGCCGAGGCGGATGGAACAAGTCCGCAAGGAGCGCTCATCAGCTCGAG 300
QY 298 GAGTCCAGACCTTCGCTTCGAGGCTGAGGCTCACCGAGGATGCGCTTCGACAGGCG 357
DB 301 GAGTCCAGACCTTCGCTTCGAGGCTGAGGCTCACCGAGGATGCGCTTCGACAGGCG 360
QY 358 TACATCTCGGCTACTTCGCGCACCGACATGAGGCGGATGAGGCGGCTGCTCGAGACCG 417
DB 361 TACATCTCGGCTACTTCGCGCACCGACATGAGGCGGATGAGGCGGCTGCTCGAGACCG 420
QY 418 TAC 420
DB 421 TAC 423
XX
RESULT 52
ADV99150
```

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Db      301 GAGTCCAGACCTTCGGTCTGGAGCTGGAACCTACCGAGGGTATGCGCTTCGACAAAGGGC 360
QY      358 TACATCTCGCGCTACTTCGCCACCGCATGGAGCGGATGGAGCGTTCGCTCGACGACCCG 417
Db      361 TACATCTCGCGCTACTTCGCCACCGCATGGAGCGGATGGAGCGCGGCTCGAGGACCCG 420
QY      418 TAC 420
Db      421 TAC 423

RESULT 53
ADV99124
ID ADV99124 standard; DNA; 420 BP.
XX
AC ADV99124;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 4.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces aculeolatus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
PI WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 4; 34pp; English.
XX
CC The present invention relates to novel primers STGR0F1 (ADV99121) and
CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 85 A; 145 C; 141 G; 49 T; 0 U; 0 Other;

Query Match 87.0%; Score 365.6; DB 14; Length 420;
Best Local Similarity 91.9%; Pred. No. 7.8e-52;
Matches 386; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY      1 AAGAGACGGAGCAGTCCCGGTACCGGTACGACACCGGACCGGTTCGCCAGCGC 60
Db      1 AAGAGACGGAGCAGTCCCGGTACCGGTACGACACCGGACCGGTTCGCCAGCGC 60
QY      61 CTCGTACCGAGGGCTTCGGCAACGTCGCGCGGTGCAACCCGATGCTCTCAAGGCG 120
Db      61 CTGTGTCAGAGAGGGCTTCGGGACGTCGCGCGCGGTGCAACCCGATGCGCTGAGGCG 120
QY      121 GGCATCGAGAAGCGGCTCGAGGCGCTCTCCGCGCGCTTCGAGGACGGCGAAGGATGTC 180

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Db      121 GGCATCGAGAAGCGGCTTCGCCCGCGCTCTCCGCGCGCTTCGAGCAGGCCAAGGACGTG 180
QY      181 GAGACCAAGGAGCAGATCGCTTCACCGGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
Db      181 GAGACCAAGGAGCAGATCGCTTCACCGGCTCCATCTCCGCGCGGACACCCAGATCGGC 240
QY      241 GAGCTCATCGCGGAGCGCATGGAACAAGGTGCGCAAGGAAGGCGTCATCAACCGTCGAGGAG 300
Db      241 GAGCTGATCGCGGAGGCCATGGAACAAGGTGCGCAAGGAAGGCGTCATCAACCGTCGAGGAG 300
QY      301 TCCGAGACCTTCGGTCTGGAGCTCAGCGAGGGTATGCGCTTCGACAAAGGCTTAC 360
Db      301 TCGCAGACCTTCGGGCTGGAGCTTGAGCTCACCAGGGGCGATGCGCTTCGACAAAGGCTTAC 360
QY      361 ATCTCGGCGTACTTCGCCACCGCATGGAGCGGATGGAGGCGTTCGTCGACGACCGGTAC 420
Db      361 ATCTCGGCGTACTTCGCCACCGCATGGAGCGGATGGAGGCGTTCGAGACCGGTAC 420

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RESULT 54

ADV99153
ID ADV99153 standard; DNA; 420 BP.

XX AC ADV99153;

XX DT 24-MAR-2005 (first entry)

XX DE groEL2 gene fragment, SEQ ID 33.

XX KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.

XX OS Streptomyces griseochromogenes.

XX PN US2004265873-A1.

XX PD 30-DEC-2004.

XX PF 15-APR-2004; 2004US-00824527.

XX PR 18-APR-2003; 2003KR-00024656.

XX PR 14-NOV-2003; 2003KR-00080580.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;

XX WPI; 2005-089568/10.

XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.

XX Claim 3; SEQ ID NO 33; 34pp; English.

XX The present invention relates to novel primers STGR0F1 (ADV99121) and
CC STGR0R2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.

XX SQ Sequence 420 BP; 86 A; 147 C; 136 G; 51 T; 0 U; 0 Other;

Query Match 86.3%; Score 362.4; DB 14; Length 420;

Best Local Similarity 91.4%; Pred. No. 2.6e-51;

Matches 384; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGCTCGCGGTGACGCTACGACACCGCGGCTTCTCGCCAGGCG 60
DB |||||
1 AAGAAGACGACGACGCTCGCGGTGACGCTACGACACCGCGGCTTCTCGCCAGGCG 60
QY 61 CTGCTAGCGAGGCGCTGCGCAACGCTCGCGCGGTGCGCAACCGCGATGGCTCTCAAGCGC 120
DB |||||
61 CTGCTCAAGGAAGCGCTCCGCAACGCTCGCGCGGTGCGCAACCGCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGCGCGCTCGAGGCGCTCGCGCGCGCTCGCGCGCGCTCGAGGCGGAGGATGTC 180
DB |||||
121 GGTATCGAGAAGCGCGCTCGAGGCGCTCGCGCGCGCTCGCGCGCGCTCGAGGCGGAGGACGTC 180
QY 181 GAGACCAAGGACGACGATCGCTTCCAGCGCGCTTCCATCTCCCGCGCGCGACACCGACGATCGGC 240
DB |||||
181 GAGACCAAGGACGACGATCGCTTCCAGCGCGCTTCCATCTCCCGCGCGCGACACCGACGATCGGC 240
QY 241 GAGCTCATCCCGAGGCGGATGGGCAAGGTCGGCAAGGTCGCAAGGTCGATCATCCCGTCGAGGAG 300
DB |||||
241 GAGCTGATCCCGAGGCGGATGGGCAAGGTCGGCAAGGTCGCAAGGTCGATCATCCCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGCTCGGAGCTGAGCTCACCGAGGCTATCGCTTCGACAGGCGCTAC 360
DB |||||
301 AGCAACACCTTCGCTCGGAGCTGAGCTCACCGAGGCGATCGCTTCGCAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCGCGACCGACGATGGAGCGGATGGAGCGGCTCGGCTCGACGACCGGTAC 420
DB |||||
361 ATCTCGGCGTACTTCGCGACCGACGATGGAGCGGATGGAGCGGCTCGGAGCGGCTCGGAGCGGCTAC 420

RESULT 55

ADV99159
ID ADV99159 standard; DNA; 423 BP.
XX
AC ADV99159;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 39.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces murinus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
XX New primer specifically amplifying groEL2 gene fragment of Streptomyces
PT species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
XX
PS Claim 3; SEQ ID NO 39; 34pp; English.
XX
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2

CC Gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 423 BP; 86 A; 148 C; 134 G; 55 T; 0 U; 0 Other;

Query Match 86.2%; Score 362.2; DB 14; Length 423;
Best Local Similarity 92.7%; Pred. No. 2.9e-51;
Matches 392; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGACGCTCGCGGTGACGCTACGACACCGCGGCTTCTCGCCAGGCG 60
DB |||||
1 AAGAAGACGACGACGCTCGCGGTGACGCTACGACACCGCGGCTTCTCGCCAGGCG 60
QY 61 CTGCT---ACGCGAGGCGCTCGCGCAACGCTCGCGCGGTGCGCAACCGCGATGGCTCTCAAG 117
DB |||||
61 CTGCTCACAGCGGAGGCGCTTGGCAACGCTCGCGCGGTGCGCAACCGCGATGGCGCTGAAG 120
QY 118 CGCGGCTATCGAGAAGGCGCTCGAGGCGCTTCCGGCGCGCTTGTGGAGCAGGCGAAGGAT 177
DB |||||
121 CGCGGCTATCGAGAAGGCGCTCGAGGCGCTTCCGGCGCGCTTGTGGAGCAGGCGCAAGGAC 180
QY 178 GTCGAGACCAAGGACGATCGCTTCCAGGCGCTTCCATCTCGCGCGCGCGACACCGAGATC 237
DB |||||
181 GTCGAGACCAAGGACGATCGCTTCCAGGCGCTTCCATCTCGCGCGCGCGACACCGAGATC 240
QY 238 GCGGAGCTCATTCGCGAGGCGGATGGCAAGGTCGCAAGGTCGCAAGGTCGATCATCCGTCGAG 297
DB |||||
241 GCGGAGCTCATTCGCGAGGCGGATGGCAAGGTCGCAAGGTCGCAAGGTCGATCATCCGTCGAG 300
QY 298 GAGTCCCAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGCTATCGCTTCGACAAAGGCG 357
DB |||||
301 GAGAGCAACACCTTCGCTTCGGAGCTTGGAGCTCACCGAGGCGATCGCTTCGACAAAGGCG 360
QY 358 TACATCTCGCGTACTTCGCGCAACGACATGGAGCGGATGGAGCGGCTCGCTTCGACGACCGG 417
DB |||||
361 TACATCTTCGCTTACTTCGCGCAACCGCATGGAGCGCATGGAGCGGCTCGCTTCGACGACCGG 420
QY 418 TAC 420
DB |||||
421 TAC 423

RESULT 56

ADV99130
ID ADV99130 standard; DNA; 420 BP.
XX
AC ADV99130;
XX
DT 24-MAR-2005 (first entry)
XX
DE groEL2 gene fragment, SEQ ID 10.
XX
KW Microorganism identification; microorganism detection; groEL2;
KW potato scab; gene; ds.
XX
OS Streptomyces albus.
XX
PN US2004265873-A1.
XX
PD 30-DEC-2004.
XX
PF 15-APR-2004; 2004US-00824527.
XX
PR 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
XX WPI; 2005-089568/10.
XX
PT New primer specifically amplifying groEL2 gene fragment of Streptomyces

OS Mycobacterium phlei.
XX W02003062470-A1.
XX 31-JUL-2003.
XX 21-JAN-2003; 2003WO-KR000131.
XX 24-JAN-2002; 2002KR-00004297.
PR 05-MAR-2002; 2002KR-00011648.
XX (BIOM-) BIOMEDLAB CORP.
PA (KIMB/) KIM B.
XX Kim B, Kook Y, Kim J;
XX WPI; 2003-598757/56.
XX Primers for amplifying a heat shock protein 65-gene fragment of
PT mycobacterial species, useful for identifying and diagnosing
PT mycobacterial species in tuberculosis infection.
XX Claim 3; Page 85-86; 102pp; English.
XX The present invention provides a pair of primers for specifically
CC amplifying a heat shock protein 65 (hsp 65) gene fragment of
CC mycobacterial species comprising those sequences shown in ACF04316-
CC ACF04317. Also provided are a number of hsp65 gene fragments, mainly from
CC mycobacterial species. The methods and compositions of the present
CC invention are useful for amplifying hsp 65 gene of mycobacterial species,
CC and identifying and diagnosing mycobacterial species in tuberculosis
CC infection. The present sequence is a gene fragment of the invention
XX
SQ Sequence 604 BP; 120 A; 188 C; 207 G; 89 T; 0 U; 0 Other;
Query Match 76.8%; Score 322.4; DB 9; Length 604;
Best Local Similarity 85.5%; Pred. No. 1e-44;
Matches 359; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGATGTCGCGGGTACGCGACACACCGCCACCGCTCTGCGCCAGGCG 60
DB 50 AAGAAGACGACGATGTCGCGGGTACGCGACACACCGCCACCGCTCTGCGCCAGGCG 109
QY 61 CTGATAGCAGAGGCTGCGACAGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 120
DB 110 CTGATAGCAGAGGCTGCGACAGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 169
QY 121 GGATATCGAGAGGCGCTGCGAGAGGTACCGAGACCTGCTGAGTCTGCGCGCGCTGCGCGCG 180
DB 170 GGATATCGAGAGGCGCTGCGAGAGGTACCGAGACCTGCTGAGTCTGCGCGCGCTGCGCGCG 229
QY 181 GAGACCAAGAGCAGATGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCG 240
DB 230 GAGACCAAGAGCAGATGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCG 289
QY 241 GAGCTATCGCGCGGCGATGCGACAGGTGCGACAGGTGCGACAGGTGCGACAGGTGCGACAG 300
DB 290 GAGCTATCGCGCGGCGATGCGACAGGTGCGACAGGTGCGACAGGTGCGACAGGTGCGACAG 349
QY 301 TCCAGACCTTGGTCTGAGCTGAGCTCAGCGAGGTATGCGCTTCAAGCGCTTCAAGCGCTTCA 360
DB 350 AGCAGACCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 409
QY 361 ATCTCGCGGTACTTTCGCGACCGACATGAGCGGATGAGCGGCTGCTTCAAGCGCTTCAAGCG 420
DB 410 ATCTCGCGGTACTTTCGCGACCGACATGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG 469
RESULT 59
ADV99161
ID ADV99161 standard; DNA; 420 BP.
XX
AC ADV99161;

XX 24-MAR-2005 (first entry)
DT groEL2 gene fragment, SEQ ID 41.
XX
DE Microorganism identification; microorganism detection; groEL2;
XX potato scab; gene; ds.
KW
XX Rhodococcus equi.
OS
XX US2004265873-A1.
PN
XX 30-DEC-2004.
PD
XX 15-APR-2004; 2004US-00824527.
PF
XX 18-APR-2003; 2003KR-00024656.
PR 14-NOV-2003; 2003KR-00080580.
PR
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA
XX Kim B, Kim C, Ko YH, Koh J, Park D, Lee HB, Kim H, Kim S;
PI WPI; 2005-089568/10.
XX
DR New primer specifically amplifying groEL2 gene fragment of Streptomyces
XX species, useful in identifying the genus Streptomyces, and for isolating
PT or purifying natural products using such microorganisms.
PT
XX Claim 3; SEQ ID NO 41; 34pp; English.
XX The present invention relates to novel primers STGROF1 (ADV99121) and
CC STGROF2 (ADV99122) which specifically amplify a groEL2 gene fragment of
CC Streptomyces species (ADV99123-ADV99162) or a groEL2 gene fragment
CC derived from a potato scab pathogenic microorganism (ADV99163-ADV99181).
CC Potato scab is a pathogenic disease caused by certain Streptomyces
CC species. Primers ADV99121 and ADV99122 are useful in a method for
CC identifying Streptomyces species, comprising amplifying groEL2 gene
CC fragment of target strain, analyzing the nucleotide sequence of groEL2
CC gene fragment amplified, and comparing the nucleotide sequence obtained
CC with that of groEL2 gene fragment of a reference strain.
XX
SQ Sequence 420 BP; 82 A; 140 C; 141 G; 57 T; 0 U; 0 Other;
Query Match 76.4%; Score 320.8; DB 14; Length 420;
Best Local Similarity 85.2%; Pred. No. 2e-44;
Matches 358; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 1 AAGAAGACGACGACGCTGCGCGGTACGCTACGACACCGCGACCGCTTCTGCGCCAGGCG 60
DB 1 AAGAAGACGACGACGCTGCGCGGTACGCTACGACACCGCGACCGCTTCTGCGCTCAGGCG 60
QY 61 CTGATACGAGAGGCTGCGCAACGCTGCGCGCGGTGCGCAACCGGATGGCTTCAAGCGCG 120
DB 61 CTGATACGAGAGGCTGCGCAACGCTGCGCGCGGTGCGCAACCGGCTTCTGCGCTCAGGCG 120
QY 121 GGCATCGAGAGGCTGCGAGCGCTTCTGCGCGCGCTTCTGCGAGCAGCGGAGGATGTC 180
DB 121 GGCATCGAGAGGCTGCGAGCGCTTCTGCGCGCGCTTCTGCGAGCAGCGGAGGATGTC 180
QY 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCATCTCGCGCGCTGCGACACCGAGTCCGC 240
DB 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCATCTCGCGCGCTGCGACACCGAGTCCGC 240
QY 241 GAGCTCATCGCGAGCGGATGGAACAAGGTGCGCAAGAGGTGCAACCGGCTCATACCGTCCAGGAG 300
DB 241 GAGCTCATCGCGAGCGGATGGAACAAGGTGCGCAAGAGGTGCAACCGGCTCATACCGTCCAGGAG 300
QY 301 TCCAGACCTTGGTCTGAGCTGAGCTTCAAGCGGATGCGCTTCAAGCGGCTTCAAGCGGCTTCA 360
DB 301 TCCAGACCTTGGTCTGAGCTGAGCTTCAAGCGGATGCGCTTCAAGCGGCTTCAAGCGGCTTCA 360
QY 361 ATCTCGCGGTACTTTCGCGACCGACATGAGCGGATGAGCGGCTGCTTCAAGCGGCTTCAAGCG 420

Db 361 ATCTCGTGTACTTCGACCGGACCGGAGCGGTACAGGAAGCGGTCTCGAGGATCCGTAC 420

RESULT 60

ACC70275
ID ACC70275 standard; DNA; 1626 BP.

XX AC ACC70275;

XX DT 11-AUG-2003 (first entry)

XX DE Nucleotide sequence of the Rhodococcus equi GroEL2 protein.
XX KW GroEL protein; protein aggregation; protein folding; immune response;
XX KW antigen; pathogenic infection; gene; ss.
XX OS Rhodococcus equi.

XX FH Key Location/Qualifiers
XX CDS 1
XX FT /*tag= a
XX FT /product= "GroEL2"
XX FT

XX PN WO2003035676-A1.

XX XX

XX PD 01-MAY-2003.

XX PF 25-OCT-2002; 2002WO-AU001460.

XX PR 26-OCT-2001; 2001AU-00008523.

XX PA (UYSA-) UNIV SOUTH AUSTRALIA.

XX PA (MEDV-) MEDVET SCI PTY LTD.

XX PA (RURA-) RURAL IND RES & DEV CORP.

XX PI Vanniasinkam T, Barton M, Heuzenroeder MW;

XX WPI; 2003-482030/45.

XX DR P-PSDB; ABR55530.

XX PT New GroEL protein, useful for preparing a composition for preventing or
XX PT treating pathogenic infections.

XX PS Disclosure; Fig 1; 77pp; English.

CC The present sequence encodes a GroEL protein. The groEL2 gene is highly
CC conserved between species, and the protein facilitates the correct
CC folding of various bacterial proteins as well as prevent the aggregation
CC of denatured proteins by an ATP-dependent mechanism. The specification
CC describes a chimeric protein, consisting of a GroEL protein which has a
CC modification or analogue comprising a surface exposed exogenous amino
CC acid sequence inserted to it. The exogenous amino acid sequence is
CC configured to elicit an immune response specifically reactive to the
CC antigenic determinant. The chimeric protein is useful for preparing a
CC composition for preventing or treating pathogenic infections

XX SQ Sequence 1626 BP; 300 A; 544 C; 549 G; 233 T; 0 U; 0 Other;

Query Match

Best Local Similarity 76.4%; Score 320.8; DB 9; Length 1626;

Matches 358; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 AAGAGAGCGGAGCGTCCGCGTACGCGTACGACCGCGACCGGTCTCGCCCGGCG 60

Db 232 AAGAGAGCGGAGCGTCCGCGTACGCGTACGACCGCGTACGCGTCTCGCGTCAAGCGC 291

QY 61 CTCGTACCGGAGCGGCGTCCGCAACCTCGCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGC 120

Db 292 CTCGTCCGCGAGGCGCTGGCAACCTCGCTGCCGCGCGCAACCGCTGGGTCTGAGCGC 351

QY 121 GGCATCGAAGAGCGGTGAGGCCCTCTCCGGCGCCCTCTGTGGAGCGCGAAGGATGTC 180

Db 352 GGCATCGAAGAGCGCGTTCGAGGCCGTCAACCGCAAGCTGTCTCGACACCGCCCAAGGAGTTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATCGCTCCACCGCGGGATCTCGCGGGGAGCTTCCACGATCGGC 471
QY 241 GAGCTCATCGCGAGGCGATGGAACAAGGTTCGCAAGGAAGGCGTTCATCAACCGTCGAGGAG 300
Db 472 GAGCTCATCGCGAGGCGATGGAACAAGGTTCGCAAGGAAGGCGTTCATCAACCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGGAGCTCAGGCTCACCAGGAGGTATGCGCTTCGACAGGCGTAC 360
Db 532 TCGAACTCCTTCGGCTTCGAGCTCAGGCTCACCAGGAGGTATGCGCTTCGACAGGCGTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATCGAGCGGATGGAGGCGTCCGTCCGACGACCGGTAC 420
Db 592 ATCTCGCTGTACTTCGCCACCGACCGCGAGGCGTCAAGGAAGGCGTCTCTGAGGATCCGTAC 651

Search completed: April 1, 2006, 22:21:36
Job time : 855.578 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:06:31 ; Search time 5784.96 Seconds
(without alignments)
3396.840 Million cell updates/sec

Title: US-10-824-527-43

Perfect score: 420

Sequence: 1 aagaagacggacgacgtgc.....cgtcgtcgacgacccgtac 420

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gsa1:*

10: gb_gsa2:*

11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	195.2	46.5	817	10	CG811365	CG811365 PSAT60TR
2	185.6	44.2	652	8	DR606790	DR606790 EST996918
3	185.6	44.2	696	8	DR606213	DR606213 EST996341
4	185.6	44.2	918	8	DR649351	DR649351 EST103946
5	179	42.6	639	7	CO977844	CO977844 BeZSPN11F
6	173.6	41.3	690	6	CF712525	CF712525 CCAG056TR
7	173.6	41.3	738	6	CF693874	CF693874 CCADM43TR
8	173.6	41.3	741	6	CF718151	CF718151 CCACZ70TR
9	173.6	41.3	749	6	CF682602	CF682602 CCABF32TR
10	173.6	41.3	752	6	CF693560	CF693560 CCAGV54TR
11	173.6	41.3	760	6	CF692108	CF692108 CCABR85TR
12	173.6	41.3	763	6	CF676179	CF676179 CCAGC90TR
13	173.6	41.3	766	6	CF722454	CF722454 CCAC270TR
14	173.6	41.3	767	6	CF710636	CF710636 CCAC87TR
15	173.6	41.3	768	6	CF709888	CF709888 CCAPF74TR
16	173.6	41.3	773	6	CF701856	CF701856 CCAD54TR
17	173.6	41.3	776	6	CF702480	CF702480 CCAS550TR
18	173.6	41.3	778	6	CF681781	CF681781 CCACW22TR
19	173.6	41.3	779	6	CF695095	CF695095 CCAC96TR
20	173.6	41.3	790	6	CF694632	CF694632 CCAGK96TR
21	173.6	41.3	797	6	CF713816	CF713816 CCADQ78TR
22	173.6	41.3	801	6	CF703574	CF703574 CCABB71TR

ALIGNMENTS

RESULT 1

CG811365/c 817 bp DNA linear GSS 13-NOV-2003

LOCUS PSAT60TR LargeInsertGenomicLibrary Fusarium virguliforme genomic clone KMV5J24, genomic survey sequence.

DEFINITION CG811365

ACCESSION CG811365

VERSION CG811365.1 GI:38264839

KEYWORDS GSS.

SOURCE Fusarium virguliforme

ORGANISM Fusarium virguliforme

REFERENCE 1 (bases 1 to 817)

AUTHORS Meksem, K., Ishihara, H., Koo, H., Shultz, J., Ali, S., Iqbal, J., Lightfoot, D. A. and Town, C. D.

TITLE End sequencing of BACs from a fingerprint physical map of the causative agent of soybean sudden death syndrome, Fusarium virguliforme

JOURNAL Unpublished (2003)

COMMENT Other GSSs: PSAT60TR

Contact: Chris Town and K. Meksem

The Center of Excellence in Soybean Research, Teaching and Outreach, Southern Illinois University at Carbondale and Plant Genomics, The Institute for Genomic Research

Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415, USA and 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 618 453 3103 and 301-838-3523

Fax: 618 453-7457 and 301-838-0208

Email: meksem@siu.edu; cdtown@igr.org (URL: http://Fusariumvirguliforme.siu.edu)

23	173.6	41.3	801	6	CF709185	CF709185 CCACN36TR
24	173.6	41.3	803	6	CF713651	CF713651 CCAHF05TR
25	173.6	41.3	804	6	CF711476	CF711476 CCAHX08TR
26	173.6	41.3	815	6	CF703324	CF703324 CCAHU57TR
27	173.6	41.3	820	6	CF699756	CF699756 CCAFP745TR
28	173.6	41.3	827	6	CF687348	CF687348 CCAG060TR
29	173.6	41.3	831	6	CF713573	CF713573 CCAFP58TR
30	173.6	41.3	833	6	CF701087	CF701087 CCAFB06TR
31	173.6	41.3	834	6	CF696500	CF696500 CCAD887TR
32	173.6	41.3	861	6	CF690854	CF690854 CCAFP192TR
33	173.6	41.3	869	6	CF699606	CF699606 CCAH574TR
34	173.6	41.3	872	6	CF695217	CF695217 CCAFB71TR
35	173.6	41.3	874	6	CF719528	CF719528 CCAEJ74TR
36	173.6	41.3	877	6	CF706367	CF706367 CCAHL29TR
37	173.6	41.3	878	6	CF682687	CF682687 CCAC161TR
38	173.6	41.3	881	6	CF700757	CF700757 CCAHL50TR
39	173.6	41.3	891	6	CF696919	CF696919 CCACL52TR
40	173.6	41.3	901	6	CF719458	CF719458 CCADQ25TR
41	173.6	41.3	910	6	CF716339	CF716339 CCAER16TR
42	173.6	41.3	921	6	CF711999	CF711999 CCAC030TR
43	173.2	41.2	716	6	CF716527	CF716527 CCAGN89TR
44	173.2	41.2	759	6	CF687310	CF687310 CCAAI41TR
45	173.2	41.2	794	6	CF679031	CF679031 CCAC445TR
46	172	41.0	758	6	CF707848	CF707848 CCAC564TR
47	172	41.0	796	6	CF697914	CF697914 CCAAS32TR
48	171.6	40.9	746	6	CF714926	CF714926 CCAHF79TR
49	171.2	40.8	752	7	CK446096	CK446096 pncs914ad
50	170.8	40.7	724	6	CF707221	CF707221 CCAHL38TR
51	170.8	40.7	731	6	CF704854	CF704854 CCAH737TR
52	170.6	40.6	707	6	CF689741	CF689741 CCACS77TR
53	170.6	40.6	778	6	CF691132	CF691132 CCAAI40TR
54	170.6	40.6	840	6	CF708616	CF708616 CCAHI55TR
55	168.8	40.2	799	6	CF711662	CF711662 CCAFR33TR
56	168.8	40.2	851	6	CF698612	CF698612 CCAAGN42TR
57	165.8	39.5	653	7	CF843128	CF843128 pshB023AN
58	165	39.3	393	6	CF640823	CF640823 D32_A12 F
59	162.6	38.7	698	8	CV899250	CV899250 PB02189 m
60	162.6	38.7	757	6	CF697565	CF697565 CCABM02TR

Seq primer: CAGGAAACGCTATGACC

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1. .817

/organism="Fusarium virguliforme"

/mol_type="genomic DNA"

/cultivar="Monticello"

/db_xref="taxon:232082"

/clone_lib="RMFV5J24"

/notes="Organ: Hypophae; Vector: pINDIGOBAC5; A single spore

derived culture was used. Hypophae were grown in an

incubator for four days. Nuclei were isolated and embedded

in agarose, restriction digested with Hind III. Large size

DNA fragments were ligated in vector pINDIGOBAC5 and

electro-transformed into DH10B cells."

ORIGIN

Query Match 46.5%; Score 195.2; DB 10; Length 817;

Best Local Similarity 68.5%; Pred. No. 1.5e-30;

Matches 285; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 4 AAGACGACGACGCTCGCGGTGACGTTACGACCAACGCGACCGTCTCTCGCCAGGGGCTC 63

DB 683 AAGACCAACGAGTTCGCGGTGACGTTACCAACGCGCACTGTCTTGGCCGCGCATC 624

QY 64 GTACGGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGGGC 123

DB 623 TTCTCCGAGACCGTCAAGAACGTCGCGCGGTGCAACCCCATGGACTTCGACGCGGT 564

QY 124 ATCGAAGACCGTTCGAGGCGCTCTCGGGCGCTGCTGAGGAGGAGGATGTCGAG 183

DB 563 ATCCAGGCTCCGTCGAGGCGCTGTCGAGTTCCTCAGAAGAACAAAGCGGGACATCACC 504

QY 184 ACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240

DB 503 ACCAGCGCGAGATCGCTCAGTCCGACCATCTCCGCCAACGGTGAAGTTCATTTGGT 444

QY 241 GAGCTCATTCGCGAGGCGATGGAACAGGTGCGGAAGAAAGCGGTATCATCGTCGAGGAG 300

DB 443 GAGATGATTGCAACGCGATGGAAGGTGCGGAAGGAGGTGTCTATCATCTGTCGAGGAG 384

QY 301 TCCGAGACCTTCGCTGAGGCTGAGCTACCGAGGGATGCGCTTCGACAGGGCTAC 360

DB 383 GCGAAGACCGTCCAGGATGAGCTGAGGTACCGAGGGATGCGATTCGACCGTGGCTTC 324

QY 361 ATCTCGGCGTACTTCGCGCACCGCATGAGCGGATGAGCGGTGCTCGACGACCC 416

DB 323 GTCTCTCCCTACTTATCATCCGACACCAAGTCCAGAGGTTCGAGTTTGAGAACCC 268

RESULT 2

DR606790

LOCUS

DEFINITION

EST996918 FVG Gibberella moniliformis cDNA clone FVGBQ50, mRNA

sequence.

DR606790

VERSION

DR606790.1 GI:70681438

KEYWORDS

SOURCE

ORGANISM

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 652)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.P., Town, C.D., and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAUR

USDA

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVGBQ50TH

Seq primer: AAT TAA CCC TCA AAG GG.

Location/Qualifiers

1. .652

/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVGBQ50"

/tissue_type="mycelia"

/clone_lib="FVG"

/note="Vector: pBlueScript II SK(+); Site: EcoRI;

Site 2: XhoI; anamorph: Fusarium verticillioides. Mycelia

was collected after growth in liquid GYM medium for 96

hours. Cultures were vacuum filtered and the mycelial mats

were frozen in liquid nitrogen, ground to a powder, and

then added to Trizol Reagent (Invitrogen, Carlsbad, CA) at

approximately 1 g mycelia per 10 ml Trizol. The cDNA was

directionally ligated into the pBlueScript II SK(+) XR

vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 44.2%; Score 185.6; DB 8; Length 652;

Best Local Similarity 67.1%; Pred. No. 1.5e-28;

Matches 279; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

QY 4 AAGACGACGACGCTCGCGGTGACGTTACGACCAACGCGACCGTCTCTCGCCAGGGGCTC 63

DB 98 AAGACCAACGAGTTCGCGGTGACGTTACCAACGCGCTACCGTTCGCGCGGTGCAATC 157

QY 64 GTACGGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGGGC 123

DB 158 TTCTCCGAGACCGTCAAGAACGTTGCGGTGCAACCTATGACCTCCGCGCGGT 217

QY 124 ATCGAAGACCGTTCGAGGCGCTCTCGGGCGCTGCTGAGGAGGAGGATGTCGAG 183

DB 218 ATCCAAGCTGCTGTTGAGGCGGTGTCGAGTTCCTCAGAAGAACAAAGCGTGAATATACC 277

QY 184 ACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240

DB 278 ACCAGCGCTGAGATCGCTCAGTCCGACCATCTCCGCCAACGGTGAATGTCACATCGGC 337

QY 241 GAGCTCATTCGCGAGGCGATGGAACAGGTGCGGAAGAAAGCGGTATCATCGTCGAGGAG 300

DB 338 CAGATGATTGCCAACGCCATGGAAGAGTTCGGAAGGAGGTGTCTATCATCCTCAGAGGAG 397

QY 301 TCCGACACCTTCGCTGAGGCTGAGCTACCGAGGGATGCGCTTCGACAGGGCTAC 360

DB 398 GCGAAGACCGTTCGCGATGAGCTCGAGGTACCGAGGGATGCGATTCGACCGTGGCTTC 457

QY 361 ATCTCGGCGTACTTCGCGCACCGCATGAGCGGATGAGCGGTGCTCGACGACCC 416

DB 458 GTCTCTCCCTACTTATCATCCGACACCAAGTCCAGAGGTTCGAGTTTGAGAACCC 513

RESULT 3

DR606213

LOCUS

DEFINITION

EST996341 FVG Gibberella moniliformis cDNA clone FVGBJ59, mRNA

sequence.

DR606213

VERSION

DR606213.1 GI:70680861

KEYWORDS

SOURCE

ORGANISM

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 696)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.P., Town, C.D., and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAUR

USDA

Utterback, T., Smith, S., Peldhlyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR

1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@nceaur.usda.gov
TIGR sequence name: FVGBU597H
Seq primer: AAT TAA CCC TCA AAG GG.

source

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1. 696
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="PVG8J59"
/tissue_type="mycelia"
/clone_lib="PVC"

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ORIGIN

Query Match	44.2%;	Score 185.6;	DB 8;	Length 696;
Best Local Similarity	67.1%;	Pred. No. 1.5e-28;		
Matches 279;	Conservative 0;	Mismatches 134;	Indels 3;	Gaps 1;
QY	4	AAGACGACGACGATCGCGGTGACGGGTACGACACACCGCGACCGCTTCGCCCCAGCGCGTC	63	
Db	96	AAGACCAACGAGGTTGCGGTGACGGGTACCAACACCGGTACCGTTCTCGCCCGTGCACATC	155	
QY	64	GTAACGAGGGCCTGCGCAACGTCGCCCGCGGTGCCAACCCGATGGCTTCAACGCGCGGC	123	
Db	156	TTCTCCGAGACCGTCAAGAAACGTTGCGCGCTGGCTGCCAACCTATGACCTCCGCGCGCGT	215	
QY	124	ATCGAAGAGCGCTCGAGGCGCTCTCGGCGCCCTGCTGGAGCAGGCGGAGGATGTCGAG	183	
Db	216	ATCCAGCTGCTGTTGAGGCGCGTGGTCGAGTCTCCAGAAAGAACAGCGTGATATTACC	275	
QY	184	ACCAAGSAGCAGATCGCTTCCACGGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC	240	
Db	276	ACCAGCGCTCAGATCGCTCAGGTCGCTACCATCTCCGCCAAGCGTGATGCCACATCGGC	335	
QY	241	GAGTCATCCGAGGCGATGGACAAGGTGGGCAAGGAAGCGTCATCACCGTTCGAGGAG	300	
Db	336	CAGATGATTCCCAACGCGCATGGAGAAGGTGGCAAGGAGGGTGTCATCACCTGCAAGGAG	395	
QY	301	TCCCGACACTTTCGCTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTTCGACAAGGGCTAC	360	
Db	396	GGGAAGACCGTTGCCGATGAGCTCGAGGTCACCGAGGGTATGCGATTGAGTCGACCGTGGCTTC	455	
QY	361	ATTCGGCGTACTTCGCGCACCGACATGGAGCGGATGGAGGGTTCGCTTCGAGGACCC	416	
Db	456	GTCTCCCCCTACTTTCATCACCGCACCAAGTCCCAAGGTCGAGTTGAGAACCC	511	

RESULT 4

DR649351
LOCUS
DEFINITION
918 bp mRNA linear
EST1039468 Pw Gibberella moniliformis cDNA clone FYNAM52, mRNA
sequence.
ACCESSION
DR649351

VERSION
KEYWORDS
SOURCE
ORGANISM

DR649351.1 GI:70737826
EST.
Gibberella moniliformis
Gibberella moniliformis
Eukaryota; Fungi; Ascom
Hypocreomycetidae; Hypo
1 (bases 1 to 918)

REFERENCE AUTHORS

TITLE

**JOURNAL
COMMENT**

Unpublished (2005)
Contact: Brown, D.W.

USDA
USDA/ARS/NCAR
1815 N. University St., Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncar.usda.gov
TIGR sequence name: FVNM52TH
Seq primer: AAT TAA CCG TCA AAG CG.

FEATURES

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1. 918
/location/qualifiers
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FPMAM52"
/tissue_type="mycelia"
/clone_lib="FVN"
/notes=Vhost: pBUEScript II SK(+)
Site_2: XhoI; anamorph: Fusarium ves.
FVN was obtained from RNA derived from
culture of strain M-125. These cultures
inoculating an autoclaved mixture of
ml distilled water with 5 ml of water
condia. The inoculated medium was mixed
distributed equally into two 100-mm
and incubated at room temperature for

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ORIGIN

Query Match	44.2%	Score 185.6;	DB 8;	Length 918;
Best Local Similarity	67.1%;	Pred. No. 1.5e-28;		
Matches 279;	Conservative 0;	Mismatches 134;	Indels 3;	Gaps 1;
QY	4	AAGACGGAGCGACTGCCCGTGCAGGTACGACCAACCGACCGGTCTTCGCCCGAGCGCTC	63	
DB	438	AAGACCAACGAGGTTCCCGTGCAGGTACCAACACCGCTACCGTTCTTCGCCCGTGCACATC	497	
QY	64	GTACCGGAGGGCTGCGCAACGTCGCGCGCGGTGSCCAACCCGATGGCTCTCAAGCGGGCC	123	
DB	498	TTCTCCGAGACCGTCAAGAACGTTGCGCGTGGCTGCAACCCCTATGACCTCCGCGCGGT	557	
QY	124	ATCCAGAACGGCGTCGACGGCGTCTCGGGCGCCCTCTGAGCAGCAGGCGAAGGATGTCCAG	183	
DB	558	ATCCAAGTGTGTTGAGGCGCGTGCAGAGTTCTCTCAGAAGAAACAAGCGTGATTAATACC	617	
QY	184	ACCAAGGAGCAGATCGCTTCCACGGCGCTCCATCTCCGC---	240	
DB	618	ACCAGCGCTGAGATCGCTCAGGTTCGTACCATCTCCGCCAACCGGTGATGCCATCGGC	677	
QY	241	GAGCTCATCCGAGGGGATGGACAAGGTTCGGCAAGGAAGGCGTCAATCACTGCGAGGAG	300	
DB	678	CAGATGATTCCAAACCCATGGAGAAAGGTGCGCAAGGAGGGTGTCTATCACTTCGAAGGAG	737	
QY	301	TCCACGACCTTCGGTCTGAGCTGAGAGCTCACCGAGGTATGCGTTTCGACAAAGGGCTAC	360	
DB	738	GGGAGAGACCTTGCCGATGAGCTCGAGGTCAACGAGGGTATGCGATTCGACCGTGGCTTC	797	
QY	361	ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGCGCTCGCTCGACGACCC	416	
DB	798	GTCTCCCGCTACTTATCATACCGACACCAAGTCCCAAGAGGTCCAGTTGAGAACCC	853	

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RESULT 5
CO977844/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN

CO977844 639 bp mRNA linear EST 11-FEB-2005
BeZSPN11F12 BeZSPN Blastoclastiella emersonii cDNA clone BeZSPN11F12
5' mRNA sequence.
CO977844 1 GI:59296937
EST.
Blastoclastiella emersonii
Blastoclastiella emersonii
Eukaryota; Fungi; Chytridiomycota; Blastocladiiales;
Blastocladiaceae; Blastocladiella.
1 (bases 1 to 639)
Navarro,L.D. and Gomes,S.L.
Gene discovery and expression profile analysis through sequencing
of expressed sequence tags from different developmental stages of
the chytridiomycete Blastoclastiella emersonii
Eukaryotic Cell 4 (2), 455-464 (2005)
Contact: Gomes, Suely Lopes
Department of Biochemistry
Institute of Chemistry, University of Sao Paulo
Av. Prof. Lineu Prestes, 748, Sao Paulo, SP, 05508-900, BRASIL
Tel: (55) 11-30913826
Fax: (55) 11-30912186
Email: sulgomes@ig.usp.br
PCR Primers
FORWARD: T7 universal forward primer
BACKWARD: SP6 universal reverse primer
Plate: 11 row: F column: 12
Seq primer: T7 universal forward primer
High quality sequence stop: 639.
Location/Qualifiers
1..639
/organism="Blastoclastiella emersonii"
/mol_type="mRNA"
/db_xref="taxon:4808"
/clone="BeZSPN11F12"
/sex="Asexual"
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/lab_host="E. coli DH5a cells (ampicillin resistant)"
/clone_lib="BeZSPN"
/notes="vector: pSPOR1; Cloned unidirectionally, 5' end
of the cDNA cloned into SalI / NotI site of pSPOR1.
Primer: Oligo (dT). Average insert size: 1 kb; Superscript
Plasmid system -5' adaptor sequence: 5'CCACGGCTCGG3' -3'
adaptor sequence:
5'GCCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT3'"

Query Match 42.6%; Score 179; DB 7; Length 639;
Best Local Similarity 65.9%; Pred. No. 3.6e-27;
Matches 276; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGTTTCGCGCCAGGCG 60
DB 627 AACAAAGACCAACGAGGTGCGCGGTGACGGTACGACACCGGACCGTTTCGCGCCAG 568
QY 61 CTGTACGCGAGGCGCTTGGCAGACGTGCGCGCGGTGCGACCGGATGGCTCTCAAGCGC 120
DB 567 ATCTTCAACGAGGCGCTTCAAGAACGTTGCGCGCGGTGCGACCGGACCGTTCGCGCGC 508
QY 121 GGCAATCAGAGAGGCGCTTCGAGGCGGTCTCGCGCGCTTCTGAGCAGGCGGAGGATGTC 180
DB 507 GGTGTCAGGTGGCGCTTCGAGCGGTCTGTCAGACACTCAAGAGACACCGCGCATGATC 448
QY 181 GAGACCAAGGACGACGATCGCTTCCACGGCTTCATCTCCGC---CGCCGACACCGACATC 237
DB 447 ACGTGCTCCGAGGAGGTGGCGGTCGCGACCATTTTCGCGCAACCGCGCACGTC 388
QY 238 GCGGAGCTCATCGCCGAGGCGGATGGACAGGTGCGGCAAGGAGCGTTCATCAGCGTCGAG 297

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Db 387 GCGCGCCTGATCGCGCAGGCCCATGAGAGGTTGCGAAGGAGGCGTTCATCAGCGTCCAG 328
QY 298 GAGTCCGACAGACTTCGGTCTGGAGCTGAGCTCACCAGGAGGTATCGCTTCACAGGCGC 357
DB 327 GAGGCGAAGAGCTCGAGGACGAGCTCCAGATTCACGAGGGGATCGCTTTTACCGCGCGC 268
QY 358 TACATCTCGGCTTACTTTCGCCACCGACATGGAGCGATGGAGCGCTCGCTCGACGACCC 416
DB 267 TTCACTCGCCCTACTTTCATCCAGTGTCAAGGCCGAGAGGTTCGATTCGAGAGCC 209

RESULT 6
CF712525
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN

CF712525 690 bp mRNA linear EST 16-AUG-2004
CCAG056TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAG056, mRNA sequence.
CF712525
CF712525.1 GI:41566684
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 690)
Loftus,B.
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCAG056TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.
Location/Qualifiers
1..690
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone_lib="CCAG056"
/notes="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

Query Match 41.3%; Score 173.6; DB 6; Length 690;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGGACCGTTTCGCGCCAGGCGCTC 63
DB 270 AAGACCAACGACACTCGCGGTGACGGTACGACACCGGACCGTTTCGCGCCAGGCGATC 329
QY 64 GTACGCGAGGCGCTTCGCGACGTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123
DB 330 TACTCTGAGGCGTGAAGAACGTCGTCGCGGTGCAACCCCATGACCTTCGTCGAGGT 389
QY 124 ATCGAGAGGCGCTTCGAGGCGGTCTCGCGCGCTTCGTCGAGCAGGCGGAGAGTGTGAG 183
DB 390 GCCAGAGAGGCTTCGACAGGTCTCTCGAGGTCTTCGTCGCAACAAAAGGTTATCACC 449
QY 184 ACCAAGAGAGAGATCGGTTTCACGGGCTTCATCTCCGC---CGCCGACACCGAGATCGGC 240
DB 450 ACCTCTGAGGAGATTGCCAGGTTCGCCACCATCTCGCCCAACCGCGGATACCCACGTCG 509

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QY 241 GAGCTCATCGCGAGCGATGACCAAGTCCGCAAGGAGGCGCTCATCCGTCGAGGAG 300
 Db 510 GCATCATTCGCCAAGCCATGAGCAGGTCCGCAAGGAGGCTGTATCATCTGTTAAGGAG 569
 QY 301 TCCAGACCTTCGCTCTGAGAGTGGAGCTCACCGAGGGTATGCGCTTCGACAAAGGCGTAC 360
 Db 570 GCGCGAACCATTCAGCAGGAGATTGAGATTACCGAGGGTATGCGCTTCGACCAAGGCGTTC 629
 QY 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGCTTCGACGACCGGTAC 420
 Db 630 ATCTCCCTTACCTCATCCGACACCAAGACGAGCGTGTGCGAGCTCGAGAGGCGCTTC 689

RESULT 7
 CF693874
 LOCUS
 DEFINITION
 CCADM43TR C.neofomans strain JEC21 mRNA linear EST 16-AUG-2004
 CF693874
 neofomans cDNA clone CCADM43, mRNA sequence.

ACCESSION
 VERSION
 CF693874.1 GI:41548033
 KEYWORDS
 EST.
 SOURCE
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)

ORGANISM
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE
 1 (bases 1 to 738)

AUTHORS
 Loftus,B.

TITLE
 End sequencing of clones from a Full length enriched, normalized

JOURNAL
 JEC21 cDNA library

COMMENT
 Other ESTs: CCADM43TF
 Contact: Brendan Loftus

The Institute for Genomic Research (TIGR: www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1..738

source

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCADM43"

/clone_lib="C.neofomans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 738;

Best Local Similarity 65.0%; Pred. No. 4.7e-26;

Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGCGGAGCGTCCGCGTACCGGTACGACCGGACCGGTTCGCCCGAGCGGTC 63

Db 318 AAGCAACAGCACTGCGCGTACCGGTACCGACCGCGCACTGCTCGCGCGAGCCATC 377

QY 64 GTACGCGAGGCGTCCGCAACGTCGCGCGGTGCGCAACCGATGCTCTCAAGCGCGC 123

Db 378 TACTCTGAGGGTGTGAGAACGTGCTGCGCGGTGCGCAACCGATGCTCTCGGTGAGGT 437

QY 124 ATCGAGAGGCGGTTCGAGCGCGTCTCGCGCGCGTTCGAGCGGCGGAGGATGTCGAG 183

Db 438 GCCCAGAGGCGTTCGACAAAGTCTCGAGGTTCTTGCTGCGCAACAAAGGTATCACC 497

QY 184 ACCAAGGAGCAGATCGCTTCACAGCGGCTCATCTCCGCGCGCGCGCGCGCGCGCGCG 240

Db 498 ACCTCTGAGGAGATTGCCGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557

QY 241 GAGCTCATCGCGAGCGATGACCAAGTCCGCAAGGAGGCGCTCATCCGTCGAGGAG 300
 Db 558 GCATCATTCGCCAAGCCATGAGCAGGTCCGCAAGGAGGCTGTATCATCTGTTAAGGAG 617
 QY 301 TCCAGACCTTCGCTCTGAGAGTGGAGCTCACCGAGGGTATGCGCTTCGACAAAGGCGTAC 360
 Db 618 GCGCGAACCATTCAGCAGGAGATTGAGATTACCGAGGGTATGCGCTTCGACCAAGGCGTTC 677
 QY 361 ATCTCGGCGTACTTCGCGACCGACATGAGCGGATGAGGCGTTCGCTTCGACGACCGGTAC 420
 Db 678 ATCTCCCTTACCTCATCCGACACCAAGACGAGCGTGTGCGAGCTCGAGAGGCGCTTC 737

RESULT 8

CF718151

LOCUS

DEFINITION

CCAHZ70TR C.neofomans strain JEC21 mRNA linear EST 16-AUG-2004

CF718151

neofomans cDNA clone CCAHZ70, mRNA sequence.

ACCESSION

VERSION

CF718151.1 GI:41572310

KEYWORDS

EST.

SOURCE

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans

var. neoformans)

ORGANISM

Cryptococcus neoformans var. neoformans

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella.

REFERENCE

1 (bases 1 to 741)

AUTHORS

Loftus,B.

TITLE

End sequencing of clones from a Full length enriched, normalized

JOURNAL

JEC21 cDNA library

COMMENT

Other ESTs: CCAHZ70TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR: www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1..741

source

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAHZ70"

/clone_lib="C.neofomans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 741;

Best Local Similarity 65.0%; Pred. No. 4.7e-26;

Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGCGGAGCGTCCGCGTACCGGTACGACCGGACCGGTTCGCCCGAGCGGTC 63

Db 316 AAGCAACAGCACTGCGCGTACCGGTACCGACCGCGCACTGCTCGCGCGAGCCATC 375

QY 64 GTACGCGAGGCGTCCGCAACGTCGCGCGGTGCGCAACCGATGCTCTCAAGCGCGC 123

Db 376 TACTCTGAGGGTGTGAGAACGTGCTGCGCGGTGCGCAACCGATGCTCTCGGTGAGGT 435

QY 124 ATCGAGAGGCGGTTCGAGCGCGTCTCGCGCGCGTTCGAGCGGCGGAGGATGTCGAG 183

Db 436 GCCCAGAGGCGTTCGACAAAGTCTCGAGGTTCTTGCTGCGCAACAAAGGTATCACC 495

QY 184 ACCAAGGAGCAGATCGCTTCACAGCGGCTCATCTCCGCGCGCGCGCGCGCGCGCG 240


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Db      496 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCCAACCGCGGATACCCACGTCGGT 555
QY      241 GAGCTCATCGCCGAGCGATGGACAAGTTCGCAAGGAGGCGCTCATCACCGTCGAGGAG 300
Db      556 GCATCATTTGCCCAAGCCATGGAGCGAGGTGCGCAAGGAGGTGTCTCATCTGTTAAGGAG 615
QY      301 TCCACAGACCTTCGGTCTGGAGCTGCGAGCTCACCGAGGGTATGCGTTTCGACAAAGGGCTAC 360
Db      616 GCGCGAACCATTTGACGACGAGATTGAGATTACCGAGGGTATGCGATTTCGACCGAGGCTTC 675
QY      361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGAGCGGTGCGTTCGACGACCGGTCAC 420
Db      676 ATCTCCCTTACCTCATCACCGACACCAAGAACGAGCGGTGTCGAGCTCGAGAAAGCCCTTC 735

RESULT 9
CF682602 749 bp mRNA linear EST 16-AUG-2004
LOCUS
DEFINITION
CF682602 C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCABP32, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
CF682602.1 GI:41536761
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE
1 (bases 1 to 749)
Loftus,B.
AUTHORS
Loftus,B.
TITLE
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: CCABP32TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES
source
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Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCABP32"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 749;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4 AAGACGACGACGTCGCGGTGACGGTACCAACCGCGGTGCGCAACCGGATGCGTCTCAAGCGCGGC 63
Db      325 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGCGGTGCGTCTCAAGCGCGGCATC 384
QY      64 GTACGCGAGCGCTCGCGGTGACGGTACCAACCGCGGTGCGTCTCAAGCGCGGC 123
Db      385 TACTCTGAGGGTGTGAAGAACGTGCTGCGCGGTGCAACCCCATCGACCTTCGTCGAGGT 444
QY      124 ATCGAGAGGCGGTGCGAGCGGTCTTCGCGCGGTGCGTCTGAGAGCGGCGAAGGATGTCGAG 183
Db      445 GCCCAGAAGGCTGTGCAAGAGTCTTCGAGGTTCTTGTCTGCAACAAAGAGGTTATCACC 504
QY      184 ACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGC---CGCGCACACCCAGATCGGC 240

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Db      505 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCCAACCGCGGATACCCACGTCGGT 564
QY      241 GAGCTCATCGCCGAGCGATGGACAAGTTCGCAAGGAGGCGTCTCATCACCGTCGAGGAG 300
Db      565 GCATCATTTGCCCAAGCCATGGAGCGAGGTGCGCAAGGAGGTGTCTCATCTGTTAAGGAG 624
QY      301 TCCACAGACCTTCGGTCTGGAGCTGCGAGCTCACCGAGGGTATGCGTTTCGACAAAGGGCTAC 360
Db      625 GCGCGAACCATTTGACGACGAGATTGAGATTACCGAGGGTATGCGATTTCGACCGAGGCTTC 684
QY      361 ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGAGCGGTGCGTTCGACGACCGGTCAC 420
Db      685 ATCTCCCTTACCTCATCACCGACACCAAGAACGAGCGGTGTCGAGCTCGAAGAGCCCTTC 744

RESULT 10
CF693560 752 bp mRNA linear EST 16-AUG-2004
LOCUS
DEFINITION
CF693560 C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAGV54, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
CF693560.1 GI:41547719
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE
1 (bases 1 to 752)
Loftus,B.
AUTHORS
Loftus,B.
TITLE
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: CCAGV54TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES
source
1..752
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAGV54"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match 41.3%; Score 173.6; DB 6; Length 752;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4 AAGACGACGACGTCGCGGTGACGGTACCAACCGCGGTGCGTCTCAAGCGCGGC 63
Db      329 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGCGGTGCGTCTCAAGCGCGGCATC 388
QY      64 GTACGCGAGCGCTCGCGGTGACGGTACCAACCGCGGTGCGTCTCAAGCGCGGC 123
Db      389 TACTCTGAGGGTGTGAAGAACGTGCGTTCGCGGTGCAACCCCATCGACCTTCGTCGAGGT 448
QY      124 ATCGAGAGGCGGTGCGAGGCGGTCTTCGCGCGGTGCGTCTGAGAGCGGCGAAGGATGTCGAG 183
Db      449 GCCCAGAAGGCTGTGCAAGAGTCTTCGAGGTTCTTGTCTGCCAACAAAGAGGTTATCACC 508

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Db      445  GCCCAGAGGCTGTGACAGAGTCTCTGAGGTTCTTGCTGCCCAACAAAAGGTTATCACC 504
QY      184  ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
Db      505  ACCTCTGAGGAGATGCGCCAGGTCGCCACCATCTCCGCCAACCGCGGATACCCACGTCGGT 564
QY      241  GAGCTCATCCCGAGGCGATGGACAGGTTCGCAAGGAAGGCGTCATCACCGTCGAGGAG 300
Db      565  GCATCATTCGCCAGCCATGGAGGTCGGCAGGAGGTTGTCATCTGTTAAGGAG 624
QY      301  TCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGTTATCGCTTCGCAAGGGCTAC 360
Db      625  GCGGACCATTCAGCAGCAGATTGAGATTACCGAGGTTATCGATTTCGACCGAGGCTTC 684
QY      361  ATCTCGGCTACTTCGCCACCGCATGGAGCGGATGGAGCGTTCGCTCGAGACCGCTAC 420
Db      685  ATCTCCCTTACCTCATCCGACACCAAGACCGGTCGTGAGCTCGAGAGGCCCTTC 744

RESULT 13
CF722454
LOCUS      766 bp      mRNA      linear      EST 16-AUG-2004
DEFINITION C.n.eoformans strain JEC21 Cryptococcus neoformans var.
ACCESSION CF722454
VERSION    1
KEYWORDS  EST.
SOURCE    Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
          var. neoformans)
ORGANISM  Cryptococcus neoformans var. neoformans
          Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
          Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
          Filobasidiella.
REFERENCE  1 (bases 1 to 766)
AUTHORS   Loftus,B.
TITLE     End sequencing of clones from a Full length enriched, normalized
JOURNAL   JEC21 cDNA library
COMMENT   Unpublished (2003)
          Contact: Brendan Loftus
          The Institute for Genomic Research (TIGR; www.tigr.org)
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-3543
          Fax: 301-838-0208
          Email: bjloftus@tigr.org
          Seq primer: TR.
FEATURES   Location/Qualifiers
            source          1..766
                        /organism="Cryptococcus neoformans var. neoformans"
                        /mol_type="mRNA"
                        /strain="JEC21"
                        /db_xref="taxon:40410"
                        /clone="CCAE270"
                        /clone_lib="C.n.eoformans strain JEC21"
                        /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
                        length, normalized library was prepared from a variety of
                        conditions using RNA provided by Joseph Heitman and
                        Jennifer Lodge"
ORIGIN
Query Match      41.3%; Score 173.6; DB 6; Length 766;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4  AAGACGAGCAGCTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCAGGCGCTC 63
Db      271  AAGACCAACGACACTCGCGGTGACGGTACGACCAACCGGACCGTCTCGCCGAGCCATC 330
QY      64  GTACGCGAGGCGCTCGGCAAGCTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123
Db      331  TACTCTGAGGGGTGAAGAACGTCGCTGCGCGGTGCAACCCCATGGACCTTCGTCGAGGT 390
QY      124  ATCGAGAAGGCGTCGAGGCGGCTCTCCGGCGCCCTGCTGGAGGAGCGGAGGATGTCGAG 183

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Db      391  GCCCAGAGGCTGTGACAGAGTCTCTGAGGTTCTTGCTGCCCAACAAAAGGTTATCACC 450
QY      184  ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
Db      451  ACCTCTGAGGAGATGCGCCAGGTCGCCACCATCTCCGCCAACCGGCGATACCCACGTCGGT 510
QY      241  GAGCTCATCCCGAGGCGATGGACAGGTTCGCAAGGAAGGCGTCATCACCGTCGAGGAG 300
Db      511  GCATCATTCGCCAGCCATGGAGGTCGGCAGGAGGTTGTCATCTGTTAAGGAG 570
QY      301  TCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGTTATCGCTTCGCAAGGGCTAC 360
Db      571  GCGGACCATTCAGCAGCAGATTGAGATTACCGAGGTTATCGATTTCGACCGAGGCTTC 630
QY      361  ATCTCGGCTACTTCGCCACCGCATGGAGCGGATGGAGCGTTCGCTCGAGACCGCTAC 420
Db      631  ATCTCCCTTACCTCATCCGACACCAAGACCGGTCGTGAGCTCGAGAGGCCCTTC 690

RESULT 14
CF710636
LOCUS      767 bp      mRNA      linear      EST 16-AUG-2004
DEFINITION C.n.eoformans strain JEC21 Cryptococcus neoformans var.
ACCESSION CF710636
VERSION    1
KEYWORDS  EST.
SOURCE    Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
          var. neoformans)
ORGANISM  Cryptococcus neoformans var. neoformans
          Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
          Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
          Filobasidiella.
REFERENCE  1 (bases 1 to 767)
AUTHORS   Loftus,B.
TITLE     End sequencing of clones from a Full length enriched, normalized
JOURNAL   JEC21 cDNA library
COMMENT   Unpublished (2003)
          Contact: Brendan Loftus
          The Institute for Genomic Research (TIGR; www.tigr.org)
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-3543
          Fax: 301-838-0208
          Email: bjloftus@tigr.org
          Seq primer: TR.
FEATURES   Location/Qualifiers
            source          1..767
                        /organism="Cryptococcus neoformans var. neoformans"
                        /mol_type="mRNA"
                        /strain="JEC21"
                        /db_xref="taxon:40410"
                        /clone="CCAF87"
                        /clone_lib="C.n.eoformans strain JEC21"
                        /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
                        length, normalized library was prepared from a variety of
                        conditions using RNA provided by Joseph Heitman and
                        Jennifer Lodge"
ORIGIN
Query Match      41.3%; Score 173.6; DB 6; Length 767;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY      4  AAGACGAGCAGCTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCAGGCGCTC 63
Db      331  AAGACCAACGACACTCGCGGTGACGGTACGACCAACCGGACCGTCTCGCCGAGCCATC 390
QY      64  GTACGCGAGGCGCTCGGCAAGCTCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123
Db      391  TACTCTGAGGGGTGAAGAACGTCGCTGCGCGGTGCAACCCCATGGACCTTCGTCGAGGT 450

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QY 124 ATCGAGAGGCCGTCGAGGCGCTCTCGGCGCCCTGCTGGAGCAGCGGAGGATGTCGAG 183
 Db 451 GCCCAGAGGCTGTGCGACAGGCTCTCGAGGTTCTTGTGTCACCAACAAAAGGTTATCACC 510
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 511 ACTCTGAGGAGATGCGCAGGTCGCACATCTCCGCAACGGCATACCCACGTCGGT 570
 QY 241 GAGCTCATCGCCGAGGCGATGGCAAGGTCGGCAAGGAAGGCGTCATCACCCTCGAGGAG 300
 Db 571 GCCATCATTCGCCAAGCCATGGAGCAGGTCGGCAAGGAGGTCATCATCTGTTAAGGAG 630
 QY 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTCGACAGGCGTAC 360
 Db 631 GGCCGAACCATTCGACGAGGATGAGATTACCGAGGATGCGATTTCGACGAGGCTTC 690
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGCGGCTCGACGACCGGTCAC 420
 Db 691 ATCTCCCTTACTCTCATCCGACACCAAGACCGGTCGAGCTCGAGAGGCCCTTC 750

RESULT 15

CF709688 768 bp mRNA linear EST 16-AUG-2004
 LOCUS CCAFP74TR C.neofomans strain JEC21 Cryptococcus neoformans var.
 DEFINITION neoformans cDNA clone CCAFP74, mRNA sequence.

ACCESSION CF709688
 VERSION CF709688.1 GI:41563847
 KEYWORDS EST.

SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 768)

AUTHORS Loftus,B.

TITLE End sequencing of clones from a Full length enriched, normalized

JOURNAL JEC21 cDNA library

COMMENT Unpublished (2003)

Other ESTs: CCAFP74TO

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1..768

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAFP74"

/clone_lib="C.neofomans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 768;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCGTCGCCGGTACGGTACGACCAACCGGACCGTTCCTGCCAGCGCTC 63
 Db 325 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGGACCTGTCTCTGCCCGGAGCCATC 384

QY 64 GTACGCGAGGCGCTCGGCAACGTCGCGCGGTCGCAACCCGATGGCTCTCAAGCGCGC 123
 Db 385 TACTCTGAGGGTGTGAAGAACGTCGCTGCCGCTGCAACCCATGGACCTCGTGAGGT 444

QY 124 ATCGAGAGGCCGTCGAGGCGCTCTCCGCGCCCTGCTGGAGCAGCGGAGGATGTCGAG 183
 Db 445 GCCCAGAGGCTGTGCGACAGGCTCTCGAGGTTCTTGTGTCACCAACAAAAGGTTATCACC 504
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 505 ACCTCTGAGGAGATGCGCCAGGTCGCCACCATCTCCGCAACGGGATACCCACGTCGGT 564
 QY 241 GAGCTCATCGCCGAGGCGATGGCAAGGTCGGCAAGGAAGGCGTCATCACCCTCGAGGAG 300
 Db 565 GCCATCATTCGCCAAGCCATGGAGCAGGTCGGCAAGGAGGTCATCATCTGTTAAGGAG 624
 QY 301 TCCGAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGATGCGCTTCGACAGGCGTAC 360
 Db 625 GGCCGAACCATTCGACGAGGATGAGATTACCGAGGATGCGATTTCGACGAGGCTTC 684
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGCGGCTCGACGACCGGTCAC 420
 Db 685 ATCTCCCTTACTCTCATCCGACACCAAGACCGGTCGAGCTCGAGAGGCCCTTC 744

RESULT 16

CF701856

LOCUS CCAAD54TR C.neofomans strain JEC21

DEFINITION Cryptococcus neoformans var.

ACCESSION CF701856

VERSION CF701856.1 GI:41556015

KEYWORDS EST.

SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

ORGANISM Cryptococcus neoformans var. neoformans

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella.

REFERENCE 1 (bases 1 to 773)

AUTHORS Loftus,B.

TITLE End sequencing of clones from a Full length enriched, normalized

JOURNAL JEC21 cDNA library

COMMENT Unpublished (2003)

Other ESTs: CCAAD54TP

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1..773

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAAD54"

/clone_lib="C.neofomans strain JEC21"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

FEATURES

source

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 773;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCGTCGCCGGTACGGTACGACCAACCGGACCGTTCCTGCCAGCGCTC 63
 Db 322 AAGACCAACGACACTGCGCGGTGACGGTACCAACCGGACCTGTCTCTGCCCGGAGCCATC 381

QY 64 GTACGCGAGGCGCTCGGCAACGTCGCCCGCGGTGCAACCCGATGGCTCTCAAGCGCGGC 123
 Db 64 GTACGCGAGGCGCTCGGCAACGTCGCCCGCGGTGCAACCCGATGGCTCTCAAGCGCGGC 123

Db 382 TACTCTGAGGCTGTGAAGAACGTCGCTGCGGCTGCACCCCATGAGACCTCCGTCGAGGT 441
 QY 124 ATCGAGAGCCGCTCGAGGCCGCTCTCGGCGCCCTGCTGAGCAGCGGAGGATGTCGAG 183
 Db 442 GCCCAGAGGCTGTGCAAGAGGCTCTGAGGCTTCTGCTCCCAACAAAAGGTTATCACC 501
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 502 ACCTCTGAGAGATTGCCAGGTGCGCACCATCTCCGCCAACGGCGATACCCAGCTCGGT 561
 QY 241 GAGCTCATCCCGAGGCGATGGAACAAGTTCGCAAGGAAGCGCTCATCACCGTCGAGGAG 300
 Db 562 GCCATCATTCGCCAAGCCATGAGCAGGTTCGCAAGGAGGTTGTCATCACTGTTAAGGAG 621
 QY 301 TCCGAGACCTTCGCTGAGCTGAGCTCACCGAGGTATGCGTTCGCAAGAGGCTAC 360
 Db 622 GGCCGACACCATTCGACGACGAGATTGAGATTACCGAGGTTATCGATTCCGACCGAGGCTTC 681
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
 Db 682 ATCTCCCTTACCTCATCCGACACCCAGACCGGTCGAGCTCGAGAACCCCTTC 741

RESULT 17

CF702480
 LOCUS
 DEFINITION CAA550TR C.neoformans strain JEC21 Cryptococcus neoformans var.
 neoformans cDNA clone CAA550, mRNA sequence.

ACCESSION
 VERSION CF702480.1 GI:41556639

KEYWORDS

SOURCE

EST.
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)

ORGANISM

Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella

REFERENCE

Loftus,B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAA550TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

FEATURES

source

1. .776
 /location="Qualifiers
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CAA550"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 776;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCTGCGCGGTGACGGTACGACACCGGACCGTTCGCGCCGAGCGCTC 63
 Db 323 AAGACCAACGACACTGCGCGGTGACGGTACGACACCGGACCGTTCGCGCCGAGCCATC 382
 QY 64 GTACGCGAGGCGCTGCGCAACGTCGCGCGGTGACCGACCGGCTCTTCAGCGCGGC 123

Db 383 TACTCTGAGGCTGTGAAGAACGTCGCTGCGGCTGCACCCCATGAGACCTCCGTCGAGGT 442
 QY 124 ATCGAGAGCCGCTCGAGGCCGCTCTCGGCGCCCTGCTGAGCAGCGGAGGATGTCGAG 183
 Db 443 GCCCAGAGGCTGTGCAAGAGGCTCTGAGGCTTCTGCTCCCAACAAAAGGTTATCACC 502
 QY 184 ACCAAGGAGCAGATCGCTTCCAGGGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 503 ACCTCTGAGAGATTGCCAGGTGCGCACCATCTCCGCCAACGGCGATACCCAGCTCGGT 562
 QY 241 GAGCTCATCCCGAGGCGATGGAACAAGTTCGCAAGGAAGCGGTTCATCACCGTCGAGGAG 300
 Db 563 GCCATCATTCGCCAAGCCATGAGCAGGTTCGCAAGGAGGTTGTCATCACTGTTAAGGAG 622
 QY 301 TCCGAGACCTTCGCTGAGCTGAGCTCACCGAGGTATGCGTTCGCAAGAGGCTAC 360
 Db 623 GGCCGACACCATTCGACGACGAGATTGAGATTACCGAGGTTATCGATTCCGACCGAGGCTTC 682
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
 Db 683 ATCTCCCTTACCTCATCCGACACCCAGACCGGTCGAGCTCGAGAACCCCTTC 742

RESULT 18

CF681781

LOCUS

DEFINITION

CF681781

ACCESSION

VERSION

KEYWORDS

SOURCE

EST.

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)

Cryptococcus neoformans var. neoformans

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella

Loftus,B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAHW22TP

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .778

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CAHW22"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 778;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGAGCAGCTGCGCGGTGACGGTACGACACCGGACCGTTCGCGCCGAGCGCTC 63
 Db 287 AAGACCAACGACACTGCGCGGTGACGGTACGACACCGGACCGTTCGCGCCGAGCCATC 346

QY 64 GTACGAGGCGCTCGCAGCTCGCGCGCGTGCACACCCGATGCTCTCAAGCGCGC 123
 Db 347 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGCTGCACACCCATGACCTCCGTCAGGT 406
 QY 124 ATCGAGAGGCGCTCGAGGCGCTCTCGGCGCGCTCTGTCGAGCAGGCGAGGATGCGAG 183
 Db 407 GCCAGAGGCTGTGCAAGGTCCTCGAGGTCCTGTCGCAACAAAAGGTTATCACC 466
 QY 184 ACCAAGAGCAGATCGTTCCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 467 ACCTCTGAGGAGATTGCCAGGTCGCCACCATCTCCGCCAACAGCGCATACCCACGTCGT 526
 QY 241 GAGCTCATCGCCGAGGATGACAGGTCGCAAGAGGTCGCAAGAGGTCATCAGCTCGAGGAG 300
 Db 527 GCCATCATTTGCCCAAGCCATGAGAGCGGTGCGCAAGGAGGTTGTCATCATCTGTTAAGGAG 586
 QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCAGCGGCTATGCTTTCGACAGGCGCTAC 360
 Db 587 GGCGAACCATTGACAGCAGATTGAGATTACGAGGTTATGCGATTTCGACGAGGCTTC 646
 QY 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCGCTAC 420
 Db 647 ATCTCCCTTACTCTATCATCCGACACCAAGACCGGTCGAGCTCGAGAGCCCTTC 706

RESULT 19
 CF695095 779 bp mRNA linear EST 16-AUG-2004
 LOCUS CCACS96TR C. neoformans strain JEC21 Cryptococcus neoformans var.
 DEFINITION neoformans cDNA clone CCACS96, mRNA sequence.
 ACCESSION CF695095
 VERSION CF695095.1 GI:41549254
 KEYWORDS EST.
 SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)

ORGANISM
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 779)
 Loftus, B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 JOURNAL JEC21 CDNA library
 COMMENT Unpublished (2003)
 CONTACT: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 Location/Qualifiers
 1..779
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCACS96"
 /clone_lib="C. neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 779;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
 QY 4 AAGACGAGCAGCTCGCGGTGACGGTACGACACCGACCGTCTCGCCAGCGGTC 63
 Db 329 AAGACAAACGACTCGCGGTGACGGTACGACACCGACCGTCTCGCCGAGCCATC 388

QY 64 GTACGAGGCGCTCGCAGCAACCTGCGCGCGTGCACACCCGATGCTCTCAAGCGCGC 123
 Db 389 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGCTGCACACCCATGACCTCCGTCAGGT 448
 QY 124 ATCGAGAGGCGCTCGAGGCGCTCTCGGCGCGCTCTGTCGAGCAGGCGAGGATGTCGAG 183
 Db 449 GCCAGAGGCTGTGCAAGGTCCTCGAGGTCCTGTCGCAACAAAAGGTTATCACC 508
 QY 184 ACCAAGAGCAGATCGTTCCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 Db 509 ACCTCTGAGGAGATTGCCAGGTCGCCACCATCTCCGCCAACGCGCATACCCACGTCGT 568
 QY 241 GAGCTCATCGCCGAGGATGACAGGTCGCAAGAGGTCGCAAGAGGTCATCAGCTCGAGGAG 300
 Db 569 GCCATCATTTGCCCAAGCCATGAGAGCGGTGCGCAAGGAGGTTGTCATCATCTGTTAAGGAG 628
 QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCAGCGGCTATGCTTTCGACAGGCGCTAC 360
 Db 629 GGCGAACCATTGACAGCAGATTGAGATTACGAGGTTATGCGATTTCGACGAGGCTTC 688
 QY 361 ATCTCGGCGTACTTTCGCCACCGACATGAGCGGATGAGCGGCTCGCTCGACGACCGCTAC 420
 Db 689 ATCTCCCTTACTCTATCATCCGACACCAAGACCGGTCGAGCTCGAGAGCCCTTC 748

RESULT 20
 CF694632 790 bp mRNA linear EST 16-AUG-2004
 LOCUS CCAGK96TR C. neoformans strain JEC21 Cryptococcus neoformans var.
 DEFINITION neoformans cDNA clone CCAGK96, mRNA sequence.
 ACCESSION CF694632
 VERSION CF694632.1 GI:41548791
 KEYWORDS EST.
 SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)

ORGANISM
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 790)
 Loftus, B.
 End sequencing of clones from a Full length enriched, normalized
 JEC21 cDNA library
 JOURNAL JEC21 CDNA library
 COMMENT Unpublished (2003)
 CONTACT: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org
 Seq primer: TR.

FEATURES
 Location/Qualifiers
 1..790
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCAGK96"
 /clone_lib="C. neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

ORIGIN
 Query Match 41.3%; Score 173.6; DB 6; Length 790;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
 QY 4 AAGACGAGCAGCTCGCGGTGACGGTACGACACCGACCGTCTCGCCAGCGGTC 63
 Db 325 AAGACAAACGACTCGCGGTGACGGTACGACACCGACCGTCTCGCCGAGCCATC 384

Qy	4	AAGA	CGGACGACGCTCGCCGGTGA	CGGTACGACCAACCGCGACCGTTCTCGCCACGAGCGCTC	63
Db	237	AAGACCAACGACAC	TGCGCGGTGACGAGTACCA	CCACCGCACCTGCTCGCCCGAGGCATC	296
Qy	64	GTACGCGAGGCGCTCGGCAC	AGTCGCGCGCGGTGCCAACCGATCGCTCTCAAGCGCGGC	123	
Db	297	TACTCTGAGGGTGTGA	AGACGTCGCTCGCGGTGCCAACCCCATGACCTTCGTCGAGGT	356	
Qy	124	ATCGAGAAGGCGCTCGAGGCG	CGCTCTCGCGCGCCCTGCTGGAGCAGCGCAAGGATGTCGAG	183	
Db	357	GCCCAGAAGGCTGTGCA	CAAGTCTCTCGAGGTCTTGCTGCCAACAAAGGTATTACCC	416	
Qy	184	ACCAAGGAGCGATCGCTTC	CACGGGCTTCATCTCCGC---CGCGCACACCCAGATCGGC	240	
Db	417	ACCTCTGAGGAGATTG	CGCCAGGTGCGCCACCATCTCGCGCAACGGCGATACCCACGTCGGT	476	
Qy	241	GAGCTCATCGCCGAGGCGAT	GGACAAGTTCGCGCAAGGAAGCGTCA	TACCCCTTCGAGGAG	300
Db	477	GCCATCATTTGCCCAAGCC	ATGGACGAGTTCGGCAAGGAGGGTGT	CATCACTGTTAAGGAG	536
Qy	301	TCCCAGACCTTCGGTCTG	AGCTCGAGCTTCACCCGAGGCTATGCGCTTCGACAAGGCGCTAC	360	
Db	537	GGCCGACCAATTGACG	ACGAGATTGAGATTACCGAGGGTATGCGATTTCGACGAGGCTTC	596	
Qy	361	ATCTCGGCGTATCTTCG	CCACCGCATGGAGCGGATGGAGGGCGT	CGCTCGACGCCGTAC	420
Db	597	ATCTCCCTCTACCTCAT	CAACCGACCAAGAAACGAGCGTGTG	CGAGTTCGAGAAGGCCCTTC	656

RESULT 24	
CF713651	
LOCUS	803 bp mRNA linear EST 16-AUG-2004
DEFINITION	CCAHP05TR C. neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAHP05, mRNA sequence.
ACCESSION	CF713651
VERSION	CF713651.1
KEYWORDS	GI:41567810
SOURCE	EST.
ORGANISM	Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
REFERENCE	Cryptococcus neoformans var. neoformans
AUTHORS	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
TITLE	1 (bases 1 to 803)
JOURNAL	Loftus, B.
COMMENT	End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library
	Unpublished (2003)
	Other ESTs: CCAHP05TF
	Contact: Brendan Loftus
	The Institute for Genomic Research (TIGR; www.tigr.org)
	9712 Medical Center Drive, Rockville, MD 20850, USA
	Tel: 301-838-3543
	Fax: 301-838-0208
	Email: bjloftus@tigr.org
	Seq primer: TR.

```

FEATURES             source
Seq Primer: taxon    Location/Qualifiers
1..803
   /organism="Cryptococcus neoformans var. neoformans"
   /mol_type="mRNA"
   /strain="JEC21"
   /db_xref="taxon:40410"
   /clone="CCAHP05"
   /clone_lib="C.neoformans strain JEC21"
   /note="Vector: pCMVSPORT6; Site: NotI EcoRV; The
length, normalized library was prepared from a vari
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

```

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 803;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGCGGACGAGCTCGCCGGTGACGGTACGACACCGCGACCGTTCTTCGCCCGAGGCGCTC 63
 DB 265 AAGACCAACGACACTCGCCGGTGACGGTACCAACACCGCCCACTGTCTTCGCCCGAGCCATC 324
 QY 64 GTACGCGAGGCGCTCGCCAAAGCTCGCCCGCGTGCCAAACCGCATGGCTCTCAAGCGCGGC 123
 DB 325 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGCTGCAACCCCATGGACCTCCGTCGAGGT 384
 QY 124 ATCGAAGGCGCGTCGAGGCGGCTTCGCGGCGCCCTGCTGAGCAGCGGGAAGATGTGAG 183
 DB 385 GCCCAGAAGGCTGTGCAACAAGGCTCTCGAGGTTCTTGCTGCCAACAACAAAGGTTATCACC 444
 QY 184 ACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 DB 445 ACCTCTGAGGAGATTGCCAGGTCGCCACCATCTCCGCCAACCGCGCATACCCACGTCGT 504
 QY 241 GAGCTCATCGCCGAGGCGATGGACAGGTCGGCAAGGAGCGCTCATCACCGTCGAGGAG 300
 DB 505 GCATCATTTGCCNAGCATGAGCAGTGGCNAAGAGGGTGTCTCATCTGTTAAGGAG 564
 QY 301 TCCGAGACCTTCGCTCGAGCTGGAGCTCACCGAGGGTATGCGTTTCGACAAGGGCTAC 360
 DB 565 GGCCGAACCATTCGACGACGAGATTGAGATTACCGAGGGTATGCGATTTCGACCGAGGCTTC 624
 QY 361 ATCTCGCGCTACTTCGCCACGACATGAGGGATGAGCGGTCGCTTCGACGACCCGCTAC 420
 DB 625 ATCTCCCTTTACCTCATCCGACACCAAGAACAGCGGTTCGAGCTCGAAGAGCCCTTC 684

RESULT 25

CF711476
 LOCUS
 DEFINITION C.n. neoformans strain JEC21 Cryptococcus neoformans var.
 neoformans cDNA clone CCAHX08, mRNA sequence.

ACCESSION
 VERSION CF711476.1 GI:41565635

KEYWORDS
 SOURCE EST.

ORGANISM
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE
 1 (bases 1 to 804)

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .804

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAAX08"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 804;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGCGGACGAGCTCGCCGGTGACGGTACGACACCGCGACCGTTCTTCGCCCGAGGCGCTC 63
 DB 333 AAGACCAACGACACTCGCCGGTGACGGTACCAACACCGCCCACTGTCTTCGCCCGAGCCATC 392
 QY 64 GTACGCGAGGCGCTCGCCAAAGCTCGCCCGCGTGCCAAACCGCATGGCTCTCAAGCGCGGC 123
 DB 393 TACTCTGAGGGTGTGAAGAACGTCGTCGCGGCTGCAACCCCATGGACCTCCGTCGAGGT 452
 QY 124 ATCGAAGGCGCGTCGAGGCGGCTTCGCGGCGCCCTGCTGAGCAGCGGGAAGATGTGAG 183
 DB 453 GCCCAGAAGGCTGTGCAACAAGGTCCTCGAGGTTCTTGCTGCCAACAACAAAGGTTATCACC 512
 QY 184 ACCAAGGACGATCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
 DB 513 ACCTCTGAGGAGATTGCCAGGTCGCCACCATCTCCGCCAACCGCGCATACCCACGTCGT 572
 QY 241 GAGCTCATCGCCGAGGCGATGGACAAAGTTCGGCAAGGAGCGCTCATCACCGTCGAGGAG 300
 DB 573 GCATCATTTGCCNAGCATGAGCAGTGGCNAAGAGGGTGTCTCATCTGTTAAGGAG 632
 QY 301 TCCGAGACCTTCGCTCGAGCTGGAGCTCACCGAGGGTATGCGTTTCGACAAGGGCTAC 360
 DB 633 GGCCGAACCATTCGACGACGAGATTGAGATTACCGAGGGTATGCGATTTCGACCGAGGCTTC 692
 QY 361 ATCTCGCGCTACTTCGCCACGACATGAGGGATGAGCGGTCGCTTCGACGACCCGCTAC 420
 DB 693 ATCTCCCTTTACCTCATCCGACACCAAGAACAGCGGTTCGAGCTCGAAGAGCCCTTC 752

RESULT 26

CF703324
 LOCUS
 DEFINITION C.n. neoformans strain JEC21 Cryptococcus neoformans var.
 neoformans cDNA clone CCAHU57, mRNA sequence.

ACCESSION
 VERSION CF703324.1 GI:41557483

KEYWORDS
 SOURCE EST.

ORGANISM
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)

Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE
 1 (bases 1 to 815)

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAHU57TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .815

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone="CCAHU57"

/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 815;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;

Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGAGCGAGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 63
DB 321 AAGACCAACGACACTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 380
QY 64 GTACGAGGCGGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 123
DB 381 TACTCTGAGGGTGTGAAGAACGTCGCTGCGGTGACACCGCGACCGTCTTCGCCCGGCGCTC 440
QY 124 ATGACGAGGCGGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 183
DB 441 GCCAGAGGCTGTGACGAGGCTCTCGAGGTTCTTCGCCCGGCGACCAAAAGGTATACCC 500
QY 184 ACCAGGAGCGAGTCTTCGCCCGGCTCTCGAGGTTCTTCGCCCGGCGACCAAAAGGTATACCC 240
DB 501 ACCTCTGAGGAGTTCGCCCGGCTCTCGAGGTTCTTCGCCCGGCGACCAAAAGGTATACCC 560
QY 241 GAGCTCATCGCGAGGCGATGACGAGGTCGCGAGGAGGCGTCTTCGCCCGGCGACCAAAAGGTATACCC 300
DB 561 GCCATCATTCGCCCGGAGTTCGCCCGGAGGTCGCGAGGAGGCGTCTTCGCCCGGCGACCAAAAGGTATACCC 620
QY 301 TCCGAGACCTTCGCGAGGTCGAGCTCAGCGGCTTCGCCCGGAGGTCGAGGAGGCTTAC 360
DB 621 GCGCGAACCATTCGACGAGGATTCGAGGATTCGCGAGGAGGTCGAGGAGGCTTAC 680
QY 361 ATCTCGGCTACTTCGCCCGGAGTTCGCCCGGAGGTCGAGGAGGCTTACGCCAGGCGCTTAC 420
DB 681 ATCTCCCTTACTTCATCCGAGGATTCGCCCGGAGGTCGAGGAGGCTTACGCCAGGCGCTTAC 740

RESULT 27
CF699756 820 bp mRNA linear EST 16-AUG-2004
LOCUS CCA745STR C. neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCA745, mRNA sequence.
ACCESSION CF699756
VERSION CF699756.1 GI:41553915
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 820)
Loftus, B.
AUTHORS End sequencing of clones from a Full length enriched, normalized
TITLE JEC21 cDNA library
JOURNAL JEC21 cDNA library
COMMENT Other ESTs: CCA745TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.
Location/Qualifiers
1..820
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCA745"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 820;

Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGAGCGAGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 63
DB 329 AAGACCAACGACACTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 388
QY 64 GTACGAGGCGGCTCGCGGTGACGGTACGACACCGCGACCGTCTTCGCCCGGCGCTC 123
DB 389 TACTCTGAGGGTGTGAAGAACGTCGCTGCGGTGACACCGCGACCGTCTTCGCCCGGCGCTC 448
QY 124 ATGACGAGGCGGCTCGAGGCGCTTCGCCCGGCGCTTCGCCCGGCGACCAAAAGGTATACCC 183
DB 449 GCCAGAGGCTGTGACGAGGTCCTCGAGGTTCTTCGCCCGGCGACCAAAAGGTATACCC 508
QY 184 ACCAGGAGCGAGTCTTCGCCCGGCTCTCGAGGTTCTTCGCCCGGCGACCAAAAGGTATACCC 240
DB 509 ACCTCTGAGGAGTTCGCCCGGCTCTCGAGGTTCTTCGCCCGGCGACCAAAAGGTATACCC 568
QY 241 GAGCTCATCGCGAGGCGATGACGAGGTCGCGAGGAGGCGTCTTCGCCCGGCGACCAAAAGGTATACCC 300
DB 569 GCCATCATTCGCCCGGAGTTCGCCCGGAGGTCGCGAGGAGGCGTCTTCGCCCGGCGCTTAC 628
QY 301 TCCGAGACCTTCGCGTTCGAGCTCAGCGGCTTCGCCCGGAGGTCGAGGAGGCTTAC 360
DB 629 GCGCGAACCATTCGACGAGGATTCGAGGATTCGCGAGGAGGTCGAGGAGGCTTAC 688
QY 361 ATCTCGGCTACTTCGCCCGGAGTTCGCCCGGAGGTCGAGGAGGCTTACGCCAGGCGCTTAC 420
DB 689 ATCTCCCTTACTTCATCCGAGGATTCGCCCGGAGGTCGAGGAGGCTTACGCCAGGCGCTTAC 748

RESULT 28
CF687348 827 bp mRNA linear EST 16-AUG-2004
LOCUS CCA6060TR C. neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION neoformans cDNA clone CCA6060, mRNA sequence.
ACCESSION CF687348
VERSION CF687348.1 GI:41541507
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 827)
Loftus, B.
AUTHORS End sequencing of clones from a Full length enriched, normalized
TITLE JEC21 cDNA library
JOURNAL JEC21 cDNA library
COMMENT Other ESTs: CCA6060TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.
Location/Qualifiers
1..827
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCA6060"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match	41.3%	Score 173.6	DB 6	Length 827
Best Local Similarity	65.0%	Pred. No. 4.7e-26		
Matches 273	Conservative 0	Mismatches 144	Indels 3	Gaps 1
Qy	4	AAGACGACGACGTCGCGGTGACGGTACGACACACCGCGACCGGTTCTCGCCCGAGGCGCTC	63	
Db	264	AAGACCMACGACACTGCGCGGTGACGGTACACCAACCGCCACTGTCTTCGCCCGAGCCATC	323	
Qy	64	GTACGCGAGGGCCTGCGCAACGTCGCGCGCGGTGCCAACCCGATGGCTCTCAAGCGCGGC	123	
Db	324	TACTCTGAGGGTGTGAAGAACGTCGCTCGCGGTGCAACCCATGGACCTCCGTCGAGGT	383	
Qy	124	ATCGAGNAGCGCGTCGAGGGCGGTCTCGCGCGCCCTGCTGAGGACGAGGAGGATGTCGAG	183	
Db	384	GCCACGAAGGCTGTGCAAGAAGGTCCTCGAGGTTCTTGCTGCAACAAAAAGGTTATCACC	443	
Qy	184	ACCAAGGAGCAGATCGCTTCCAGCGGCTTCATCTCTCCGC--CGCGGACACCCAGATCGGC	240	
Db	444	ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCCAACGGCGATACCCACGTCGGT	503	
Qy	241	GAGCTATCCCGAGGGCGATGZCAAGTTCGGCGAAGGAGCGGTATCATCCGTGCGAGGAG	300	
Db	504	GCCATCATTTGCCCAAGCCNTGAGACAGGTGGGCAAGGAGGGTGTCACTACTGTTAAGGAG	563	
Qy	301	TCCACAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGGTATGCGCTTTCGACAAGGGCTAC	360	
Db	564	GSCCGACCATTGACGACGAGATTGAGATTACCGAGGGTATGCGATTTCGACCGAGGCTTC	623	
Qy	361	ATCTCGCGGTACTTTGCGCAACGACATCGAGCGGATGAGGGGTCGTCTGACGACCCGTAC	420	
Db	624	ATCTCCCTTTACTCTCATCAGCGACCAAGAACCAAGCGGTGTGCGAGCTCGAAGACCCCTTC	683	

RESULT 29
CF713573
LOCUS
DEFINITION
CF713573 831 bp mRNA linear EST 16-AUG-2004
CCAF558TR C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAF558. mRNA sequence.

ACCESSION	CF713573
VERSION	CF713573.1
KEYWORDS	GI:41567732 EST.
SOURCE	Cryptococcus neoformans var. neoformans (Filobasidiella neoformans)

ORGANISM
var. neoformans)
Cryptococcus neoformans var. *neoformans*
Eukaryota; Fungi; Basidiomycota; Hymenomyces;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Pilobasidium

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 831)	Loftus, B.	End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library

JOURNAL COMMENT
Unpublished (2003)
Other_ESTs: CCAP558TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

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FEATURES
source
Location/Qualifiers
1..831
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mrna"
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/strain="JEC21"  
/db_xref="taxon:40410"  
/clone="CCAF58"  
/clone_lib="C. neoformans strain JEC21"  
/seq_type="contigs" size 1 Nety pccbv. mba full
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ORIGIN

/nucleo-vector: pucmvsppico; site:1; nctt_200av; the full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

Query Match	41.3%;	Score 173.6;	DB 6;	Length 831;
Best Local Similarity	65.0%;	Pred. No. 4,7e-26;		
Matches 273;	Conservative 0;	Mismatches 144;	Indels 3;	Gaps 1;
QY	4	AAGACGGACGACGTCCGCGGTGACGGTAGACACACCGCGACCGGTTCCTCGCCACGAGGCGCTC	63	
DB	238	AGAGCCAAACGACACTGCCGTTGACGGTATACCAACCGCCACTGTCTCGCCCGAGCCATC	297	
QY	64	GTACGGGAGGGCTGGCGAAAGTTCGGCGCGCGGTGCCAACCCGATGGCTCTCAAGCGCGC	123	
DB	298	TACTCTGAGGGGTGTGAAGAACCTGCGTGC CGGTGCAACCCCATGGACCTTCGCTCGAGGT	357	
QY	124	ATCGAAGGCGGTTCGAGGCGGTCTCCGGCGCCCTCTCTGGAGCAGCGCGAAGGATGTCGAG	183	
DB	358	GCCACGAAGGCTGTGCAACAGGTCTCGAGGTCTTGTCTGCCAAACAAAAGGTATATACC	417	
QY	184	ACGAGGACGAGTCCGTTCCAGGCGCTCCATCTCGC-- --GC CGCACACCCAGATCGGC	240	
DB	418	ACCTCTGAGGAGANTGCCAGGTGCGCACATCTCCGCCAACGGCGATATCCACGTCGGT	477	
QY	241	GAGCTCATCCGAGGCGGATGGCAAGGTCGGCAAGGAGGGGTCTATCAACCGTCGAGGAG	300	
DB	478	GCCATCATTTGCCAAGCCATGAGCAGGTGCGGCAAGGAGGGTGTCTATCATCTGTTAAGGAG	537	
QY	301	TCCACAGACCTTCGGTCTGAGCTTGGAGCTCACCGAGGGTATGGCTTTCGACAAAGGCGTAC	360	
DB	538	GGCCGAACATTGACGACGAGATTGAGATTACGAGGGGTATGCGAATTCGACCGAGGCTTC	597	
QY	361	ATCTCGGCGTACTTTCGCCACCGACATGGAGCGGATGGAGGCGTTCGTCGACGACCCGTCAC	420	
DB	598	ATCTCCCTTACTCTCATACCGACACAAGAAACGACGTGTCCAGTTCGAGTTCGAGAAGCCCTTC	657	

RESULT 30	CF701087	833 bp	linear	EST 16-AUG-2004
LOCUS	CF701087			
DEFINITION	CCAFB06PR C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans CDNA clone CCAFB06, mRNA sequence.			

ACCESSION	CF701087
VERSION	CF701087.1
KEYWORDS	GI:4155246
SOURCE	Cryptococcus neoformans var. neoformans (Filobasidiella neoformans EST.)

ORGANISM
var. *neoformans*)
Cryptococcus neoformans var. *neoformans*
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Pilobasidiella

REFERENCE	1 (bases 1 to 833)
AUTHORS	Loftus B.
TITLE	End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library

JOURNAL COMMENT
Unpublished (2003)
Other_ESTs: CCAPB06TO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
Washington, DC 20060 USA

9112 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

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FEATURES             Location/Qualifiers
     source            1..833
                        /organism="Cryptococcus neoformans var. neoformans"
                        /mol_type="mRNA"

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/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAFB06"
/clone_lib="C.neoformans strain JEC21"
/contig_vector.ncmvsport6.Site.1.Nori.ECBPV.The.full

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length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 833;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGGAGCGCTCGCGGTGACGGTACGACACCGGACCGTTCCTCGCCAGGCGCTC 63
 DB 332 AAGACCAACGACACTCGCGGTGACGGTACGACACCGGACCGTTCCTCGCCAGGCGCTC 391
 QY 64 GTACGCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCCTCGCCAGGCGCTC 123
 DB 392 TACTCTGAGGGTGTGAAGACGTCGCTGCGGTGCAACCCATGACCTTCGTCGAGT 451
 QY 124 ATGAGAGGCGCTCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCCTCGCCAGGCGCTC 183
 DB 452 GCCCAGAGGCGCTCGAGGCGCTCGCGGTGACGGTACGACACCGGACCGTTCCTCGCCAGGCGCTC 511
 QY 184 ACCAAGGAGCGATCGCTTCACGGCTCCATCTCCG---CGCCGACACCGGACCGTTC 240
 DB 512 ACCTCTGAGGAGATTCGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 571
 QY 241 GAGCTCATCGCGAGCGGATGACAGGTGCGGCAAGAGGCGTTCATCAACCGTTCGAGGAG 300
 DB 572 GCATCATTCGCGAGCGGATGACAGGTGCGGCAAGAGGCGTTCATCAACCGTTCGAGGAG 631
 QY 301 TCCAGACCTTCGCTGAGGCTGAGGCTACCGAGGCTATCGCTTCGACAGGCGCTAC 360
 DB 632 GCGCGAAGCAATTCGACGAGGATTCGAGTTCGAGGCTATCGGATTCGACGAGGCTTC 691
 QY 361 ATCTCGGCTTCTCGCAGCGGATTCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 420
 DB 692 ATCTCCCTTACCTCATCCGACACCAAGAGGCGGTGCGAGTTCGAGGCGGCTTC 751

RESULT 31

CF696500 834 bp mRNA linear EST 16-AUG-2004
 CCADB87TR C.neoformans strain JEC21 Cryptococcus neoformans var.
 neoformans cDNA clone CCADB87, mRNA sequence.

ACCESSION CF696500
 VERSION
 KEYWORDS
 SOURCE EST. GI:41550659

ORGANISM Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 834)

AUTHORS Loftus, B.
 TITLE End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library
 JOURNAL Unpublished (2003)
 COMMENT Other_ESTS: CCADB87TF
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org

Seq primer: TR.
 Location/Qualifiers
 1. .834

FEATURES

source
 1. .834
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCADB87"
 /clone_lib="C.neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site_1: NotI EcorV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and

Jennifer Lodge

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 834;
 Best Local Similarity 65.0%; Pred. No. 4.7e-26;
 Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGGAGCGCTCGCGGTGACGGTACGACACCGGACCGTTCCTCGCCAGGCGCTC 63
 DB 325 AAGACCAACGACACTCGCGGTGACGGTACGACACCGGACCGTTCCTCGCCAGGCGCTC 384
 QY 64 GTACGCGAGGCGCTCGGCAACGTCGCGCGCGGTGCAACCCGATGGCTTCGAGCGCGC 123
 DB 385 TACTCTGAGGGTGTGAAGACGTCGCTGCGGTGCAACCCGATGGACCTTCGTCGAGT 444
 QY 124 ATGAGAGGCGCTCGAGGCGCTTCGCGCGCGCTGCGGAGCGGACGAGGATTCGAG 183
 DB 445 GCCCAGAGGCTTCGACAGGCTTCGAGGCTTCGTCGCCAACAAAAGGTTATCACC 504
 QY 184 ACCAAGGAGCGATCGCTTCACCGCTTCATCTCCG---CGCCGACACCGGACCGTTC 240
 DB 505 ACCTCTGAGGAGATTCGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 564
 QY 241 GAGCTCATCGCGAGGCGATGACAGGTGCGGCAAGAGGCGTTCATCAACCGTTCGAGGAG 300
 DB 565 GCCATCATTCGCGAGGCGATGACAGGTGCGGCAAGAGGCGTTCATCACTGTTAAGGAG 624
 QY 301 TCCCAGAGCTTCGCTGAGGCTGAGGCTACCGAGGCTATCGCTTCGACAAAGGCTAC 360
 DB 625 GCGCGACCATTCGACGAGGATTCGAGGATTCGAGGCTATCGGATTCGAGGCTTC 684
 QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGGCGGTGCTCGACGACCGCTAC 420
 DB 685 ATCTCCCTTACCTCATCCGACACCAAGAGGCGGTGCGAGTTCGAGGCGGCTTC 744

RESULT 32

CF690854 861 bp mRNA linear EST 16-AUG-2004
 CCAFI92TR C.neoformans strain JEC21 Cryptococcus neoformans var.
 neoformans cDNA clone CCAFI92, mRNA sequence.

ACCESSION CF690854
 VERSION
 KEYWORDS
 SOURCE EST. GI:41545013

ORGANISM Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
 Cryptococcus neoformans var. neoformans
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE 1 (bases 1 to 861)

AUTHORS Loftus, B.
 TITLE End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library
 JOURNAL Unpublished (2003)
 COMMENT Other_ESTS: CCAFI92TO
 Contact: Brendan Loftus
 The Institute for Genomic Research (TIGR; www.tigr.org)
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: bjloftus@tigr.org

Seq primer: TR.
 Location/Qualifiers
 1. .861

FEATURES

source
 1. .861
 /organism="Cryptococcus neoformans var. neoformans"
 /mol_type="mRNA"
 /strain="JEC21"
 /db_xref="taxon:40410"
 /clone="CCAFI92"
 /clone_lib="C.neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site_1: NotI EcorV; The full length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
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QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
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RESULT 33		RESULT 34	
CF699606		CF695217	
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DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
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REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
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COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
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QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
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Db	464	Db	505
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Db	524	Db	565
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Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
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COMMENT		COMMENT	
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source		source	

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Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
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QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
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REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	124
Db	404	Db	445
QY	184	QY	184
Db	464	Db	505
QY	241	QY	241
Db	524	Db	565
QY	301	QY	301
Db	584	Db	625
QY	361	QY	361
Db	644	Db	685
RESULT 33		RESULT 34	
CF699606		CF695217	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
FEATURES		FEATURES	
source		source	

ORIGIN		ORIGIN	
Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 861; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;	Query Match Best Local Similarity Matches 273; Conservative	41.3%; Score 173.6; DB 6; Length 869; 65.0%; Pred. No. 4.7e-26; 0; Mismatches 144; Indels 3; Gaps 1;
QY	4	QY	4
Db	284	Db	325
QY	64	QY	64
Db	344	Db	385
QY	124	QY	12

/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 872;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGAGTACGACACCGCGCGTTCGCGCCAGGCGCTC 63
| | | | |
Db 331 AAGACCAACGACACTGCGGTGACGAGTACCAACACCGCCACTGTCCTCGCCCGAGCCATC 390
| | | | |
QY 64 GTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCGATGCGTCTCAAGCGCGGC 123
| | | | |
Db 391 TACTCTGAGGCTGTGAAGACGTCGCTGCGGCTGCAACCCATGACCTCCCTCGAGGT 450
| | | | |
QY 124 ATCGAAGGCGCTCGAGGCGCTTCGCGCGCTTCGCGAGCAGGCGAAGGATGTCGAG 183
| | | | |
Db 451 GCCCAGAAGGCTGTGCAAGAGTCTCGAGGTCTTGTCTGCCAACAAAAGGTTATCACC 510
| | | | |
QY 184 ACCAAGGACGAGATGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCGAGATCGGC 240
| | | | |
Db 511 ACCTCTGAGGAGATTGCCAGGTGCGCAGCTGCGCACCATTCTCGGCCAACCGCGATACCCACGTCGT 570
| | | | |
QY 241 GAGCTCATCGCCGAGGCGATGCAAGGTGCGCAAGGAGCGCTCATCCGCTCGAGGAG 300
| | | | |
Db 571 GCCATCATTTGCCAAGCCATGAGGAGTGGAGTGGCAAGGAGGTGTCATCTGTTAAGGAG 630
| | | | |
QY 301 TCCGACGACTTCGGTCTGAGCTGAGCTCACCGAGGTATGCGTTCGACAAAGGCGCTAC 360
| | | | |
Db 631 GGCCGAACCATTCACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 690
| | | | |
QY 361 ATCTCGCGTACTTCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCGCTAC 420
| | | | |
Db 691 ATCTCCCTTACCTCATCCGACACCAAGACGAGCGTGTGAGCTCGAGAGAGCCCTTC 750
| | | | |

RESULT 35
CP719528
LOCUS
DEFINITION
CCAEJ74TR C.neoformans strain JEC21 Cryptococcus neoformans var.
CP719528
ACCESSION
VERSION
CP719528.1 GI:41573687
KEYWORDS
SOURCE
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE
AUTHORS
TITLE
Loftus, B.
JEC21 cDNA library
End sequencing of clones from a Full length enriched, normalized
Unpublished (2003)
JOURNAL
COMMENT
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.
Location/Qualifiers
1. .874
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAEJ74"
/clone_lib="C.neoformans strain JEC21"

FEATURES
source
1. .874
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAEJ74"
/clone_lib="C.neoformans strain JEC21"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 874;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGAGTACGACACCGCGCGTTCGCGCCAGGCGCTC 63
| | | | |
Db 325 AAGACCAACGACACTGCGCGGTGACGAGTACCAACCGCCACTGTCCTCGCCCGAGCCATC 384
| | | | |
QY 64 GTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCGATGCGTCTCAAGCGCGGC 123
| | | | |
Db 385 TACTCTGAGGCTGTGAAGACGTCGCTGCGGCTGCAACCCATGACCTCCCTCGAGGT 444
| | | | |
QY 124 ATCGAAGGCGCTCGAGGCGCTTCGCGCGCTTCGCGAGCAGGCGAAGGATGTCGAG 183
| | | | |
Db 445 GCCCAGAAGGCTGTGCAAGGTCCTCGAGGTCTTGTCTGCCAACAAAAGGTTATCACC 504
| | | | |
QY 184 ACCAAGGACGAGATGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCGAGATCGGC 240
| | | | |
Db 505 ACCTCTGAGGAGATTGCCAGGTGCGCAGCTGCGCACCATTCTCGGCCAACCGCGATACCCACGTCGT 564
| | | | |
QY 241 GAGCTCATCGCCGAGGCGATGCAAGGTGCGCAAGGAGCGTTCATCCGCTCGAGGAG 300
| | | | |
Db 565 GCCATCATTTGCCAAGCCATGAGGAGTGGAGTGGCAAGGAGGTGTCATCTGTTAAGGAG 624
| | | | |
QY 301 TCCGACGACTTCGGTCTGAGCTGAGCTCACCGAGGTATGCGTTCGACAAAGGCGCTAC 360
| | | | |
Db 625 GGCCGAACCATTCACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 684
| | | | |
QY 361 ATCTCGCGTACTTCGCCACGACATGAGCGGATGAGGCGTCTCGACGACCGCTAC 420
| | | | |
Db 685 ATCTCCCTTACCTCATCCGACACCAAGACGAGCGTGTGAGCTCGAGAGAGCCCTTC 744
| | | | |

RESULT 36
CP706367
LOCUS
DEFINITION
CCAHJ29TR C.neoformans strain JEC21 Cryptococcus neoformans var.
CP706367
ACCESSION
VERSION
CP706367.1 GI:41560526
KEYWORDS
SOURCE
EST.

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE
AUTHORS
TITLE
Loftus, B.
JEC21 cDNA library
End sequencing of clones from a Full length enriched, normalized
Unpublished (2003)
JOURNAL
COMMENT
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.
Location/Qualifiers
1. .877
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAHJ29"

FEATURES
source
1. .877
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAHJ29"

/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

/db xref="taxon:40410"
/clone="CAH150"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 881;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGACGACGTCGCGGTGACGGTACGACCAACCGGCGGCTCTCAAGCGGCTC 63
DB 34 AAGACCAACGACACTGCGGTGACGGTACGACCAACCGGCGGCTCTCTCGCGGCGGCTC 93
QY 64 GTACGGGAGGCGCTGCGCAAGCTGCGCGGCGGCTGCGGCGGCTCTCAAGCGGCTC 123
DB 94 TACTCTGAGGGTGTGAAGAACGTCGCTGCGGCGGCTGCAACCGGCGGCTCTCGGCTC 153
QY 124 ATCGAGAGGCGCTGCGGCGGCTCTCGGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 183
DB 154 GCCACGAGGCTGTGACGAGGCTCTCGGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 213
QY 184 ACCAGGAGGAGTTCGTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 240
DB 214 ACCTCTGAGGAGTTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 273
QY 241 GAGCTCATGCGGCGGCTGCGGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 300
DB 274 GCATCATGCGGCGGCTGCGGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 333
QY 301 TCCGAGACCTTCGCGTCTGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 360
DB 334 GCGCGACCATTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 393
QY 361 ATCTCGGCTACTTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 420
DB 394 ATCTCGGCTACTTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 453

RESULT 39

CF696919 891 bp mRNA linear EST 16-AUG-2004
LOCUS
DEFINITION
neoformans strain JEC21 Cryptococcus neoformans var.
CF696919
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
GI:41551078

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 891)
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
UNPUBLISHED (2003)
Other ESTs: CCACL52T0
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

Location/Qualifiers
1. .891
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"

FEATURES

source
Location/Qualifiers
1. .891
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"

/strain="JEC21"
/db xref="taxon:40410"
/clone="CCACL52"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 891;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;
QY 4 AAGACGACGACGTCGCGGTGACGGTACGACCAACCGGCGGCTCTCAAGCGGCTC 63
DB 273 AAGACCAACGACACTGCGGTGACGGTACGACCAACCGGCGGCTCTCTCGCGGCGGCTC 332
QY 64 GTACGGGAGGCGCTGCGCAAGCTGCGCGGCTCTCAAGCGGCTCTCAAGCGGCTC 123
DB 333 TACTCTGAGGGTGTGAAGAACGTCGCTGCGGCGGCTGCAACCGGCGGCTCTCGGCTC 392
QY 124 ATCGAGAGGCGCTGCGGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 183
DB 393 GCCACGAGGCTGTGACGAGGCTCTGCGGCGGCTCTCAAGCGGCTCTCAAGCGGCTC 452
QY 184 ACCAGGAGGAGTTCGTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 240
DB 453 ACCTCTGAGGAGTTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 512
QY 241 GAGCTCATGCGGCGGCTGCGGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 300
DB 513 GCATCATGCGGCGGCTGCGGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 572
QY 301 TCCGAGACCTTCGCGTCTGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 360
DB 573 GCGCGACCATTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 632
QY 361 ATCTCGGCTACTTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 420
DB 633 ATCTCGGCTACTTCGCGGCTCTCAAGCGGCTCTGCGGCGGCTCTCAAGCGGCTC 692

RESULT 40

CF719458 901 bp mRNA linear EST 16-AUG-2004
LOCUS
DEFINITION
neoformans strain JEC21 Cryptococcus neoformans var.
CF719458
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
GI:41573617

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 901)
End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
UNPUBLISHED (2003)
Other ESTs: CCADQ25TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

Location/Qualifiers
1. .901
/organism="Cryptococcus neoformans var. neoformans"

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/mol_type="mRNA"  
/strain="JEC21"  
/db_xref="taxon:40410"  
/clone_lib="C.neoformans strain JEC21"  
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full  
length, normalized library was prepared from a variety of  
conditions using RNA provided by Joseph Heitman and  
Jennifer Lodge"
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ORIGIN

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Query Match 41.3%; Score 173.6; DB 6; Length 901;  
Best Local Similarity 65.0%; Pred. No. 4.7e-26;  
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;  
  
QY 4 AAGACGAGACGACGTCGCGGTGACGATACGACACCGCGGATCTTCGCGCCAGGCGCTC 63  
D 325 AAGACCAACGACACTGCGGTGACGATACGACACCGCGGATCTTCGCGCCAGGCGCTC 384  
  
QY 64 GTACGCGAGGCGCTGCGCAAGCTGCGCGGTCGCCAACCGGATGGCTCTCAAGCGCGGC 123  
D 385 TACTCTGAGGCTGGAAGACGTCGTCGCGGCTGCAACCCCATGGACCTCCGTCGAGGT 444  
  
QY 124 ATCAGAGAGGCGCTGAGGCGCTCTCCGCGCCCTGCTGGAGCAGGCGAAGGATGTCGAG 183  
D 445 GCCAGAGGCTGCGACAGGTCTCTGAGGTCTTCTGCTGCCAACAAAGGTTATCACC 504  
  
QY 184 ACCAAGGAGCAGATGCGTTTCCAGCGCTTCATCTCCGC---CGCCGACACCCAGATCGGC 240  
D 505 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCCAACCGCGATACCCACGTCGGT 564  
  
QY 241 GAGCTCATCGCGAGGCGATGACAGGTGCGGCAAGGCGTCATCCGTCGAGGAG 300  
D 565 GCCATCATTTGCCAAGCCATGGACAGTCCGCAAGGAGGTGTCATCTGTTAAGGAG 624  
  
QY 301 TCCAGACCTTCGCTGAGCTGAGCTCACCGAGGTATGCGCTTCGCAAGGGGCTAC 360  
D 625 GGCGAACCATTGACGAGGATTTGAGATTACCGAGGATGCGATTGCGACCGAGGCTTC 684  
  
QY 361 ATCTCGGCGTACTTTCGACCGACATGAGCGGATGAGGCGTCTGCGACGACCCGTAC 420  
D 685 ATCTCCCTTACCTCATCACCAGACCAAGAAACAGCGGTGTCGAGCTCGAAGAGCCCTTC 744
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RESULT 41  
CF716339  
LOCUS  
DEFINITION  
CCAE16TR C.neoformans strain JEC21 Cryptococcus neoformans var.  
neoformans cDNA clone CCAER16, mRNA sequence.  
CF716339  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
CF716339.1 GI:41570498  
EST.  
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans  
var. neoformans)  
ORGANISM  
Cryptococcus neoformans var. neoformans  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;  
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;  
Filobasidiella.  
REFERENCE  
1 (bases 1 to 910)  
Loftus, B.  
AUTHORS  
TITLE  
End sequencing of clones from a Full length enriched, normalized  
JEC21 cDNA library  
JOURNAL  
COMMENT  
Other ESTs: CCAER16TO  
Contact: Brendan Loftus  
The Institute for Genomic Research (TIGR; www.tigr.org)  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: b.loftus@tigr.org  
Seq primer: TR.  
Location/Qualifiers  
1..910
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FEATURES
source

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/organism="Cryptococcus neoformans var. neoformans"  
/mol_type="mRNA"  
/strain="JEC21"  
/db_xref="taxon:40410"  
/clone_lib="CCAER16"  
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full  
length, normalized library was prepared from a variety of  
conditions using RNA provided by Joseph Heitman and  
Jennifer Lodge"
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ORIGIN

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Query Match 41.3%; Score 173.6; DB 6; Length 910;  
Best Local Similarity 65.0%; Pred. No. 4.7e-26;  
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;  
  
QY 4 AAGACGAGACGACGTCGCGGTGACGATACGACACCGCGGATCTTCGCGCCAGGCGCTC 63  
D 325 AAGACCAACGACACTGCGGTGACGATACGACACCGCGGATCTTCGCGCCAGGCGCTC 384  
  
QY 64 GTACGCGAGGCGCTGCGCAAGCTGCGCGGTCGCCAACCGGATGGCTCTCAAGCGCGGC 123  
D 385 TACTCTGAGGCTGGAAGAACGTCGTCGCGGCTGCAACCCCATGGACCTCCGTCGAGGT 444  
  
QY 124 ATCAGAGAGGCGCTGAGGCGCTCTCCGCGCCCTGCTGGAGCAGGCGAAGGATGTCGAG 183  
D 445 GCCAGAGGCTGCGACAGGTCTCTGAGGTCTTCTGCTGCCAACAAAGGTTATCACC 504  
  
QY 184 ACCAAGGAGCAGATGCGTTTCCAGCGCTTCATCTCCGC---CGCCGACACCCAGATCGGC 240  
D 505 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCCAACCGCGATACCCACGTCGGT 564  
  
QY 241 GAGCTCATCGCGAGGCGATGACAGGTGCGGCAAGGCGTCATCCGTCGAGGAG 300  
D 565 GCCATCATTTGCCAAGCCATGGACAGTCCGCAAGGAGGTGTCATCTGTTAAGGAG 624  
  
QY 301 TCCAGACCTTCGCTGAGCTGAGCTCACCGAGGTATGCGCTTCGCAAGGGGCTAC 360  
D 625 GGCGAACCATTGACGAGGATTTGAGATTACCGAGGATGCGATTGCGACCGAGGCTTC 684  
  
QY 361 ATCTCGGCGTACTTTCGACCGACATGAGCGGATGAGGCGTCTGCGACGACCCGTAC 420  
D 685 ATCTCCCTTACCTCATCACCAGACCAAGAAACAGCGGTGTCGAGCTCGAAGAGCCCTTC 744
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RESULT 42

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CF711999  
LOCUS  
DEFINITION  
CCAC030TR C.neoformans strain JEC21 Cryptococcus neoformans var.  
neoformans cDNA clone CCAC030, mRNA sequence.  
CF711999  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
CF711999.1 GI:41566158  
EST.  
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans  
var. neoformans)  
ORGANISM  
Cryptococcus neoformans var. neoformans  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;  
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;  
Filobasidiella.  
REFERENCE  
1 (bases 1 to 921)  
Loftus, B.  
AUTHORS  
TITLE  
End sequencing of clones from a Full length enriched, normalized  
JEC21 cDNA library  
JOURNAL  
COMMENT  
Other ESTs: CCAC030TO  
Contact: Brendan Loftus  
The Institute for Genomic Research (TIGR; www.tigr.org)  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: b.loftus@tigr.org  
Seq primer: TR.  
Location/Qualifiers
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FEATURES
Location/Qualifiers

source 1..921
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAC030"
/clone_lib="C.neoformans strain JEC21"
/note="vector: pCMVSPORT6; Site 1: NotI EcorV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.3%; Score 173.6; DB 6; Length 921;
Best Local Similarity 65.0%; Pred. No. 4.7e-26;
Matches 273; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGCGGATCTTCGCGCCAGCGCTC 63
DB 322 AAGACCAACGACACTGCGGTGACGGTACGACACCGCGGATCTTCGCGCCAGCATC 381
QY 64 GTACGCGAGGCGCTCGCGGTCGCGCGGTCGCGGATCTTCGCGCCAGCGCTC 123
DB 382 TACTCTGAGGGTGTGAGAACGTCGTCGCGGTGCGAACCCGATGACCTTCGCGAGGT 441
QY 124 ATCGAGAAGCGCGTCGAGGCGGTCTCCGCGCCCTCTCTGGAGCAGCGAGGATGTCGAG 183
DB 442 GCCCAGAAGCGGTGTCGACAGGTCCTCGAGGTCTTCTGCCAACAAAAGGTTATCACC 501
QY 184 ACCAAGGACGATCGTTCACGGGCTCCATCTCCGCGCGACACCGGATCGGC 240
DB 502 ACCTCTGAGGAGATGTCGCGAGGTGCGCACCATCTCCGCGCAACGCGGATACCCACGCGGT 551
QY 241 GAGCTCATCGCGAGGCGATGCGACAGGTGCGCAAGGAGCGGTCTCATCCGTCGAGGAG 300
DB 562 GCATCATCTGCGCAGCATGAGCAGGTGCGCAGGAGGAGGTCTCATCTGTAAGGAG 621
QY 301 TCCGACGACCTTCGCGTCTGGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
DB 622 GCGCGAACCATTGACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 681
QY 361 ATCTCGGCTACTTCCGCGGACATGAGCGGATGAGGCGGTCTCGACGACCGGTAC 420
DB 682 ATCTCCCTTACCTCATCTACCGGACCAAGAACCGGTGTCGAGCTCGAGAGCGCTTC 741

RESULT 43
CF716527
LOCUS
DEFINITION
CF716527 C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAGN89, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
CF716527.1 GI:41570686
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
Loftus, B.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library
Other ESTs: CCAGN89TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

FEATURES
source 1..716
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAGN89"
/clone_lib="C.neoformans strain JEC21"
/note="vector: pCMVSPORT6; Site 1: NotI EcorV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 41.2%; Score 173.2; DB 6; Length 716;
Best Local Similarity 65.1%; Pred. No. 5.7e-26;
Matches 272; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGGTACGACACCGCGGATCTTCGCGCCAGCGCTC 63
DB 298 AAGACCAACGACACTGCGGTGACGGTACGACACCGCGGATCTTCGCGCCAGCATC 357
QY 64 GTACGCGAGGCGCTCGCGGTCGCGCGGTCGCGGATCTTCGCGCCAGCGCTC 123
DB 358 TACTCTGAGGGTGTGAGAACGTCGTCGCGGTGCGAACCCGATGACCTTCGCGAGGT 417
QY 124 ATCGAGAAGCGCGTCGAGGCGGTCTCCGCGCGCTCTCTGGAGCAGCGAGGATGTCGAG 183
DB 418 GCCCAGAAGCGGTGTCGACAGGTCCTCGAGGTCTTCTGCCAACAAAAGGTTATCACC 477
QY 184 ACCAAGGACGATCGTTCACGGGCTCCATCTCCGCGCGACACCGGATCGGC 240
DB 478 ACCTCTGAGGAGATTGCCAGGTGCGCACCATCTCCGCGCAACGCGGATACCCACGCGGT 537
QY 241 GAGCTCATCGCGAGGCGATGCGACAGGTGCGCAGGAGGAGGTCTCATCCGTCGAGGAG 300
DB 538 GCATCATCTGCGCAGCATGAGCAGGTGCGCAGGAGGAGGTCTCATCTGTTAAGGAG 597
QY 301 TCCGACGACCTTCGCGTCTGGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
DB 598 GCGCGAACCATTGACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 657
QY 361 ATCTCGGCTACTTTCGCGGACCATGAGCGGATGAGGCGGTCTCGACGACCGGT 418
DB 658 ATCTCCCTTACCTCATCTACCGGACCAAGAACCGGTGTCGAGCTCGAGAGCGCT 715

RESULT 44
CF687310
LOCUS
DEFINITION
CF687310 C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAA141, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
CF687310.1 GI:41541469
EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
Loftus, B.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library
Unpublished (2003)
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TR.

```

FEATURES             Location/Qualifiers
  source              1..759
                     /organism="Cryptococcus neoformans var. neoformans"
                     /mol_type="mRNA"
                     /strain="JEC21"
                     /db_xref="taxon:40410"
                     /clone="CCAA141"
                     /clone_lib="C.neoformans strain JEC21"
                     /note="Vector: pCMVSPORT6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match      41.2%; Score 173.2; DB 6; Length 759;
Best Local Similarity 65.1%; Pred. No. 5.7e-26;
Matches 272; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY  4 AAGACGACGACGTCGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 63
DB  332 AAGACCAACGACACTGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 391
QY  64 GTACGCGAGGCGCTGCGCAACGTGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
DB  392 TACTCTGAGGTGTGAAGACGTGCGTGGCGGTGCAACCCATGGACCTCGTCCGAGGT 451
QY  124 ATCAGAGGCGGTGCGAGCGGTCTCGCGCGCTCTCGCGCGCTCTGAGGAGGCGAAGGATGTCGAG 183
DB  452 GCCGAGAAGGTGTGCAACAGGTCTCTCGAGGTCTCTGCTGCAACAAAGAGGTATCACC 511
QY  184 ACCAAGGACGAGTCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCGACATCGGC 240
DB  512 ACCTCTGAGGAGATTGCCAGGTGCGCAACCATCTCCGCAACGCGGATACCCAGTGGT 571
QY  241 GAGCTCATCGCGGAGCGATGACAAAGGTGCGGCAAGGAGCGTCATCACCGTCGAGGAG 300
DB  572 GCCATCATGCGCAAGCATGAGCAGTGGCAGGTGCGCAAGGAGGTGTCATCACTGTTAAGGAG 631
QY  301 TCCAGACCTTCGCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
DB  632 GGCCGAACCATGACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 691
QY  361 ATCTCGGCTACTTCGCCACCGATGAGCGGATGAGGCGTCTCGACGACCCGT 418
DB  692 ATCTCCCTTACCTCATCACCACCAACAGACGCTGTCGAGCTCGAAGACCTT 749

RESULT 45
CF679031
LOCUS      CF679031      794 bp      mRNA      linear      EST 16-AUG-2004
DEFINITION CCAC445TR C.neoformans strain JEC21 Cryptococcus neoformans var.
            neoformans cDNA clone CCAC445, mRNA sequence.
ACCESSION  CF679031
VERSION     CF679031.1 GI:41533190
KEYWORDS   EST.
SOURCE     Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
            var. neoformans)
ORGANISM   Cryptococcus neoformans var. neoformans
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
            Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
            Filobasidiella.
REFERENCE  1 (bases 1 to 794)
AUTHORS   Loftus,B.
TITLE     End sequencing of clones from a Full length enriched, normalized
JOURNAL   JEC21 cDNA library
COMMENT   Unpublished (2003)
Other_ESTs: CCAC445TF
Contact: Brendan Loftus
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Fax: 301-838-0208
Email: bjloftus@tigr.org

FEATURES             Location/Qualifiers
  source              1..794
                     /organism="Cryptococcus neoformans var. neoformans"
                     /mol_type="mRNA"
                     /strain="JEC21"
                     /db_xref="taxon:40410"
                     /clone="CCAC445"
                     /clone_lib="C.neoformans strain JEC21"
                     /note="Vector: pCMVSPORT6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match      41.2%; Score 173.2; DB 6; Length 794;
Best Local Similarity 65.1%; Pred. No. 5.7e-26;
Matches 272; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

QY  4 AAGACGACGACGTCGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 63
DB  332 AAGACCAACGACACTGCGGTGACGTACGACACCGACCGTTCCTCGCCAGGCGCTC 381
QY  64 GTACGCGAGGCGCTGCGCAACGTGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
DB  382 TACTCTGAGGTGTGAAGACGTGCGTGGCGGTGCAACCCATGGACCTCGTCCGAGGT 441
QY  124 ATCAGAGGCGGTGCGAGCGGTCTCGCGCGCTCTCGCGCGCTCTGAGGAGGCGAAGGATGTCGAG 183
DB  442 GCCGAGAAGGTGTGCAACAGGTCTCTCGAGGTCTCTGCTGCAACAAAGAGGTATCACC 501
QY  184 ACCAAGGACGAGTCGCTTCCACGCGCTCCATCTCCGC---CGCCGACACCGACATCGGC 240
DB  502 ACCTCTGAGGAGATTGCCAGGTGCGCAACCATCTCCGCAACGCGGATACCCAGTGGT 561
QY  241 GAGCTCATCGCGGAGCGATGACAAAGGTGCGGCAAGGAGCGTCATCACCGTCGAGGAG 300
DB  562 GCCATCATGCGCAAGCATGAGCAGTGGCAGGTGCGCAAGGAGGTGTCATCACTGTTAAGGAG 621
QY  301 TCCAGACCTTCGCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
DB  622 GGCCGAACCATGACGACGAGATTGAGATTACCGAGGATGCGATTTCGACCGAGGCTTC 681
QY  361 ATCTCGGCTACTTCGCCACCGATGAGCGGATGAGGCGTCTCGACGACCCGT 418
DB  682 ATCTCCCTTACCTCATCACCACCAACAGACGCTGTCGAGCTCGAAGACCTT 739

RESULT 46
CF707648
LOCUS      CF707648      758 bp      mRNA      linear      EST 16-AUG-2004
DEFINITION CCAC64TR C.neoformans strain JEC21 Cryptococcus neoformans var.
            neoformans cDNA clone CCAC64, mRNA sequence.
ACCESSION  CF707648
VERSION     CF707648.1 GI:41561807
KEYWORDS   EST.
SOURCE     Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
            var. neoformans)
ORGANISM   Cryptococcus neoformans var. neoformans
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
            Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
            Filobasidiella.
REFERENCE  1 (bases 1 to 758)
AUTHORS   Loftus,B.
TITLE     End sequencing of clones from a Full length enriched, normalized
JOURNAL   JEC21 cDNA library
COMMENT   Unpublished (2003)
Other_ESTs: CCAC64TF
Contact: Brendan Loftus
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```


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 Seq primer: TK.

248 Noble Research Center, Stillwater OK, 74078

Tel: 405-744-6209
 Fax: 405-744-7799
 Email: ayoubi@okstate.edu

FEATURES
 source

Location/Qualifiers
 1. 746
 /organism="Cryptococcus neoformans var. neoformans"
 /strain="JEC21"
 /mol_type="mRNA"
 /db_xref="taxon:40410"
 /clone="CCAHF79"
 /clone_lib="C. neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 40.9%; Score 171.6; DB 6; Length 746;
 Best Local Similarity 65.4%; Pred. No. 1.2e-25;
 Matches 268; Conservative 0; Mismatches 139; Indels 3; Gaps 1;
 QY 4 AAGACGACGACGTCGCGGTGACGTTACGACCGACCGCGTTCCTCGCCGAGCGCTC 63
 DB 333 AAGACGACGACGTCGCGGTGACGTTACGACCGACCGCGTTCCTCGCCGAGCGCTC 392
 QY 64 GTACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
 DB 393 TACTCTGAGGTGTGAAGACGTCGTCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 452
 QY 124 ATCCAGAGGCGGTGCGAGCGCTCTCCGCGCGCTGCTGGAGCGGAGGATGTCGAG 183
 DB 453 GCCCAGAGGCGGTGTCGACAGGCTCTCGAGGTTCTTGCTGCCAACAAGAGTTATCACC 512
 QY 184 ACCAAGGACGACGTCGTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
 DB 513 ACCTCTGAGGAGATTGCCAGGTGCGCCACCATCTCCGCAAGCGGATACCCAGTCGCT 572
 QY 241 GAGTCATTCGCGGAGGATGACAGATGCGGCAAGGAGGCGTCATCAGCGTCGAGGAG 300
 DB 573 GCCATCATTCGCCAAGCATTGAGCAGGTGCGGCAAGGAGGCGTCATCAGTCATGTTAAGGAG 632
 QY 301 TCCAGAGCTTCGCTGCGAGCTGCGAGCTACCGAGGATGCGCTTCGACCAAGGCGTAC 360
 DB 633 GGCGCAACATTGACGACGATGAGATTACCGAGGATGCGATTCGACCGAGGCTTC 692
 QY 361 ATCTCCGCGTACTTTCGCCACGACATGAGCGGATGAGGCGTCTCGTCTGA 410
 DB 693 ATCTCCCTTACCTCATCACCACGACCAAGAACGAGCGTGTGAGCTCGA 742

RESULT 49

CK446096
 LOCUS
 DEFINITION pncs914ad05.SP6 Aspergillus nidulans negative subtraction hybridization polysaccharide related cDNA plasmid library
 accession CK446096
 version CK446096.1 GI:40883579
 keywords EST.
 organism Emericella nidulans (anamorph: Aspergillus nidulans)
 reference Ray, A., Macwana, S., Ayoubi, P., Hall, L. T., Prade, R. and Mort, A. J.
 authors Negative subtraction hybridization: An efficient method to isolate large numbers of condition-specific cDNAs
 title BMC Genomics 5 (1), 22 (2004)
 journal 15050035
 comment Contact: Patricia Ayoubi
 Department of Biochemistry and Molecular Biology
 Oklahoma State University

FEATURES
 source

Location/Qualifiers
 1. 752
 /organism="Emericella nidulans"
 /mol_type="mRNA"
 /strain="FGSC C26"
 /db_xref="taxon:162425"
 /clone="pncs914ad05"
 /tissue_type="vegetative mycelia"
 /lab_host="E. coli"
 /clone_lib="Aspergillus nidulans negative subtraction hybridization polysaccharide related cDNA plasmid library"
 /note="Vector: pCMVSPORT6.0; Site 1: EcoRI; Site 2: HindIII; 5' end of cDNA cloned near EcoRI site of pCMVSPORT6.0 and 3' end cloned near HindIII site of pCMVSPORT6.0. Average length of insert is 1.49 kb"

ORIGIN

Query Match 40.8%; Score 171.2; DB 7; Length 752;
 Best Local Similarity 64.9%; Pred. No. 1.5e-25;
 Matches 270; Conservative 0; Mismatches 143; Indels 3; Gaps 1;
 QY 4 AAGACGACGACGTCGCGGTGACGTTACGACCGACCGCGTTCCTCGCCGAGCGCTC 63
 DB 99 AAGACGACGACGTCGCGGTGACGTTACGACCGACCGCGTTCCTCGCCGAGCGCTC 158
 QY 64 GTACGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGC 123
 DB 159 TTTTCCGAGACCGTTAAGAACGTTGCTGCTGGTGCACACCCCATGGATCTGCGCCGCGGT 218
 QY 124 ATCCAGAGGCGGTGCGAGCGGTCTCCGCGCGCTGCTGGAGCGGAGGATGTCGAG 183
 DB 219 ATCCAGGCTCTGTCGAGGCGGTGTCGACTACTCTCAGCAGAACAGCGTGAATTA 278
 QY 184 ACCAAGGACGACGTCGTTCCACGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
 DB 279 ACTGAGAGGAGATTGCTGCTGCTGCTACCATCTCTGCTAACCGTGACACCCAGTTGGC 338
 QY 241 GAGTCATTCGCGGAGGATGACAGGTCGCGCAAGGAGGCGTCATCAGCGTCGAGGAG 300
 DB 339 AAGCTTATCTCCACTGCTGAGCGCGCTGCTGAGGAGCGCGCTTATCACTGTCAAGGAG 398
 QY 301 TCCAGAGCTTCGCTGCGAGCTGCGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
 DB 399 GGCAAGACCTTGGAGGACGAGCTTGGATTACTGAGGATGCGCTTCGACCGTGGTTAC 458
 QY 361 ATCTCCGCGTACTTTCGCCACCGACATGAGCGGATGAGGCGTCTGCTGAGCGACCC 416
 DB 459 ACCTCCCTTACTTTCATTCAGCTGCGCGCGCGCGCGCTTATCACTGTCAAGGAG 514

RESULT 50

CF707221
 LOCUS
 DEFINITION CCAH138TR C. neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAH138, mRNA sequence.
 accession CF707221
 version CF707221.1 GI:41561380
 keywords EST.
 source Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
 organism Cryptococcus neoformans var. neoformans
 reference Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAB155TF

Contact: Brendan Loftus

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Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .840

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAB155TF

Contact: Brendan Loftus

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Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .840

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAB155TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .840

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="taxon:40410"

/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Loftus, B.

End sequencing of clones from a Full length enriched, normalized

JEC21 cDNA library

Unpublished (2003)

Other ESTs: CCAB155TF

Contact: Brendan Loftus

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

Location/Qualifiers

1. .840

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

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/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSPORT6; Site_1: NotI EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge"

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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 851)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCAGN42TF
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjlloftus@tigr.org
Seq primer: TR.
FEATURES Location/Qualifiers
source
1..851
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAGN42"
/clone_lib="C.neoformans strain JEC21"
/notes="vector: pcwSport6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"
ORIGIN
Query Match 40.2%; Score 168.8; DB 6; Length 851;
Best Local Similarity 64.8%; Pred. No. 4.7e-25;
Matches 267; Conservative 0; Mismatches 142; Indels 3; Gaps 1;
Qy 12 CGAGCTCGCGGTGACGTGACGACCGGACCGTCTCGCCCGAGCGCTCGTACGCGA 71
Db 1 CGACACTGCGGTGACGTGACGACCGGACCGTCTCGCCCGAGCCATCTACTCTGA 60
Qy 72 GGGCTCTCGCAACGCTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGCGGCGATCGAGAA 131
Db 61 GGGGTGTAAGAACGCTGCTGCGGCTGCAACCCGATGACCTCGTGGTGGCCAGAA 120
Qy 132 GCGCGTGGAGCGCTCTCGCGCGCCCTGCTGGAGCAGCGGAGGATGTCGAGACCAAGGA 191
Db 121 GGTGTGCGCAAGGTCTCTCGAGGTCTTGTGTCGCAACAAAGAGGTATCAACCACTCTGA 180
Qy 192 GCAGATCGTCTCCACGCGCTCCATCTCGCG---CGCCGACACCCAGATCGCGAGCTCAT 248
Db 181 GGAGATTGCCAGTGCACCATCTCGCCCAACGGCGATACCCAGTGGTGCCATCAT 240
Qy 249 CGCCGAGCGGATGACCAAGGTTCGCAAGGAGGCGTTCATCACCGTCGAGGAGTCCCGAGAC 308
Db 241 TGCCCAAGCCATGAGCAGGTTCGCAAGGAGGCGTTCATCATCTTTAAGGAGGCGCGAAC 300
Qy 309 CTTGCGGTGAGAGTGGAGCTCACCGAGGGTATCGGCTTCGCAAGGAGGCTATCTCGGC 368
Db 301 CATTTGACGACGAGATTGAGATTACCGAGGGTATCGGATTCGACGAGGCTTCATCTCCCC 360
Qy 369 GTACTTCGCCACCGACATGGAGCGGATGGAGCGTTCGTCGACGACCCGTAC 420
Db 361 TTACTCTATCACCGACCAAGAACCGGTGTGCGAGCTCGAAGAGCCCTTC 412
RESULT 57
LOCUS CF843128 653 bp mRNA linear EST 30-OCT-2003
DEFINITION pSHB023xN17f USDA-IPAFS:Expression of Phytophthora sojae genes
during infection and propagation_SHB Phytophthora sojae cDNA clone
SHB023N17 5, mRNA sequence.
ACCESSION CF843128
VERSION CF843128.1 GI:38058782

KEYWORDS
SOURCE ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Phytophthora sojae
Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
Tyler,B.
Tyler,B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
VBI

1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtylev@vt.edu
PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 023 row: N column: 17
Seq primer: BK reverse primer
High quality sequence stop: 653.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="SHB023N17"
/tissue="mycelium"
/cell_line="P6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="USDA-IPAFS:Expression of Phytophthora sojae
genes during infection and propagation_SHB"
/notes="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

FEATURES
source

1..653
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="SHB023N17"
/tissue="mycelium"
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/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="USDA-IPAFS:Expression of Phytophthora sojae
genes during infection and propagation_SHB"
/notes="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 39.5%; Score 165.8; DB 7; Length 653;
Best Local Similarity 64.0%; Pred. No. 2e-24;
Matches 267; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
Qy 7 ACGGAGCAGCTCGCCGTTGACGTGACGACCGGACCGTCTCGCCCGAGCGCTCGTA 66
Db 144 ACCAAGCAGCGCGCGGTGACGCGACCGTCTCGCCCGAGCGCTCGTA 203
Qy 67 CGGAGGCGCTCGCGAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGGATC 126
Db 204 AGCGAGGCGTGCAGGTGCGGTGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGCGGATC 263
Qy 127 GAGAAGGCGCTCGAGCGCGTCTCGCGCGCGTCTCGCGCGCGGTGCGCAACCGGATGCTCGAGAC 186
Db 264 CAGATGGCGGTGAGCCACCGTCTGAGCGCGTCTGAGAGCTGTCGAGGAGCGTGGCGGAC 323
Qy 187 AAGGAGCAGATCGCTTCCACGCGCTTCATCTCGCG---CGCCGACACCGGATGCGGAG 243
Db 324 AAGGAGAGGTGCGCCAGGTGCGCGCGGTGCGCAACCGGATGCTCTCGCGCGGATGCGGAG 383
Qy 244 CTATCGCCGAGCGGATGCGCAAGGTGCGCAACCGGATGCTCTCAAGCGCGGATGCGGAG 303
Db 384 CTATCGAGCGCGCGATGCGCAAGGTGCGCAACCGGATGCTCTCAAGCGCGGATGCGGAG 443
Qy 304 CAGACCTTCGCTCTGAGAGCTGAGAGCTCAGCGGAGTATCGGCTTCGCAAGGAGGCTATC 363
Db 444 AAGACGCTGTACACGAGCTAGAGGTGCTGAGGCGCATGAATTCGACCGCGGCTTCATC 503
Qy 364 TCGCGGTACTTCGCGCGGATGCGCAAGGTGCGCAAGGTGCGGATGCGGAGCGGCTGCTCGAG 420
Db 504 TCGCGCTTACTTCGTCGCGGACCAAGACCGGATGCGGAGCGGATGCGGAGCGGATGCGGAG 560

RESULT 58
LOCUS CF640823
DEFINITION D32_A12 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

CF640823 393 bp mRNA linear
EST 02-OCT-2003
D32_A12 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

sequence.
CF640823
CF640823.1 GI:37406706
EST.
Ustilago maydis
Ustilago maydis
Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
1 (bases 1 to 393)
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
Fungal Genet. Biol. 41 (3), 349-360 (2004)
14761795
Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: beaville@utmsi.utoronto.ca
Plate: UTM-UM-D126/7-032-UTM row: 12 column: A
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 393.
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSPORT; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."

FEATURES

source

ORIGIN

Query Match 39.3%; Score 165; DB 6; Length 393;
Best Local Similarity 66.4%; Pred. No. 2.9e-24;
Matches 253; Conservative 0; Mismatches 125; Indels 3; Gaps 1;
QY 13 GAGTCGCCGGTACGGTACGACACCGGACCGTTCGCGCAGCGCTCGTACGCGAG 72
DB 12 GAGTCGCCGGTACGGTACGACACCGGACCGTTCGCGCAGCGCTCGTACGCGAG 71
QY 73 GGCCTGCGCAACGTCGCCCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGATCGAGAG 132
DB 72 GGTGTCAAGACGTCGCTGCGTGTGCGTCAACCGGATGGCTCTCGAGCGTGTGTCAGGCT 131
QY 133 GCGTCGAGCGCTCTCGCGCGCTCTGCGGAGCGGCGAAGGATGTCGAGACCAAGGAG 192
DB 132 GGTGTGAGCGCGTCTATCAAGTTCCTCGAGACCAACGCGTGTCTACCACTTCGCGC 191
QY 193 CAGATCGCTTCCACGCGCTCTCATCTCGCG---CGCGCACACCGAGATCGCGGAGTCTATC 249
DB 192 GAGATCGCGCGAGTGCACCATCTCAGCCACCGGCGGACGAGATGTCGCTCAGCTCATC 251
QY 250 GCGGAGCGATGACGAGTTCGCGAAGGAGGCTCATCACCCTGAGAGGTCCAGAC 309
DB 252 GCCACCGCCATGAGAGGTTGGCAGGAGGTTGTCATCATCTGTCAAGGAGGGAAGACG 311
QY 310 TTGCGTCTGAGCTGAGCTCACCGGAGGTATGCGCTTCGACAGAGGCTTACATCTCGCG 369
DB 312 CTCGAGAGCGATCGAGATCACCGAGGCGATGCGCTTCGACCGTGGCTTACATCTCGCT 371
QY 370 TACTTCGCCACCGACATGAG 390
DB 372 TACTTCATCACCGAGCTGAG 392

RESULT 59

CV899250

LOCUS

DEFINITION

PB021E9 mycelium, sporulating growth

Phytophthora infestans cDNA,

mRNA sequence.

CV899250

VERSION

KEYWORDS

SOURCE

ORGANISM

Phytophthora infestans (potato late blight agent)

Phytophthora infestans

Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;

Phytophthora.

REFERENCE

AUTHORS

1 (bases 1 to 698)

Randal, T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C.,

Kelkar, H., Fong, A.M., Gates, K., Roberts, S., Yazkan, E., Gaffney, T.,

Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, L., Mueller, E.,

Windass, J., Binder, A., Birch, P.R.J., Gisl, U., Govers, F., Gow, N.A.,

Mauch, F., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S.,

Lam, S.T., and Judelson, H.S.

Large-scale gene discovery in the oomycete Phytophthora infestans

reveals likely components of phytopathogenicity shared with true

fungi

Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)

15782637

CONTACT: Judelson HS

Department of Plant Pathology

University of California

Webster Hall, Riverside, CA 92521, USA

Tel: 909 787 4199

Fax: 909 787 4294

Email: howard.judelson@ucr.edu.

Location/Qualifiers

1..698

/organism="Phytophthora infestans"

/mol_type="mRNA"

/strain="88069"

/db_xref="taxon:4787"

/sex="M"

/clone_lib="mycelium, sporulating growth"

/note="Vector: pSPORT1"

ORIGIN

Query Match 38.7%; Score 162.6; DB 8; Length 698;
Best Local Similarity 63.5%; Pred. No. 9.1e-24;
Matches 265; Conservative 0; Mismatches 149; Indels 3; Gaps 1;
QY 7 ACGGACGAGTGGCGGTGACGAGTACGACCGGACCGTTCGCGCAGCGCTCGTACGCG 66
DB 111 ACCAACGACGCGCGGTGACGCGCACCGTTCGCGCACCGTTCGCGCGCGCCATCTTC 170
QY 67 CGCGAGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGCGATC 126
DB 171 AGCGAGGCTGCAAGTGGTGGCGCGCGGATGAAACCGACCGCTGGCGCGCGCGATC 230
QY 127 GAGAGGCGCTGAGGCGCTCTCGCGCGCGCTCTGAGAGCGGCGGAGAGTTCGAGAC 186
DB 231 CAATGGCGGTGAGCACGCTGAGCGGTCTGAGAGGCTGTCGATGAGAGTTCGAGCGCG 290
QY 187 AAGGAGCAGATGCTTCCACGCGCTTCATCTCCGC---CGCGCACCGAGATCGCGGAG 243
DB 291 AAGGAGAGGTGGCGCGCGGTGGCGCACCATCTCGCGCAACTCGGAGACGAGATCGGCA 350
QY 244 CTCATCGCGGAGGCGATGAGCAAGTGGCAAGGAGCGCTCATCAGCGTCGAGAGTCC 303
DB 351 CTCATCGTACGCGATGAGCGGTGGCGGAGGCGGCGTATCAGCGTCGAGAGTCC 410
QY 304 CAGACCTTCGCTGAGGCTGAGCTCACCGAGGATGTCGCTTCGACAGAGGCTTACATC 363
DB 411 AAGAGCGTGTACACGAGCTGAGGTGCTGAGGAGCATGAAGTTTCGACCGCGCTTCATC 470
QY 364 TCGGCGTACTTTCGCGCACCGATGAGGCGGTGAGGCGGTGCTCGAGACCGCGTAC 420
DB 471 TCGCGCTACTTTCGTCGCGCAATAAGACCGACCGTGTGCGGAGATGAGAGACCGGTAC 527

RESULT 60	CF697565	757 bp	mRNA	linear	EST 16-AUG-2004
LOCUS	CCABM02TR	C.neoformans strain JEC21	Cryptococcus	neoformans	var.
DEFINITION	neoformans	CDNA clone CCABM02	mRNA	sequence.	
ACCESSION	CF697565				
VERSION	CF697565.1	GI:41551724			
KEYWORDS	EST.				
SOURCE	Cryptococcus	neoformans	var.	neoformans	(Filobasidiella neoformans
ORGANISM	var. neoformans)				
	Cryptococcus	neoformans	var.	neoformans	
	Eukaryota:	Fungi:	Basidiomycota:	Hymenomycetes:	
	Heterobasidiomycetes;	Tremellomycetidae;	Tremellales;	Tremellaceae;	
	Filobasidiella.				
REFERENCE	1	(bases 1 to 757)			
AUTHORS	Loftus,B.				
TITLE	End sequencing of clones from a Full length enriched, normalized				
JOURNAL	JEC21 CDNA library				
COMMENT	Unpublished (2003)				
	Other ESTs: CCABM02TF				
	Contact: Brendan Loftus				
	The Institute for Genomic Research (TIGR; www.tigr.org)				
	9712 Medical Center Drive, Rockville, MD 20850, USA				
	Tel: 301-838-3543				
	Fax: 301-838-0208				
	Email: bjlloftus@tigr.org				
FEATURES	Seq primer: TR.				
source	Location/Qualifiers				
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	/strain="JEC21"				
	/db_xref="taxon:40410"				
	/clones="CCABM02"				
	/clone_lib="C.neoformans strain JEC21"				
	/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV; The full				
	length, normalized library was prepared from a variety of				
	conditions using RNA provided by Joseph Heitman and				
	Jennifer Lodge"				
ORIGIN					
	Query Match	38.7%;	Score 162.6;	DB 6;	Length 757;
	Best Local Similarity	64.8%;	Pred. No. 9.1e-24;		
	Matches 273;	Conservative 0;	Mismatches 144;	Indels 4;	Gaps 2;
Qy	4	AAGACGACGACGCTGCGCGGTGACGGTACGACCCACCGACCGTTCGTGCGCCAGCGCGTC	63		
Db	328	AAGACCAACGACACTGCGCGGTGACGGTACCAACCAACCGGCACTGCTCTCGCCGACGCCATC	387		
Qy	64	GTACGCGAGGCGCTGCGGCAAGCTGCGCGCGGTGCCAACCCGATGGCTCTCAAGGGCGGC	123		
Db	388	TACTCTGAGGGGTGTGAAGAACCTGCTGCGCGGTGCAACCCCAATGAGACCTCCGTCGAGGT	447		
Qy	124	ATCGAGAAGGCGCTCGAGGCGGTCTCTCGGCGCCCTCTGTGGAGCAGGCGAAGGATGTCGAG	183		
Db	448	GCCCAGAAGGCTGTGCAACAGTCTCTCGAGGTTCTTGCTGCCAACAAAAGGTTATCACC	507		
Qy	184	ACC--AAGGAGCAGATCGCTTCCACGGGCTCCATCTCGC---CGCCGACACCCAGATCGG	239		
Db	508	ACCTTCTGAGGAGATTGCCAGGTGCGCCACCATCTCGGCCAACGGCGATACCCACGTCGG	567		
Qy	240	CGAGCTCATGCCGAGGCGATGGACAGGTGCGCAAGGAGCGTCATCACCCTCGAGGA	299		
Db	568	TGCCATCATTTGCCCAAGCAATGAGACAGGTGCGCAAGGAGGTTGTCACTCACTGTTAAGGA	627		
Qy	300	GTCCACAGACCTTCGTCTGAGCTGGAGCTCACCGAGGATGGCTTCGCAACAGGGGCTA	359		
Db	628	GGGCGGACCAATTGACGACGAGATTGATTAACGAGGGTATGCGATTCGACCGAGGCTT	687		
Qy	360	CATCTGGCGGTACTTGGCCACCGACATGAGCGGATGAGGCGGTGCTCTCGACGACCCGTA	419		
Db	688	CATCTCCCTTACTCTCATCAACGACACCAAGAACACAGCGTGTGAGCTTCGAGATCGAGACCCCTT	747		


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; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-113

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Best Local Similarity	83.3%	Pred. No. 1.2e-50		
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Db	232	AAGNAGACCGACGAGCTGCGGGCGACGGCACACACACCGCCACCGTCTCAGGCT	291	
Qy	61	CTCGTACGGAGGGCTTGGGAAGCTGCGCGCGGTGCCAACCCGATGGCTCTCAAGCGC	120	
Db	292	CTGGTTTCGGAAGGCTTGGCAACGTGCGACCGCGGCCAACCCGCTCGGCCTCAAGCGT	351	
Qy	121	GGCATCGAAGAAGGCGCTCGAGGGCGTCTCGGGCGCCCTGCTGGAGCAGGCGGAAGGATGC	180	
Db	352	GGCATCGAAGAAGGCTGTCGAGGCTGTCAACCAAGTCGCTGTCTAAGTCGGCCAGAGGTC	411	
Qy	181	GAGACCAAGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGGCACACCCAGATCGC	240	
Db	412	GAGACCAAGAGCAGATTTCTGCGCACCGCGCGGATTTTCGCGCGGCACACCCAGATCGC	471	
Qy	241	GAGCTCATCCCGGGCGATGGACAAAGTTCGGCAAGGAAGGCGTCATCACCGTCGAGAG	300	
Db	472	GAGCTCATCCCGAGGCCATGGACAAGTTCGGCAACGAGGGTGTTCATCACCGTCGAGAG	531	
Qy	301	TCCACAGACCTTCGCTCTGGAGCTGGAGCTCACCGAGGGTATGCGCTTTCGACAAGGGCTAC	360	
Db	532	TCGNAACACTTCGCGCTTCAGCTCGAGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC	591	
Qy	361	ATCTCGCGGTACTTTCGCCACCGAATGGAGCGGATGGAGGGTTCGCTCGACGACCCGCTAC	420	
Db	592	ATCTCGGGTTACTTTCGTGACCGACCGCGAGCGCCAGGAAGCGCTCTCTGGAGGATCCCTAC	651	

RESULT 6

US-08-997-080-159
; Sequence 159, Application US/08997080
; Patent No. 5968524

/ PATENT NO. 520802
 / GENERAL INFORMATION:
 / APPLICANT: WATSON, JAMES D.
 / APPLICANT: TAN, PAUL L.J.
 / TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
 / NUMBER OF SEQUENCES: 194
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Law Offices of Ann W. Speckman
 / STREET: 2601 Elliott Avenue, Suite 4185
 / CITY: Seattle
 / STATE: WA
 / COUNTRY: USA
 / ZIP: 98121
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/997,080
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Sleath, Janet
 / REGISTRATION NUMBER: 37,007
 / REFERENCE/DOCKET NUMBER: 11000.1007

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

Query Match	73.3%;	Score 308;	DB 2;	Length 1626;
Best Local Similarity	83.3%;	Pred. No. 1.2e-50;		
Matches 350;	Conservative 0;	Mismatches 70;	Indels 0;	Gaps 0;
Qy	1	AAGAAGACGGACGACGTCGCGCGGTGACGGGTACGACACACCGCGACCGGTTCCTCGCCACGCGC	60	
Db	232	AAGNAGACCGNAGOGTTCGGGGCGACGGCACACACCGCCACCGTCTCGCTCAGGCT	291	
Qy	61	CTCGTACCGGAGGGCCTTCGGCAACGTCCGCCCGCGTGCCTAAACCCGATGGCTCTCAAGGCG	120	
Db	292	CTGCTTCGCGAAGCCTTCGCGCAACGTTCGACGCGGGCGCCAAACCGCTTCGGCTCAAGCGT	351	
Qy	121	GGCATCCAGAAAGCGCGTCGAGGGCGTCTCCGGCGCCCTGCTGGAGCAGGGCGGAAGGATGC	180	
Db	352	GGCATCCAGAAAGGCTGTGAGAGGCTGTCAACCAAGTCGCTGTGAAGTCGGGCCAAGGAGGTC	411	
Qy	181	GAGACCAAGGAGCAGATCGCTTCCACGGGCTTCCATCTCCGCGCGCGCACCCACGATCGGC	240	
Db	412	GAGACCAAGGAGCAGATTTCTGCGCACCGCGGCGATTTCCGCGCGCGCACCCAGATCGGC	471	
Qy	241	GAGCTCATCGCGAGGGCGATGACCAAGGTCGGGCAGGAAGGCGGTCTACACGTCGAGGAG	300	
Db	472	GAGCTCATCGCGAGGGCCATGAGCAAGGTCGGCAACGAGGGGTGTATCATCCGTCGAGGAG	531	
Qy	301	TCCCGAGACCTTCGCTCTGGAGCTTGAGCTCACCGAGGGTATGGCTTCGACAAAGGGGTAC	360	
Db	532	TCGNAACACTTCGGGCTCTGAGCTCGAGCTCACCGAGGGTATGGCTTCGACNAGGGGTAC	591	
Qy	361	ATCTCGGCTACTTCGCCACCGACNAGGAGCGGATGGAGGGCTGGCTCGACGACCCGTAC	420	
Db	592	ATCTCGGGTTACTTCGTGACCGACCGCGAGCGCCAGGAACCGCTTCCTGGAGGATCCCTAC	651	

RESULT 7

US-08-997-362-159
; Sequence 159, Application US/08997362
; Patent No. 5985287

GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362


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; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-159

Query Match 73.3%; Score 308; DB 3; Length 1626;
Best Local Similarity 83.3%; Pred. No. 1.2e-50;
Matches 350; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGGTACGACACACCGCGACCGGTCTCTCGCCACGCG 60
   |||
Db 232 AAGAAGACGACGACGTCGCGGGGCGGACGACACACCGCGACCGGTCTCGCTCAGGCT 291
   |||

QY 61 CTCGTATCGGAGGGCCTTGCACAACTGTCGCCCGCGGTGCCAAACCGATGGCTCTCAAGCGC 120
   |||
Db 292 CTGTTTCGCGAAGGCTTCGCGCAAGCTGCGAGCGCGGCGCAACCCGCTCGGCTCAAGCGT 351
   |||

QY 121 GGCATCGAAGAGCGCTCGAGGGCGGTCTCCGGCGCCCTGCTGGAGCAGGCGGAAGGATGTC 180
   |||
Db 352 GGCATCGAAGAGCTGTGAGGGGTGTACCACTGCTGCTGAAGTCGCGCAAGGAGGTC 411
   |||

QY 181 GAGACCAAGAGCAGATCGCTTCACGGCTCTCATCTCCGCCCGCGACACCCAGATCGGC 240
   |||
Db 412 GAGACCAAGAGCAGATTTCTGCAACCGCGCGATTTCCGCGGCGACACCCAGATCGGC 471
   |||

QY 241 GAGCTCATCTCCGAGGCGATGGCAAGGTTCGGCAAGGAAGCGCTCATCACCGTCGAGGAG 300
   |||
Db 472 GAGCTCATCTCCGAGGCGATGGCAAGGTTCGGCAAGTCGAGGCTGTCATCACCGTCGAGGAG 531
   |||

QY 301 TCCGAGACCTTCGCTGAGAGCTGGAGCTCACCAGGGGTATGCGCTTCGACAGGGGCTAC 360
   |||
Db 532 TCGAACAACCTTCGCGCTGCGAGCTCGAGCTCACCAGGGGTATGCGCTTCGACAGGGGCTAC 591
   |||

QY 361 ATCTCGCGGTACTTCGCGACCGACATGGAGCGGATGGAGGCGCTCGCTTCGACAGCCCTAC 420
   |||
Db 592 ATCTCGGGTTACTTCTGTGACCGAGCGCGCGGAGGAGGAGGAGGATCCCTTC 651
   |||

RESULT 11
US-08-997-080-115
; Sequence 115, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICAL
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563

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241 GAGCTGTTTCCCGACCAATATATATGTCCTCAGGAGGGGTGTATCATCACCGTTCAGGAG
472 GAGCTCATCGCGGAGGCCATGGAACAAGGTGGCAACAGGGGTGTATCATCACCGTTCAGGAG
301 TCCCAGACTTTCGGTCTTGAGAGCTCAGAGCTCACCGAGGGTATGGCGTTCGCACAAGGGCTAC
532 TCGAACACTTTCGGCGTCACGCTCGAGCTCACCGAGGGTATGGCTTCGCACAAGGGCTAC
361 ATCTCGGGGTACTTCGCCACCAGCATGGAGCGGATGGAGCGGTGCGTTCGACGACCCGCTAC
592 ATCTCGGGGTACTTTCGTGACCGGAGCGCCGAGGAGCGGTCTCTGGAGGATCCCTTAC
        RESULT 10
US-09-205-426-159
; Sequence 159, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 159

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TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
US-08-997-080-115

Query Match          72.8%; Score 305.6; DB 2; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 291
QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 120
DB 292 CTGCTTCGCAAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 351
QY 121 GGCATCGCAAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 180
DB 352 GGCATCGCAAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGTGCGCAACCGCGATGCG 240
DB 412 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGTGCGCAACCGCGATGCG 471
QY 241 GAGCTCATCGCGAGGCGATGACAAAGTTCGCGAGGAGGAGGCGTATCATCGTTCGAGGAG 300
DB 472 GAGCTCATCGCGAGGCGATGACAAAGTTCGCGAGGAGGAGGCGTATCATCGTTCGAGGAG 531
QY 301 TCCAGACCTTCGCTCGAGCTCGAGGCTCACGAGGAGTATCGCTTCGACAGGCGTAC 360
DB 532 TCGAACACCTTCGCTCGAGCTCGAGGCTCACGAGGAGTATCGCTTCGACAGGCGTAC 591
QY 361 ATCTCGGGTACTTTCGCCACCGCATGAGCGGATGAGGCGTCTCGTCGACGACCC 416
DB 592 ATCTCGGGTACTTTCGCCACCGCATGAGCGGATGAGGCGTCTCGTCGAGGATCC 647

RESULT 12
US-08-997-362-115
; Sequence 115, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiya, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
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PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
US-08-997-362-115

Query Match          72.8%; Score 305.6; DB 2; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 60
DB 232 AAGAAGACGAGCAGCTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 291
QY 61 CTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 120
DB 292 CTGCTTCGCAAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 351
QY 121 GGCATCGCAAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 180
DB 352 GGCATCGCAAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCGCGATGCGTCTCAAGCG 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGTGCGCAACCGCGATGCG 240
DB 412 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTTCCATCTCCGCGCGGTGCGCAACCGCGATGCG 471
QY 241 GAGCTCATCGCGAGGCGATGACAAAGTTCGCGAGGAGGAGGCGTATCATCGTTCGAGGAG 300
DB 472 GAGCTCATCGCGAGGCGATGACAAAGTTCGCGAGGAGGAGGCGTATCATCGTTCGAGGAG 531
QY 301 TCCAGACCTTCGCTCGAGCTCGAGGCTCACGAGGAGTATCGCTTCGACAGGCGTAC 360
DB 532 TCGAACACCTTCGCTCGAGCTCGAGGCTCACGAGGAGTATCGCTTCGACAGGCGTAC 591
QY 361 ATCTCGGGTACTTTCGCCACCGCATGAGCGGATGAGGCGTCTCGTCGACGACCC 416
DB 592 ATCTCGGGTACTTTCGCCACCGCATGAGCGGATGAGGCGTCTCGTCGAGGATCC 647
```

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RESULT 13
US-09-095-855-115
; Sequence 115, Application US/09095855
; Patent No. 616093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITL OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
```

```
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 647 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
; US-09-095-855-115

Query Match 72.8%; Score 305.6; DB 3; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGCGGACCGGTCCTCGGCCGAGGCG 60
Db 232 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGCGGACCGGTCCTCGGCCGAGGCT 291
QY 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGACCGGTCCTCGGCCGAGGCG 120
Db 292 CTGGTTCCGAGAGGCTGCGCAACGTCGCGCGCGGTGACCGGTCCTCGGCCGAGGCT 351
QY 121 GGCATCGAGAAGCGCGTCGAGGCGGTCCTCGCGCGCGGTGACCGGTCCTCGGCCGAGGATGC 180
Db 352 GGCATCGAGAAGCGTCGCGAGGCTGTCACCCAGTCGTCGTCGAGGAGGTC 411
QY 181 GAGACCAAGAGCAGATCGCTTCACGGGCTTCATCTCCGCGCGGTGACCGGTCCTCGGCCGAGGATGC 240
Db 412 GAGACCAAGAGCAGATTTCTGCCACCGCGCGGTGACCGGTCCTCGGCCGAGGATGC 471
QY 241 GAGCTCATCGCGAGGCGGTCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTC 300
Db 472 GAGCTCATCGCGAGGCGGTCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTC 531
QY 301 TCCACAGACCTTCGGCTCGGAGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTC 360
Db 532 TCGAACACCTTCGGCTCGGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAG 591
QY 361 ATCTCGGCTACTTCCGCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTC 416
Db 592 ATCTCGGCTACTTCCGCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTC 647

RESULT 15
US-09-205-426-115
; Sequence 115, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115

; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-115

Query Match 72.8%; Score 305.6; DB 3; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGCGGACCGGTCCTCGGCCGAGGCG 60
Db 232 AAGAAGACGACGACGTCGCGCGGTGACGGTACGACACCGCGGACCGGTCCTCGGCCGAGGCT 291
QY 61 CTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGACCGGTCCTCGGCCGAGGCG 120
Db 292 CTGGTTCCGAGAGGCTGCGCAACGTCGCGCGCGGTGACCGGTCCTCGGCCGAGGCT 351
QY 121 GGCATCGAGAAGCGCGTCGAGGCGGTCCTCGCGCGCGGTGACCGGTCCTCGGCCGAGGATGC 180
Db 352 GGCATCGAGAAGCGTCGCGAGGCTGTCACCCAGTCGTCGTCGAGGAGGTC 411
QY 181 GAGACCAAGAGCAGATCGCTTCACGGGCTTCATCTCCGCGCGGTGACCGGTCCTCGGCCGAGGATGC 240
Db 412 GAGACCAAGAGCAGATTTCTGCCACCGCGCGGTGACCGGTCCTCGGCCGAGGATGC 471
QY 241 GAGCTCATCGCGAGGCGGTCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTC 300
Db 472 GAGCTCATCGCGAGGCGGTCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTCGCGCAAGGTC 531
QY 301 TCCACAGACCTTCGGCTCGGAGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTC 360
Db 532 TCGAACACCTTCGGCTCGGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAGCTCGAG 591
QY 361 ATCTCGGCTACTTCCGCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTC 416
Db 592 ATCTCGGCTACTTCCGCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTC 647

RESULT 14
US-09-324-542-115
; Sequence 115, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
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; LENGTH: 647
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-205-426-115

Query Match      72.8%; Score 305.6; DB 3; Length 647;
Best Local Similarity 83.4%; Pred. No. 3.5e-50;
Matches 347; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGACGCTCGCGGTGACGGTACGACACACCGCGACCGTTCGCGCCAGGGCG 60
DB 232 AAGAAGACGAGACGCTCGCGGTGACGGTACGACACACCGCGACCGTTCGCTCAGGCT 291
QY 61 CTCGTACGAGGGCTCGCGCAACGTCGCGCGGTGCGCAACCGTTCGCGCGGTTCGCGCGG 120
DB 292 CTGCTTCGCGAAGGCTCGCGCAACGTCGCGCGGTGCGCAACCGTTCGCGCGGTTCGCGCGG 351
QY 121 GGCATCGAGAGGCTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 180
DB 352 GGCATCGAGAGGCTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGCACACCGAGGCTAC 240
DB 412 GAGACCAAGGAGCAGATTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGG 471
QY 241 GAGCTCATCGCGAGCGGATGACAAAGGTCGCGCAAGGAGGCTCATCCCGTTCGAGGAG 300
DB 472 GAGCTCATCGCGAGCGGATGACAAAGGTCGCGCAAGGAGGCTCATCCCGTTCGAGGAG 531
QY 301 TCCGACACCTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGG 360
DB 532 TCGAACACCTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGG 591
QY 361 ATCTCGGGGTACTTCCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 416
DB 592 ATCTCGGGGTACTTCCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 647

RESULT 16
US-10-068-059-5
; Sequence 5, Application US/10068059
; Patent No. 6921534
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acids encoding fusion protein
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
US-10-068-059-5

Query Match      70.3%; Score 295.2; DB 3; Length 2241;
Best Local Similarity 81.4%; Pred. No. 3.5e-48;
Matches 342; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGACGCTCGCGGTGACGGTACGACACACCGCGACCGTTCGCGCCAGGGCG 60
DB 850 AAGAAGACGAGATGAGTTCGCGGTGACGGTACGACACACCGCGACCGTTCGCGCCAGGGCG 909
QY 61 CTCGTACGCGAGGGCTCGCGCAACGTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 120

Query Match      69.9%; Score 293.6; DB 3; Length 1623;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGACGCTCGCGGTGACGGTACGACACACCGCGACCGTTCGCGCCAGGGCG 60
DB 232 AAGAAGACGAGATGAGTTCGCGGTGACGGTACGACACACCGCGACCGTTCGCGCCAGGGCG 291
QY 61 CTCGTACGCGAGGGCTTCGCGCAACGTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 120
DB 292 TTGGTTTCGCGAGGGCTTCGCGCAACGTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGG 351
QY 121 GGCATCGAGAGGCGCTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 180
DB 352 GGCATCGAGAGGCGCTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGCACACCGAGGCTAC 240
DB 412 GAGACCAAGGAGCAGATTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGG 471
QY 241 GAGCTCATCGCGAGGGCTTCGCGCAACGTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGG 300
DB 472 GACCTGATCGCGAGGGCTTCGCGCAACGTCGCGCGGTTCGCGCGGTTCGCGCGGTTCGCGCGG 531
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QY 301 TCCAGAGACCTTCGGTTCGAGCTGAGCTCACCGAGGATGCGTTTCGACAAAGGGCTAC 360
Db 532 TCCAAACACCTTTGGCTGCGAGCTCGAGCTCACCGAGGATGCGTTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCGCACCGACGATGAGCGGATGAGCGGCTCGCTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGCGCACCGACGATGAGCGGATGAGCGGCTCGCTCGACGACCGGTAC 651

RESULT 18

US-10-267-311-3
; Sequence 3, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match 69.9%; Score 293.6; DB 3; Length 1623;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAGAGCGACGACGTCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 60
Db 232 AAGAGAGCGACGATGACGTCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 291
QY 61 CTGCTAGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 120
Db 292 TTGGTTTCGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 351
QY 121 GGCAATCGAAGAGCGGCTCGAGGCGGCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 180
Db 352 GGCAATCGAAGAGCGGCTCGAGGCGGCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 411
QY 181 GAGACCAAGAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCGCGGACACCGAGATCGGC 240
Db 412 GAGACCAAGAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCGCGGACACCGAGATCGGC 471
QY 241 GAGCTCATTCGCGAGGCGATGGAACAGGTGGCAAGGAGGCGCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATTCGCGAGGCGATGGAACAGGTGGCAAGGAGGCGCTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTTCGAGCTGAGCTCACCGAGGATGCGTTTCGACAAAGGGCTAC 360
Db 532 TCCAAACACCTTTGGCTGCGAGCTCGAGCTCACCGAGGATGCGTTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCGCACCGACGATGAGCGGATGAGCGGCTCGCTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGCGCACCGACGATGAGCGGATGAGCGGCTCGCTCGACGACCGGTAC 651

RESULT 19

US-09-712-363-23
; Sequence 23, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eissenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match 69.9%; Score 293.6; DB 3; Length 1623;
Best Local Similarity 81.2%; Pred. No. 7.1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAGAGCGACGACGTCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 60
Db 232 AAGAGAGCGACGATGACGTCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 291
QY 61 CTGCTAGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 120
Db 292 TTGGTTTCGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 351
QY 121 GGCAATCGAAGAGCGGCTCGAGGCGGCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 180
Db 352 GGCAATCGAAGAGCGGCTCGAGGCGGCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 411
QY 181 GAGACCAAGAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCGCGGACACCGAGATCGGC 240
Db 412 GAGACCAAGAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCGCGGACACCGAGATCGGC 471
QY 241 GAGCTCATTCGCGAGGCGATGGAACAGGTGGCAAGGAGGCGCTCATCACCGTCGAGGAG 300
Db 472 GAGCTCATTCGCGAGGCGATGGAACAGGTGGCAAGGAGGCGCTCATCACCGTCGAGGAG 531
QY 301 TCCAGACCTTCGGTTCGAGCTGAGCTCACCGAGGATGCGTTTCGACAAAGGGCTAC 360
Db 532 TCCAAACACCTTTGGCTGCGAGCTCGAGCTCACCGAGGATGCGTTTCGACAAAGGGCTAC 591
QY 361 ATCTCGGCGTACTTCGCGCACCGACGATGAGCGGATGAGCGGCTCGCTCGACGACCGGTAC 420
Db 592 ATCTCGGCGTACTTCGCGCACCGACGATGAGCGGATGAGCGGCTCGCTCGACGACCGGTAC 651

RESULT 20
US-09-613-303-16

Qy	121	GGCATCGAAGAGCGCTCGAGGCCCTCTCCGGCGCCCTCTGCGAGCAGCGCAAGGATGTC	181
Db	676	GGCATCGAAGAGCGCTCGAGGAAGGTCAACGAGACCCCTGCTCAAGGGCGCCCAAGGAGTTC	735
Qy	181	GAGACCAAGGAGCAGATCGCTTCCACGGCCTTCATCTCCGGCGCGACACCCAGATCGGC	240
Db	736	GAGACCAAGGAGCAGATTCGGCCACCGAGGATTTTCGGCGGGTGACCACTCCATCGGT	795
Qy	241	GAGCTCATCGCCGAGCGCATGATGCAAGGTTCGGCAAGGAGGCGTTCATCACCGTTCGAGGAG	300
Db	796	GACCTGATCGCCGAGCGCATGATGCAAGGTTCGGCAAGGAGGCGTTCATCACCGTTCGAGGAG	855
Qy	301	TCCAGACCTTCGGTTCGAGCTGAGCTCACCGAGGGTATGCGCTTCGACACAGGGCTTAC	360
Db	856	TCCAAACACCTTTGGGCTGCAGCTTCGAGCTCACCGAGGGTATGCGCTTCGACACAGGGCTTAC	915
Qy	361	ATCTCGGGCTACTTCGCCACCGACATGAGCGGATGAGAGGGCTCGCTCGACGACCCGTAC	420
Db	916	ATCTCGGGCTACTTCGTGTGACCGACCCGAGCGTTCAGGAGGGCTCTCTGAGGAGCCCCCTAC	975
RESULT 24			
US-10-068-059-9			
; Sequence 9, Application US/10068059			
; Patent No. 6921534			
; GENERAL INFORMATION:			
; APPLICANT: Mizzen, Lee A.			
; APPLICANT: Hongwei, Liu			
; APPLICANT: Siegel, Marvin			
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT			
; FILE REFERENCE: 12071-017002			
; CURRENT APPLICATION NUMBER: US/10/068,059			
; PRIOR FILING DATE: 2002-06-04			
; PRIOR APPLICATION NUMBER: US 60/266,733			
; PRIOR FILING DATE: 2001-02-05			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 9			
; LENGTH: 2073			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)...(2070)			
; OTHER INFORMATION: Nucleic acids encoding fusion protein			
US-10-068-059-9			
Query Match 69.9%; Score 293.6; DB 3; Length 2073;			
Best Local Similarity 81.2%; Pred. No. 7.1e-48;			
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;			
Qy	1	AAGAAGACGAGCAGCTCGCGGTGACCGTACGAGCAGCGACCGTCTCGCCCGAGCG	60
Db	682	AAGAAGACGATGACGTGCGCGGTGACCGTACGAGCAGCGACCGTCTCGCCCGAGCG	741
Qy	61	CTCGTACGCGAGCGCTCGCGCAACGTTCGCGCGCGGTGCAACCCGATGGCTCTCAAGCGC	120
Db	742	TTGGTTGCGAGGGCTCTGCGCAACGTTCGCGCGCGGTGCAACCCGCTCGGTCTCAAGCGC	801
Qy	121	GGCATCGAAGAGCGCTCGAGGCCCTCTCCGGCGCCCTCTGCGAGCAGCGCAAGGATGTC	180
Db	802	GGCATCGAAGAGCGCTCGAGGAAGGTTCACCGAGACCCCTGCTCAAGGGCGCCCAAGGAGTTC	861
Qy	181	GAGACCAAGGAGCAGATCGCTTCCACGGCCTTCATCTCCGGCGCGACACCCAGATCGGC	240
Db	862	GAGACCAAGGAGCAGATTCGGCCACCGAGGATTTTCGGCGGGTGACCACTCCATCGGT	921
Qy	241	GAGCTCATCGCCGAGCGCATGATGCAAGGTTCGGCAAGGAGGCGTTCATCACCGTTCGAGGAG	300
Db	922	GACCTGATCGCCGAGCGCATGATGCAAGGTTCGGCAAGGAGGCGTTCATCACCGTTCGAGGAG	981
Qy	301	TCCAGACCTTCGGTTCGAGCTGAGCTCACCGAGGGTATGCGCTTCGACACAGGGCTTAC	360
Best Local Similarity 81.2%; Pred. No. 7.1e-48;			
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;			
Query Match 69.9%; Score 293.6; DB 3; Length 1947;			
Best Local Similarity 81.2%; Pred. No. 7.1e-48;			
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;			
Qy	1	AAGAAGACGAGCAGCTCGCGGTGACCGTACGAGCAGCGACCGTCTCGCCCGAGCG	60
Db	556	AAGAAGACGATGACGTTCGCGGTGACCGTACGAGCAGCGACCGTCTCGCCCGAGCG	615
Qy	61	CTCGTACGCGAGCGCTCGCGCAACGTTCGCGCGGTGCAACCCGATGGCTCTCAAGCGC	120
Db	616	TTGGTTGCGAGGGCTTCGCGCAACGTTCGCGCGGTGCAACCCGCTCGGTCTCAAGCGC	675
Qy	121	GGCATCGAAGAGCGCTCGAGGCCCTCTCCGGCGCCCTCTGCGAGCAGCGCAAGGATGTC	180
Db	676	GGCATCGAAGAGCGCTCGAGGAAGGTTCACCGAGACCCCTGCTCAAGGGCGCCCAAGGAGTTC	735
Qy	181	GAGACCAAGGAGCAGATCGCTTCCACGGCCTTCATCTCCGGCGCGACACCCAGATCGGC	240
Db	736	GAGACCAAGGAGCAGATTCGGCCACCGAGGATTTTCGGCGGGTGACCACTCCATCGGT	795
Qy	241	GAGCTCATCGCCGAGCGCATGATGCAAGGTTCGGCAAGGAGGCGTTCATCACCGTTCGAGGAG	300
Db	796	GACCTGATCGCCGAGCGCATGATGCAAGGTTCGGCAAGGAGGCGTTCATCACCGTTCGAGGAG	855
Qy	301	TCCAGACCTTCGGTTCGAGCTGAGCTCACCGAGGGTATGCGCTTCGACACAGGGCTTAC	360
Db	856	TCCAAACACCTTTGGGCTGCAGCTTCGAGCTCACCGAGGGTATGCGCTTCGACACAGGGCTTAC	915
Qy	361	ATCTCGGGCTACTTCGCCACCGACATGAGCGGATGAGAGGGCTCGCTCGACGACCCGTAC	420
Db	916	ATCTCGGGCTACTTCGTGTGACCGACCCGAGCGTTCAGGAGGGCTCTCTGAGGAGCCCCCTAC	975
RESULT 23			
US-10-267-311-28			
; Sequence 28, Application US/10267311			
; Patent No. 6657055			
; GENERAL INFORMATION:			
; APPLICANT: Siegel, Marvin			
; APPLICANT: Chu, N. Randall			
; APPLICANT: Mizzen, Lee A.			
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO			
; FILE REFERENCE: 12071/002001			
; CURRENT APPLICATION NUMBER: US/10/267,311			
; CURRENT FILING DATE: 2002-10-09			
; PRIOR APPLICATION NUMBER: US/09/613,303			
; PRIOR FILING DATE: 2000-07-10			
; PRIOR APPLICATION NUMBER: US 60/143,757			
; PRIOR FILING DATE: 1999-07-08			
; NUMBER OF SEQ ID NOS: 55			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 28			
; LENGTH: 1947			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: fusion sequence			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)...(1944)			
US-10-267-311-28			
Query Match 69.9%; Score 293.6; DB 3; Length 1947;			
Best Local Similarity 81.2%; Pred. No. 7.1e-48;			
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;			
Qy	1	AAGAAGACGAGCAGCTCGCGGTGACCGTACGAGCAGCGACCGTCTCGCCCGAGCG	60
Db	556	AAGAAGACGATGACGTTCGCGGTGACCGTACGAGCAGCGACCGTCTCGCCCGAGCG	615
Qy	61	CTCGTACGCGAGCGCTCGCGCAACGTTCGCGCGGTGCAACCCGATGGCTCTCAAGCGC	120
Db	616	TTGGTTGCGAGGGCTTCGCGCAACGTTCGCGCGGTGCAACCCGCTCGGTCTCAAGCGC	675

Db 982 TCACACACCTTTGGGCTGAGCTCAGCGGATGCGGTTTCGACAGGGCTAC 1041
Qy 361 ATCTCGGCTACTTCCACCGCATGAGCGGATGAGCGGCTGCTCGACGACCGGTAC 420
Db 1042 ATCTCGGCTACTTCCGACCGACCGGAGCGTCAAGGCGGCTCTCGAGGACCCCTAC 1101

RESULT 25

US-10-068-059-7

; Sequence 7, Application US/10068059

; Patent No. 6921534

; GENERAL INFORMATION:

; APPLICANT: Mizzen, Lee A.

; APPLICANT: Hongwei, Liu

; APPLICANT: Siegel, Marvin

; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT

; FILE REFERENCE: 12071-017002

; CURRENT APPLICATION NUMBER: US/10/068,059

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 60/266,733

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 2130

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2127)

; OTHER INFORMATION: Nucleic acids encoding fusion protein

US-10-068-059-7

Query Match 69.9%; Score 293.6; DB 3; Length 2130;
Best Local Similarity 81.2%; Pred. No. 7,1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACCGACCGGACCGTTCTCGCCGAGGG 60
Db 739 AAGAAGACCGATGAGTCCCGGTGACGGTACGACCGACCGGACCGTCTCGCCGAGGG 798
Qy 61 CTCGTACGCGAGGGCTCGGCAACGTCCGCGCGGTGCGCAACCGATGGTCTCAAGCGC 120
Db 799 TTGGTTCCGCGAGGGCTCGGCAACGTCCGCGCGGTGCGCAACCGTCTCGGTTCAAGCGC 858
Qy 121 GGCATCGAGAGCGCGTCCGAGCGCTCTCCGCGCGCTTCCGCGCGGTGCGCAACCGATGTC 180
Db 859 GGCATCGAGAGCGCGTCCGAGCGCTCTCCGCGCGGTGCGCAACCGATGTC 918
Qy 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGGTGCGCAACCGATGTC 240
Db 919 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGGTGCGCAACCGATGTC 978
Qy 241 GAGTCTATCGCGAGCGGATGAGCAAGGTGCGCAAGGAGGCTCATCCGTCGAGGAG 300
Db 979 GACCTGATCGCGAGCGGATGAGCAAGGTGCGCAAGGAGGCTCATCCGTCGAGGAG 1038
Qy 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGGTATGCGTTCGACAGGGGCTAC 360
Db 1039 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGGTATGCGTTCGACAGGGGCTAC 1098
Qy 361 ATCTCGGCGTACTTCCGACCGCATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 420
Db 1099 ATCTCGGCGTACTTCCGACCGCATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 1158

RESULT 26

US-10-068-059-11

; Sequence 11, Application US/10068059

; Patent No. 6921534

; GENERAL INFORMATION:

; APPLICANT: Mizzen, Lee A.

; APPLICANT: Hongwei, Liu

; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match 69.9%; Score 293.6; DB 3; Length 2175;
Best Local Similarity 81.2%; Pred. No. 7,1e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACCGACCGGACCGTTCTCGCCGAGGG 60
Db 784 AAGAAGACCGATGAGTCCCGGTGACGGTACGACCGGACCGGACCGTCTCGCCGAGGG 843
Qy 61 CTCGTACGCGAGGGCTCGGCAACGTCCGCGCGGTGCGCAACCGATGGTCTCAAGCGC 120
Db 844 TTGGTTCCGCGAGGGCTCGGCAACGTCCGCGCGGTGCGCAACCGGCTCGGTTCAAGCGC 903
Qy 121 GGCATCGAGAGCGCGTCCGAGCGCTCTCCGCGCGCTTCCGCGCGGTGCGCAACCGATGTC 180
Db 904 GGCATCGAGAGCGCGTCCGAGCGCTCTCCGCGCGGTGCGCAACCGATGTC 963
Qy 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCGCGCGGTGCGCAACCGATGTC 240
Db 964 GAGACCAAGGAGCAGATCGCTTCCAGCGCTTCCATCTCCGCGCGGTGCGCAACCGATGTC 1023
Qy 241 GAGTCTATCGCGAGGGGATGAGCAAGGTCCGCAAGGAGGCGTCCATCCGTCGAGGAG 300
Db 1024 GAGTCTATCGCGAGGGGATGAGCAAGGTCCGCAAGGAGGCGTCCATCCGTCGAGGAG 1083
Qy 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGGTATGCGTTCGACAGGGGCTAC 360
Db 1084 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGGTATGCGTTCGACAGGGGCTAC 1143
Qy 361 ATCTCGGCGTACTTCCGACCGCATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 420
Db 1144 ATCTCGGCGTACTTCCGACCGCATGAGCGGATGAGGCGTCTCGACGACCGGCTAC 1203

RESULT 27

US-09-613-303-20

; Sequence 20, Application US/09613303

; Patent No. 6495347

; GENERAL INFORMATION:

; APPLICANT: Siegel, Marvin

; APPLICANT: Chu, N. Randall

; APPLICANT: Mizzen, Lee A.

; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

; FILE REFERENCE: 12071/002001

; CURRENT APPLICATION NUMBER: US/09/613,303

; CURRENT FILING DATE: 2000-07-10

; PRIOR APPLICATION NUMBER: US 60/143,757

; PRIOR FILING DATE: 1999-07-08

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 2847

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

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; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-09-613-303-20

Query Match      69.9%; Score 293.6; DB 3; Length 2847;
Best Local Similarity 81.2%; Pred. No. 7.2e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 60
    |||||
Db 292 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 120
    |||||
QY 292 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 351
    |||||
Db 61 CTCGTACGAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 120
    |||||
QY 61 CTCGTACGAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 411
    |||||
Db 121 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 180
    |||||
QY 121 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 471
    |||||
Db 181 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 240
    |||||
QY 472 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 531
    |||||
Db 241 GAGCTCATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 300
    |||||
QY 532 GACCTGATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 591
    |||||
Db 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 360
    |||||
QY 592 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 651
    |||||
Db 361 ATCTCGCGTACTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 420
    |||||
QY 652 ATCTCGCGTACTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 711
    |||||

RESULT 28
US-10-267-311-20
; Sequence 20, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match      69.9%; Score 293.6; DB 3; Length 2847;
Best Local Similarity 81.2%; Pred. No. 7.2e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 60
    |||||
Db 292 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 120
    |||||
QY 61 CTCGTACGAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 120
    |||||
Db 543 TTGGTTTCGCGAGGGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 602
    |||||
QY 121 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 180
    |||||
Db 603 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 662
    |||||
QY 181 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 240
    |||||
Db 663 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 722
    |||||
QY 241 GAGCTCATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 300
    |||||
Db 723 GACCTGATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 782
    |||||
QY 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 360
    |||||
Db 783 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 842
    |||||

; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-09-613-303-20

Query Match      69.9%; Score 293.6; DB 3; Length 2847;
Best Local Similarity 81.2%; Pred. No. 7.2e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 60
    |||||
Db 292 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 351
    |||||
QY 61 CTCGTACGAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 120
    |||||
Db 352 TTGGTTTCGCGAGGGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 411
    |||||
QY 121 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 180
    |||||
Db 412 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 471
    |||||
QY 181 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 240
    |||||
Db 472 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 531
    |||||
QY 241 GAGCTCATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 300
    |||||
Db 532 GACCTGATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 591
    |||||
QY 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 360
    |||||
Db 592 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 651
    |||||
QY 361 ATCTCGCGTACTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 420
    |||||
Db 652 ATCTCGCGTACTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 711
    |||||

RESULT 28
US-10-267-311-20
; Sequence 20, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2844)
US-10-267-311-20

Query Match      69.9%; Score 293.6; DB 3; Length 2847;
Best Local Similarity 81.2%; Pred. No. 7.2e-48;
Matches 341; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 60
    |||||
Db 292 AAGAAGACGACGACGTCGCGGTGACGGTACGACACACCGGACCGTTCGCGCCAGGGCG 120
    |||||
QY 61 CTCGTACGAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 120
    |||||
Db 543 TTGGTTTCGCGAGGGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 602
    |||||
QY 121 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 180
    |||||
Db 603 GGCATCGAAGAGGCGCTCGCGCAACGCTCGCGCGCGGTGCCAACCGGATGCTCTCAAGCGC 662
    |||||
QY 181 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 240
    |||||
Db 663 GAGACCAAGAGAGAGATGCTTCACGGGCTTCATCTCCGCGCGGACACCGGATCGGC 722
    |||||
QY 241 GAGCTCATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 300
    |||||
Db 723 GACCTGATCGCGAGGCGATGACAGGTTCGCGCAAGGAGGCGTCAACCGTCGAGGAG 782
    |||||
QY 301 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 360
    |||||
Db 783 TCCAGACCTTCGCTCGAGCTGAGCTCACCGAGGGTATCGGTTTCGACAAAGGGCTAC 842
    |||||
```


APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,775
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-08-461-775-10

Query Match 64.2%; Score 269.8; DB 2; Length 1620;
Best Local Similarity 77.9%; Pred. No. 2.6e-43;
Matches 325; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 4 AAGACGAGCAGTCCGCGGTGACGGTACGACCGGACCGGCGGTCTTCGCCCGAGCGGCTC 63
DB 235 AAGACCAACGACATCGCGGTGAGGGCACCACCGCGGACCGTGTGCGCCAGGGCTG 294

QY 64 GTACGGAGGGCTCGGCAAGCTCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGGCG 123
DB 295 GTCCGCGAGGGCTCGGCAAGCTCGCGCGGTGCGCGCGGTCTCCCGCGCGCTCGAAGAGG 354

QY 124 ATCGAGAGGGCTCGGCGGCGGTCTCGCGCGGTCTCGGCGCGGTCTCGAGCGCGCGGTCTCGAG 183
DB 355 ATCGAGCGCGGTCTCGCGCGGTCTCGCGCGGTCTCGAGCGCGCGGTCTCGAGCGCGCGGTCTCGAG 414

QY 184 ACCAAGAGCAGATCGCTTCCAGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAG 243
DB 415 GACAAGTCCGACATCGCGCGGTCTCGCGCGGTCTCGCGCGGTCTCGAGCGCGGTCTCGAGCGGTCTCGAG 474

QY 244 CTCATCGCGAGCGGTGAGCAAGGTGCGCAAGAGGCTCATCAGCGTCGAGAGTCC 303
DB 475 CTCATCGCGAGCGGTGAGCAAGGTGCGCAAGAGGCTCATCAGCGTCGAGAGTCC 534

QY 304 CAGACCTCGGTCTGAGCTGAGCTCACCGAGGTATGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAG 363
DB 535 AACACCTTCGGTGTGACCTGACCTTACCGAGGGGATGCGCTTCGACAAAGGGCTACCTG 594

QY 364 TCGCGGTACTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGAGACCGCGTAC 420
DB 595 TCCCGGTACATGGTACCGACCGAGGCGGTATGAGGGCGTCTCGAGACCGCGTAC 651

RESULT 35
US-09-031-606-10
Sequence 10, Application US/09031606
Patent No. 6153404
GENERAL INFORMATION:
APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, Gerard
TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,606
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1620
US-09-031-606-10

Query Match 64.2%; Score 269.8; DB 3; Length 1620;
Best Local Similarity 77.9%; Pred. No. 2.6e-43;
Matches 325; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 4 AAGACGAGCAGTCCGCGGTGACGGTACGACCGGACCGGCGGTCTTCGCCCGAGCGGCTC 63
DB 235 AAGACCAACGACATCGCGGTGAGGGCACCACCGCGGACCGTGTGCGCCAGGGCTG 294

QY 64 GTACGGAGGGCTCGGCAAGCTCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGGCG 123
DB 295 GTCCGCGAGGGCTCGGCAAGCTCGCGCGGTCTCGCGCGGTCTCGAGCGCGGTCTCGAGCGGTCTCGAG 354

QY 124 ATCGAGAGGGCTCGGCGGCGGTCTCGCGCGGTCTCGCGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAG 183
DB 355 ATCGAGCGCGGTCTCGCGCGGTCTCGCGCGGTCTCGAGCGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAG 414

QY 184 ACCAAGAGCAGATCGCTTCCAGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAGCGGTCTCGAG 243

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Db 415 GACAAGTCCGACATCGCCGCGTCTCCGCGCAGGACAGGTCGGCGAG 474
Qy 244 CTGATCCCGAGGCGATGGACAGGTTCGGAAGGAGGCTCATCAGCGTCGAGGAGTCC 303
Db 475 CTGATCCCGAGGCGATGGACAGGTTCGGAAGGAGGCTCATCAGCGTCGAGGAGTCC 534
Qy 304 CAGACCTTCGGTCTGGAGCTGGAGCTCAGCGAGGATGCGTTCGGAAGGAGGCTATCATC 363
Db 535 AACACCTTCGGTCTGGAGCTGGAGCTCAGCGAGGATGCGTTCGGAAGGAGGCTATCATC 594
Qy 364 TCGCGCTACTTCGCCACCGCATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
Db 595 TCCCGGTACATGGTGACCGAGGAGCGTATGAGGCGCTCTCGACGACCCGCTAC 651

RESULT 36
US-08-461-775-9
; Sequence 9, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/461,775
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-461-775-9

Query Match 63.9%; Score 268.2; DB 2; Length 2167;
Best Local Similarity 77.7%; Pred. No. 5.3e-43;
Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 4 AAGACGACGACGTCGCGGTGACGTACGACACCGGACCGTCTCGCCCGAGCGCTC 63
Db 1083 AAGACCAACGACATCGCGGTGACGCGACACACCGGACCGTCTCGCCCGAGCGCTG 1142
Qy 64 GTACGCGAGGCGCTGCGCAAGTCCGCGCGGTGCCAACCGGATGGCTCTCAAGCGCGGC 123
Db 1143 GTCCGCGAGGCGCTGCGCAAGTCCGCGCGGTGCCAACCGGATGGCTCTCAAGCGGCG 1202

124 ATCGAAGGCGCGTTCGAGGCGCGTCTCCGCGCCCTGCTGAGCAGCGAGGATGTCGAG 183
1203 ATCGAGCGCGCGTTCGCGCGCGTCTCCGCGAGTCTGTCACACCGCGCGCGGATCGAC 1262
Qy 184 ACCAAGGAGCAGATCGCTTTCACGGGCTCCATCTCCGCGCGCGACACCCAGATCGCGGAG 243
1263 GACAACTCCGACATCGCGCGCGTTCGCGCGCTCTCCGCGCAGGACGAGGTCGCGGAG 1322
Qy 244 CTGATCCCGAGGCGATGGACAGGTTCGGAAGGAGGCTCATCAGCGTCGAGGAGTCC 303
1323 CTGATCCCGAGGCGATGGACAGGTTCGGAAGGAGGCTCATCAGCGTCGAGGAGTCC 1382
Qy 304 CAGACCTTCGGTCTGGAGCTGGAGCTCAGCGAGGATGCGTTCGGAAGGAGGCTATCATC 363
1383 AACACCTTCGGTCTGGAGCTGGAGCTCAGCGAGGATGCGTTCGGAAGGAGGCTATCATC 1442
Qy 364 TCGCGCTACTTCGCCACCGCATGAGCGGATGAGGCGTCTCGACGACCCGCTAC 420
1443 TCCCGGTACATGGTGACCGAGGAGCGTATGAGGCGCTCTCGACGACCCGCTAC 1499

RESULT 37
US-09-031-606-9
; Sequence 9, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUGLIEMI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/031,606
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 9011186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-031-606-9

Query Match 63.9%; Score 268.2; DB 3; Length 2167;
Best Local Similarity 77.7%; Pred. No. 5.3e-43;
Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2668 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-09-031-606-11

Query Match      63.9%; Score 268.2; DB 3; Length 2668;
Best Local Similarity 77.7%; Pred. No. 5.4e-43;
Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY      4 AAGACGGACGACGTCCGCGGTGACGGTACGACCAACCGCGACCGCTTCTCGCCGAGGGGCTC 63
DB      1083 AAGACCAACACATCGCGGTGACGGTACGACCAACCGCGACCGTGTGCGCCGAGGGCTG 1142

QY      64 GTACGCGAGGGCTCGCGCAACGTGCGCGCGGTGCGCAACCGCGATGGCTCTCAAGCGCGGC 123
DB      1143 GTGCGGAGGGCTCGCGCAACGTGCGCGCGGTGCGCAACCGCGCTTCCCGCGCGCTGAAGAAGGGC 1202

QY      124 ATCGAAGAGCGCTCGAGGCGCGTCTCGCGCGCTTCTCGGCGCGCTTCTGAGCAGGCGAAGGATGTCGAG 183
DB      1203 ATCGAGCGCGCTCGCGCGCGTCTCGCGCGAGCTGCTCGACACCGCGCGCGCGATCGAC 1262

QY      184 ACCAAGGACGATCGTTTCCAGGCGCTTCCATCTTCGCGCGCGCGACACCGCGATCGGCGAG 243
DB      1263 GACAAGTCCGACATCGCGCGCGTCTCGCGCGCGCTTCTCGCGCGAGGACGACGATCGCGGAG 1322

QY      244 CTATCGCGCGAGCGATGGAACAGGTGCGCAAGGAGGCGTCTATCACCCTCGAGGAGTCC 303
DB      1323 CTATCGCGCGAGCGATGGAACAGGTGCGCAAGGAGGCGTCTATCACCCTCGAGGAGTCC 1382

QY      304 CAGACCTTCGGTTCGGAGCTCGAGCTCACCAGGCGTATGCGCTTCGACCAAGGCGCTACATC 363
DB      1383 AACACCTTCGGTTCGACCTGGACTTCACCGAGGCGATGCGCTTCGACCAAGGCGTACCTG 1442

QY      364 TCGGCGTACTTCGCGCGGATGAGCGGATGAGGCGTTCGCTCGACGACCGGTAC 420
DB      1443 TCCCCGTACATGTTGACCGGACGAGGCGTATGAGGCGCTCTCTCGACGACCGCGTAC 1499

RESULT 40
US-09-613-303-32
; Sequence 32, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-09-613-303-32

Query Match      60.7%; Score 254.8; DB 3; Length 888;
Best Local Similarity 81.5%; Pred. No. 1.9e-40;
Matches 295; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY      1 AAGACGCGACGACGTCCGCGGTGACGGTACGACCAACCGCGACCGCTTCTCGCCGAGGGC 60
DB      232 AAGACGCGATGACGTCCGCGGTGACGGTACGACCAACCGCGACCGCTTCTCGCCGAGGGC 291

QY      61 CTCGTACGCGAGGGCTTCGCAACGTCGCGCGGTGCGCAACCGCGATGGCTCTCAAGCGC 120
DB      292 TTGGTTTCGCGAGGGCTTCGCAACGTCGCGCGGTGCGCAACCGCGCTCGTCTCAAGCGC 351

QY      121 GGCATCGAAGGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCAGGAGGATGTC 180
DB      352 GGCATCGAAGGCGCGTGGAGGAGGTCAACCGAGACCGCTCTCAAGGCGCGCAAGGAGGTC 411

QY      181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCGATCGGC 240
DB      412 GAGACCAAGGAGCAGATTCGCGCGCACCGCAGCGATTCGCGCGGTGACCCAGTCCATCGGT 471

QY      241 GAGCTCATCGCGAGCGATGGAACAGGTGCGCAAGGTGCGCAAGGAGGCGTCAACCGCTCGAGGAG 300
DB      472 GACCTGATCGCGAGGCGATGGAACAGGTGCGCAAGGTGCGCAAGGAGGCGTCAACCGCTCGAGGAG 531

QY      301 TCCGACACCTTCGCTTCGAGCTGAGCTCAGGAGGTATGCGCTTCGACGAGGCGTAC 360
DB      532 TCCAACACCTTTGGGCTGCGCTCGAGCTCAGGAGGTATGCGGTTCGACGAGGCGCAT 591

QY      361 AT 362
DB      592 AT 593
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RESULT 41
US-10-267-311-32
; Sequence 32, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(885)
US-10-267-311-32

Query Match      60.7%; Score 254.8; DB 3; Length 888;
Best Local Similarity 81.5%; Pred. No. 1.9e-40;
Matches 295; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY      1 AAGACGCGACGACGTCCGCGGTGACGGTACGACCAACCGCGACCGCTTCTCGCCGAGGGC 60
DB      232 AAGACGCGATGACGTCCGCGGTGACGGTACGACCAACCGCGACCGCTTCTCGCCGAGGGC 291

QY      61 CTCGTACGCGAGGGCTTCGCAACGTCGCGCGGTGCGCAACCGCGATGGCTCTCAAGCGC 120
DB      292 TTGGTTTCGCGAGGGCTTCGCAACGTCGCGCGGTGCGCAACCGCGCTCGTCTCAAGCGC 351

QY      121 GGCATCGAAGGCGCTCGAGGCGCTCTCGGCGCGCTCTCGGAGCAGGAGGATGTC 180
DB      352 GGCATCGAAGGCGCGTGGAGGAGGTCAACCGAGACCGCTCTCAAGGCGCGCAAGGAGGTC 411

QY      181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCCATCTCCGCGCGCGACACCGATCGGC 240
DB      412 GAGACCAAGGAGCAGATTCGCGCGCACCGCAGCGATTCGCGCGGTGACCCAGTCCATCGGT 471

QY      241 GAGCTCATCGCGAGCGATGGAACAGGTGCGCAAGGTGCGCAAGGAGGCGTCAACCGCTCGAGGAG 300
DB      472 GACCTGATCGCGAGGCGATGGAACAGGTGCGCAAGGTGCGCAAGGAGGCGTCAACCGCTCGAGGAG 531

QY      301 TCCGACACCTTCGCTTCGAGCTGAGCTCAGGAGGTATGCGCTTCGACGAGGCGTAC 360
DB      532 TCCAACACCTTTGGGCTGCGCTCGAGCTCAGGAGGTATGCGGTTCGACGAGGCGCAT 591

QY      361 AT 362
DB      592 AT 593
```


	Matches	270;	Conservative	0;	Mismatches	48;	Indels	0;	Gaps	0;
Qy	1	AAGAAGACGGACGACGTCGGCGGTGACGGGTACGACCAACCGCGACCGTGTCTCGCCACGCG	60							
Db	43	AAGNAGCCGACGACGTCGGGGCGACGGCACCAACACCGCCACCGTGTCTCGCTCAGGCT	102							
Qy	61	CTCGTACGCGAGGGCCTGCGCAACGTCGCGCGCCGGTGCCAACCCGATGGTCTCAAGCGC	120							
Db	103	CTGGTTCGCGAAGGCCCTCGCAACGTCGACGCGCGCCCAACCCGCTCGGCGCTCAAGCGT	162							
Qy	121	GGCATCAGAAAGCCGTCGAGGCCGCTCTCCGGCGCCCTGCTGGAGCAGGCGGAAGGATGTC	180							
Db	163	GGCATCAGAAAGGCTGTGAGGGCTGTCAACCCAGTCGCTGTGAAAGTCGGGCCAAGGAGTC	222							
Qy	181	GAGACCAAGGAGCAGATCGCTTCCACCGCCCTCCATCTCCGCGCGGACACCCAGATCGGC	240							
Db	223	GAGACCAAGGAGCAGATTTCTGCCACCGCGCGATCTCCGCGCGGACACCCAGATCGGC	282							
Qy	241	GAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGAAGCGTCAATCACCGTCGAGGAG	300							
Db	283	GAGCTCATCGCGAGGCCATGGACAAGTGGCACAACGAGGGTGTCAACCGTCGAGGAG	342							
Qy	301	TCCGAGACCTTCGGTCTG	318							
Db	343	TCGAACACCTTCGGCCTG	360							

```

RESULT 44
US-08-873-970-79
; Sequence 79, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-873-970-79

Query Match 57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGGACACGCTCGCCGTTGACGGTACGACACCGCGACACCGCTTCTCGCCCAAGCG 60
DB 43 AAGAAGACCGACGACGCTCGCGGGCGACGCGACACACCGCGACACCGCTCGCTCAGGCT 102
QY 61 CTCGTACGGAGGGCTTCGGCGAAGCGTTCGGCGCGCGGTGCGAACCAGATGGCTTCAAGCGC 120
DB 103 CTGGTTTCGGAAGGCTTCGCGAAGCTCGAGCGCGCGCGCAACCGCTCGGCTTCAAGCGT 162
QY 121 GGCATCGAGNAGGCGCTCGAGGCGCTTCGGGCGCGCTCTGCTGGAGCAGGCGAAGGATGTC 180
DB 163 GGCATCGAGNAGGCTCTGAGAGGCTGTACCCAGTCTGCTGAAGTCGGCAAGGAGGTC 222
QY 181 GAGACCAAGGAGCAGATCGCTTCACGCGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 223 GAGACCAAGGAGCAGATTCCTGCACCGCGCGCATCTCCGCGCGCGACACCCAGATCGGC 282
QY 241 GAGCTCATCCCGAGGCGATGGACAAGGTTCGGCAAGGAAGGCGGTCTATCATCCGTTCGAGGAG 300
DB 283 GAGCTCATCCCGAGGCGCATGGACAAGGTTCGGCAAGGCGGTCTCATCACCGTCGAGGAG 342
QY 301 TCCAGACCTTCGGTCTG 318
DB 343 TCGAACACCTTCGCGCTG 360

RESULT 45
US-09-095-855-79
; Sequence 79, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Viseer, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TREATMENT: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-09-095-855-79

Query Match          57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGCTCGCGGTGACGCTAGCAGCAGCAGCGGACCGTCTCGCCGAGGCG 60
DB 43 AAGNAGACCGACGACGCTCGCGGCGAGCGGACGACGACCGCCACCGCTCGCTCAGGCT 102
QY 61 CTGTTACGCGAGGCGCTCGCGCAACGCTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
DB 103 CTGTTTCGCGAAGGCTCGCGCAACGCTCGCGAGCGCGGCGCAACCGCTCGAGCT 162
QY 121 GGCATCGAAGCGCTCGAGCGCTCTCGCGGCGCTCTCGTGGAGCAGCGAAGGATGTC 180
DB 163 GGCATCGAAGCGCTCGAGCGCTCTCACCCAGTCTGCTGAAGTCGGCCCAAGGAGTTC 222
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 223 GAGCTCATCGCGAGCGCATGACCAAGGTTCGGCAACGAGGGTGTCTATCACCGTCGAGGAG 282
QY 241 GAGCTCATCGCGAGCGCATGACCAAGGTTCGGCAACGAGGGTGTCTATCACCGTCGAGGAG 300
DB 283 GAGCTCATCGCGAGCGCATGACCAAGGTTCGGCAACGAGGGTGTCTATCACCGTCGAGGAG 342
QY 301 TCCAGACCTTCGGCTCG 318
DB 343 TCGAACACCTTCGGCCTG 360

RESULT 47
US-09-205-426-79
; Sequence 79, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-205-426-79

Query Match          57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGCTCGCGGTGACGCTAGCAGCAGCAGCGGACCGTCTCGCCGAGGCG 60
DB 43 AAGAAGACCGACGACGCTCGCGGCGAGCGGACGACGACCGCCACCGCTCGCTCAGGCT 102
QY 61 CTGTTACGCGAGGCGCTCGCGCAACGCTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
DB 103 CTGTTTCGCGAAGGCTCGCGCAACGCTCGCGAGCGCGGCGCAACCGCTCGAGCT 162
QY 121 GGCATCGAAGCGCTCGAGCGCTCTCGCGGCGCTCTCGTGGAGCAGCGAAGGATGTC 180
DB 163 GGCATCGAAGCGCTCGAGCGCTCTCACCCAGTCTGCTGAAGTCGGCCCAAGGAGTTC 222
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 223 GAGCTCATCGCGAGCGCATGACCAAGGTTCGGCAACGAGGGTGTCTATCACCGTCGAGGAG 282
QY 241 GAGCTCATCGCGAGCGCATGACCAAGGTTCGGCAACGAGGGTGTCTATCACCGTCGAGGAG 300
DB 283 GAGCTCATCGCGAGCGCATGACCAAGGTTCGGCAACGAGGGTGTCTATCACCGTCGAGGAG 342
QY 301 TCCAGACCTTCGGCTCG 318
DB 343 TCGAACACCTTCGGCCTG 360

RESULT 46
US-09-324-542-79
; Sequence 79, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-09-324-542-79

Query Match          57.4%; Score 241.2; DB 3; Length 360;
Best Local Similarity 84.9%; Pred. No. 7.7e-38;
Matches 270; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGCTCGCGGTGACGCTAGCAGCAGCAGCGGACCGTCTCGCCGAGGCG 60
DB 43 AAGAAGACCGACGACGCTCGCGGCGAGCGGACGACGACCGCCACCGCTCGCTCAGGCT 102
QY 61 CTGTTACGCGAGGCGCTCGCGCAACGCTCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
```

[illegible]

Db 41 AAGAGAGCCGACGCTCGCGGTGACGGCACCACCAACCGCCACCGTGTCTCGCCAGCG 100
Qy 61 CTGCTAGCCGAGGCTTCCCAAGCTCGCCCGCGGTGCGCAACCGGATGGCTCTCAAGCGC 120
Db 101 CTGCTCGCGAGGCTTCTGCGCAACGCTGGCCGCGCGCGCAACCGCTGGCGCTCAAGCGC 160
Qy 121 GGATCGAGAAGCCGCTCGAGGCGCTCTCCGGCGCCCTGCTGGAGCAGGCGAAGGATGTC 180
Db 161 GGATCGAAGAGCCGCTCGAGGCGCGTACCGCAAGCTGTCTGACACCGCCAAAGAGGTC 220
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 221 GAGACCAAGGAGCAGATCGCGCGCCACCGCGGCGATCTCCGCGCGCGAGCGGTCCATCGGT 280
Qy 241 GAGCTCATTCGCGAGGCGATGACAGGTCGCGCAAGAGCGGTCTATCACCCTCGAGGAG 300
Db 281 GAGCTGATCGCGAGGCGATGACAGGTCGCGCAAGGCGGTCTATCACCCTCGAGGAG 340

RESULT 52

US-09-902-540-3255

; Sequence 3255, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 3255

; LENGTH: 1651

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-3255

Query Match 50.5%; Score 212.2; DB 3; Length 1651;

Best Local Similarity 71.0%; Pred. No. 2.9e-32;

Matches 296; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

Qy 4 AAGACGACGACGCTCGCGGTGACGTAACGACCAACCGGACCGCTTCTCGCCAGGCGCTC 63

Db 235 AAGACGCTGACGCTCGCGGTGACGTCACGCGCACCAACGCGGACCGCTGTGGCGGCGGCATC 294

Qy 64 GTACGCGAGGCGCTGCGCAAGCTCGCCCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123

Db 295 TTCCGCGAGGCGCGAAGCTGGTGGCGCGCGCGCACCAACCGGATGGACATCAAGCGCGGC 354

Qy 124 ATCGAGAAGCCGCTCGAGGCGCTCTCCGGCGCCCTGCTGGAGCAGGCGAAGGATGTCGAG 183

Db 355 ATCGAAGGCGCTGGCGGCGCATGCTCGCGAGCTGAAGAGTGGCGCAAGCGGACCAAG 414

Qy 184 ACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGCACCCAG---ATCGGC 240

Db 415 GACAAAGGAGATTGCCAGGTGCGGTACCATCTCCGCCAACCGTGACGAGACCATCGGC 474

Qy 241 GAGCTCATTCGCGAGGCGATGACAGGTCGGCAGGAGCGGTCTATCACCCTCGAGGAG 300

Db 475 ACCATCATCGCGACGCGATGGAGAGGTGGCGAAGGCGGTCTATCACCCTCGAAGAG 534

Qy 301 TCCGAGACCTTCGCTCGAGGCTGGAGCTCACCAGGAGTATGCGTTTCGACAAGGCGTAC 360

Db 535 GCCAAGGCGCTGGAGACGCTGGAGCGTGGTGGAGAGCGATGACATTCGACCGCGGCTAC 594

Qy 361 ATCTCGCGGTACTTCCGCCACCGACATGGAGCGGATGGAGCGGTGCTCGACGACCGG 417

Db 595 CTGTCCCGGTACTTCTGTCGAGCGGACCGCGGCGCATGGAGCGGCGCTCAACGACGCG 651

RESULT 53

US-09-902-540-1150

; Sequence 1150, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1150

; LENGTH: 19954

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-1150

Query Match 50.5%; Score 212.2; DB 3; Length 19954;

Best Local Similarity 71.0%; Pred. No. 3.1e-32;

Matches 296; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

Qy 4 AAGACGACGACGCTCGCGGTGACGTAACGACCAACCGGACCGCTTCTCGCCAGGCGCTC 63

Db 7835 AAGACGCTGACGCTCGCGGTGACGTCACGCGCACCAACCGGCGGCGGTGTGGCGGCGGCATC 7894

Qy 64 GTACGCGAGGCGCTGCGCAAGCTCGCCCGCGGTGCGCAACCGGATGGCTCTCAAGCGCGGC 123

Db 7895 TTCCGCGAGGCGCGAAGCTGGTTCGCGCGCGGCGCACCAACCGGATGGACATCAAGCGCGGC 7954

Qy 124 ATCGAGAAGCCGCTCGAGGCGCTCTCCGGCGCCCTGCTGGAGCAGGCGAAGGATGTCGAG 183

Db 7955 ATCGAAGGCGCTGGCGGCGCATGTCGCGGAGCTGAAGAGTGGCGGCGGACCAAG 8014

Qy 184 ACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCGCGCGCACCCAG---ATCGGC 240

Db 8015 GACAAAGGAGATTGCCAGGTGCGGTACCATCTCCGCCAACCGTGACGAGACCATCGGC 8074

Qy 241 GAGCTCATTCGCGAGGCGATGACAGGTCGCGCAAGGAGGCGGTCTATCACCCTCGAGGAG 300

Db 8075 ACCATCATCGCGACCGGATGGAGAGGTGGCGAAGGCGGTCTATCACCCTCGAAGAG 8134

Qy 301 TCCGAGACCTTCGCTCGAGGCTGGAGCTCACCAGGCTATGCGTTTCGACAAGGCGTAC 360

Db 8135 GCCAAGGCGCTGGAGACGACGCTGGAGCGTGGTTCGAGGCGATGCGAGCGCGCTAC 8194

Qy 361 ATCTCGCGGTACTTCCGCCACCGACATGGAGCGGATGGAGCGGTGCTCGACGACCGG 417

Db 8195 CTGTCCCGGTACTTCTGTCGAGCGGACCGCGGCGCATGGAGCGGCGCTCAACGACGCG 8251

RESULT 54

US-08-105-168B-22

; Sequence 22, Application US/08105168B

; Patent No. 5589585

; GENERAL INFORMATION:

; APPLICANT: MABILAT et al.

; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION

; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE

; TITLE OF INVENTION: MYCOBACTERIA

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oliff & Berridge

; STREET: 700 South Washington Street, Suite 300

; CITY: Alexandria,

; STATE: Virginia

; ZIP: 22314

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" DS/HD
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS DOS 3.1
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; FILING DATE: August 12, 1993
;; APPLICATION NUMBER: US/08/105,168B
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR9210094
;; FILING DATE: August 8, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: William P. Berridge
;; REGISTRATION NUMBER: 30,024
;; REFERENCE/DOCKET NUMBER: WPB 28835
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6400
;; TELEFAX: (703) 836-2787
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single-stranded
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 438-787
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
US-08-105-168B-22

Query Match 50.1%; Score 210.6; DB 2; Length 350;
Best Local Similarity 80.7%; Pred. No. 5.7e-32;
Matches 246; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY	1	AAGAGACGAGCGACGTCCCGGTGACGCTACGACCGACCGACCGTCTCTCGCCCGAGCGG	60
DB	46	AAGAGACCGATGACGTCCCGGTGACGCTACGACCGACCGACCGTCTCTCGCCCGAGCGG	105
QY	61	CTCGTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCGCATGGCTCTCAAGCGC	120
DB	106	TTGGTTCCGAGGCGCTCGCAACGTCGCGCGGTGCAACCGCATGGCTCTCAAGCGC	165
QY	121	GGCATCGAAGCGCGTCGAGCGCGTCTCCGCGCGCTCTCGGAGCGCGCAAGATGTC	180
DB	166	GGCATCGAAGCGCGTCGAGCGCGTCTCCGCGCGCTCTCGGAGCGCGCAAGATGTC	225
QY	181	GAGACCAAGCGCGATCGTCTCCAGCGCTCCATCTCCGCGCGCGACCGCATCGGC	240
DB	226	GAGACCAAGCGCGATCGTCTCCAGCGCTCCATCTCCGCGCGCGACCGCATCGGC	285
QY	241	GAGCTCATCGCGAGCGCGATGCAAGGTCGCGCAAGGAGGCGTCTATCACCGTCCAGGAG	300
DB	286	GACCTGATCGCGAGCGCGATGCAAGGTCGCGCAAGGAGGCGTCTATCACCGTCCAGGAG	345
QY	301	TCCCA 305	
DB	346	TCCAA 350	

RESULT 55
US-08-698-948-22

;; Sequence 22, Application US/08698948
;; Patent No. 5849901
;; GENERAL INFORMATION:
;; APPLICANT: MABILAT et al.
;; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
;; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETECTION
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oliff & Berridge
;; STREET: 700 South Washington Street, Suite 300
;; CITY: Alexandria,
;; STATE: Virginia
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" DS/HD
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS DOS 3.1
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/698,948
;; FILING DATE: August 16, 1996
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/105,168
;; FILING DATE: August 12, 1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR9210094
;; FILING DATE: August 8, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: William P. Berridge
;; REGISTRATION NUMBER: 30,024
;; REFERENCE/DOCKET NUMBER: WPB 28835A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6400
;; TELEFAX: (703) 836-2787
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single-stranded
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 438-787
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
US-08-698-948-22

Query Match 50.1%; Score 210.6; DB 2; Length 350;
Best Local Similarity 80.7%; Pred. No. 5.7e-32;
Matches 246; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY	1	AAGAGACGAGCGACGTCCCGGTGACGCTACGACCGACCGACCGTCTCTCGCCCGAGCGG	60
DB	46	AAGAGACCGATGACGTCCCGGTGACGCTACGACCGACCGACCGTCTCTCGCCCGAGCGG	105
QY	61	CTCGTACGCGAGGCGCTCGCAACGTCGCGCGGTGCAACCGCATGGCTCTCAAGCGC	120
DB	106	TTGGTTCCGAGGCGCTCGCAACGTCGCGCGGTGCAACCGCATGGCTCTCAAGCGC	165
QY	121	GGCATCGAAGCGCGTCGAGCGCGTCTCCGCGCGCTCTCGGAGCGCGCAAGATGTC	180

Db 166 GGATCGAAGGCGCGTGGAGAGGTCAACGAGACCTGCTCAAGGGCGCCAAAGGAGTC 225
Qy 181 GAGACCAAGGAGCAGATCGCTTCAAGCGCTTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 226 GAGACCAAGGAGCAGATCGCGGCCACCGCAGCGGATTTCCGCGGGGTGACCAAGTCCATCGGT 285
Qy 241 GAGCTCATCGCGGAGGCGATGGACAAAGTGGCAAGGCGGCAAGGCGGTCATCACCGTCCGAGGAG 300
Db 286 GACCTGATCGCGGAGGCGATGGACAAAGTGGCAAGGCGGTCATCACCGTCCGAGGAG 345
Qy 301 TCCCA 305
Db 346 TCCAA 350

RESULT 56

US-08-473-020A-2
; Sequence 2, Application US/08473020A
; Patent No. 5877273
; GENERAL INFORMATION:
; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desraux, Bernard
; APPLICANT: Levy-Frebault, Veronique
; APPLICANT: Gicquel, Brigitte
; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; TITLE OF INVENTION: applications to the synthesis or detection of nucleic
; TITLE OF INVENTION: acids, products of expression of such sequences and
; TITLE OF INVENTION: application as immunogenic compositions.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,020A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/623,729
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24190
; REFERENCE/DOCKET NUMBER: A54435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-473-020A-2

Query Match 50.1%; Score 210.4; DB 2; Length 343;
Best Local Similarity 81.3%; Pred. No. 6.3e-32;
Matches 244; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
Qy 1 AAGAAGCGGACGACGTCGCGGTCAGCGTACGACACCGGACCGTCTTCGCCCGGCG 60
Db 41 AAGAAGACCGGACGACGTCGCGGTCAGCGTACGACACCGGACCGTCTTCGGCACAGGCC 100
Qy 61 CTCGTACGCGAGGGCGCTGCGGCAACGTCGCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120

Db 101 CTGTTGTTGTAAGGTCTGCGCAAGCTGCTGCGGCGCCAAACCGCTCGGCTGAAGCGC 160
Qy 121 GGATCGAAGGCGCGTCGAGGCGCTCTCGGGCGCCCTGCTGGAGCAGGCGAGGATGTC 180
Db 161 GGATCGAAGGCGCGTCGAGGAGGTCACCGGAGACGCTGCTGAAGAGCGCCAAAGGAGGTG 220
Qy 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 221 GAGACCAAGGAGCAGATCGCTGCCACCGCGGTATCTCCGCGGTGACCAAGTCCATCGGT 280
Qy 241 GAGCTCATCGCGGAGGCGATGGACAAAGTGGCAAGGTCGCGCAAGGCGGTCATCACCGTCCGAGGAG 300
Db 281 GACCTGATCGCGGAGGCGATGGACAAAGTGGCAAGGTCGCGCAACGAGGTCATCACCGTCCGAGGAG 340

RESULT 57

US-08-473-020A-31
; Sequence 31, Application US/08473020A
; Patent No. 5877273
; GENERAL INFORMATION:
; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desraux, Bernard
; APPLICANT: Levy-Frebault, Veronique
; APPLICANT: Gicquel, Brigitte
; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; TITLE OF INVENTION: applications to the synthesis or detection of nucleic
; TITLE OF INVENTION: acids, products of expression of such sequences and
; TITLE OF INVENTION: application as immunogenic compositions.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,020A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/623,729
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24190
; REFERENCE/DOCKET NUMBER: A54435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-473-020A-31

Query Match 50.0%; Score 210.2; DB 2; Length 342;
Best Local Similarity 80.9%; Pred. No. 6.9e-32;
Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Qy 1 AAGAAGCGGACGACGTCGCGGTCAGCGTACGACACCGGACCGTCTTCGCCCGGCG 60
Db 40 AAGAAGACCGGACGACGTCGCGGTCAGCGTACGACACCGGACCGTCTTCGCCCGGCG 99

QY 61 CTGTAAGGAGGCGCTGCGCAACGCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 120
Db 100 TTGGTTGCGAGGCGCTGCGCAACGCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 159
QY 121 GGCATCGAAGGCGCTGCGAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 180
Db 160 GGCATCGAAGGCGCTGCGAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 219
QY 181 GAGACCAAGGAGGAGATGCTTCCAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 240
Db 220 GAGACCAAGGAGGAGATGCTTCCAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 279
QY 241 GAGCTCATCGCGAGGCGATGCGAAGGCTCGCGCAAGGCGCTCTCAACCCGATGCTCTCAAGCG 300
Db 280 GAGCTCATCGCGAGGCGATGCGAAGGCTCGCGCAAGGCGCTCTCAACCCGATGCTCTCAAGCG 339
QY 301 TCC 303
Db 340 TCC 342

RESULT 58

US-08-473-020A-4

; Sequence 4, Application US/08473020A

; Patent No. 587273

; GENERAL INFORMATION:

; APPLICANT: Hance, Allan J

; APPLICANT: Grandchamp-Desraux, Bernard

; APPLICANT: Levy-Frebault, Veronique

; APPLICANT: Gicquel, Brigitte

; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,

; TITLE OF INVENTION: applications to the synthesis or detection of nucleic

; TITLE OF INVENTION: acids, products of expression of such sequences and

; TITLE OF INVENTION: application as immunogenic compositions.

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Walter H. Dreger

; STREET: 4, Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/473,020A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/623,729

; FILING DATE: 14-DEC-1990

; NAME: Dreger, Walter H

; ATTORNEY/AGENT INFORMATION:

; REGISTRATION NUMBER: 24190

; REFERENCE/DOCKET NUMBER: A54435

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 343 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-08-473-020A-4

Query Match

Best Local Similarity 50.0%; Score 210.2; DB 2; Length 343;

Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTACGAGTACGACCGGACCGCTTCTCCGCCAGGCG 60
Db 41 AAGAAGACGACGACGTCGCGGTACGAGTACGACCGGACCGCTTCTCCGCCAGGCG 100
QY 61 CTGTAAGGAGGCGCTGCGCAACGCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 120
Db 101 TTGGTTGCGAGGCGCTGCGCAACGCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 160
QY 121 GGCATCGAAGGCGCTGCGAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 180
Db 161 GGCATCGAAGGCGCTGCGAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 220
QY 181 GAGACCAAGGAGGAGATGCTTCCAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 240
Db 221 GAGACCAAGGAGGAGATGCTTCCAGGCGCTCTCGCGCGCGGTCGCAACCCGATGCTCTCAAGCG 280
QY 241 GAGCTCATCGCGAGGCGATGCGAAGGCTCGCGCAAGGCGCTCTCAACCCGATGCTCTCAAGCG 300
Db 281 GAGCTCATCGCGAGGCGATGCGAAGGCTCGCGCAAGGCGCTCTCAACCCGATGCTCTCAAGCG 340
QY 301 TCC 303
Db 341 TCC 343

RESULT 59

US-08-473-020A-5

; Sequence 5, Application US/08473020A

; Patent No. 587273

; GENERAL INFORMATION:

; APPLICANT: Hance, Allan J

; APPLICANT: Grandchamp-Desraux, Bernard

; APPLICANT: Levy-Frebault, Veronique

; APPLICANT: Gicquel, Brigitte

; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,

; TITLE OF INVENTION: applications to the synthesis or detection of nucleic

; TITLE OF INVENTION: acids, products of expression of such sequences and

; TITLE OF INVENTION: application as immunogenic compositions.

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Walter H. Dreger

; STREET: 4, Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/473,020A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/623,729

; FILING DATE: 14-DEC-1990

; NAME: Dreger, Walter H

; ATTORNEY/AGENT INFORMATION:

; REGISTRATION NUMBER: 24190

; REFERENCE/DOCKET NUMBER: A54435

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 343 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-08-473-020A-5

Query Match 50.0%; Score 210.2; DB 2; Length 343;
Best Local Similarity 80.9%; Pred. No. 6.9e-32;
Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 AAGAAGACCGACGACGTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 60
DB 41 AAGAAGACCGACGACGTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 100

QY 61 CTGCTACGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 120
DB 101 TTGCTCAAGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 160

QY 121 GGCATCAGAGGCGCGTCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 180
DB 161 GGCATCAGAGGCGCGTCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 220

QY 181 GAGACCAAGGAGGAGTCTCCACCGCTTCCATCTCCCGCGCGACACCGGATGGCTCTCAAGCGC 240
DB 221 GAGACCAAGGAGGAGTCTCCACCGCTTCCATCTCCCGCGCGACACCGGATGGCTCTCAAGCGC 280

QY 241 GAGCTCATCGCGAGGCGATGGACCAAGGTCCGCAAGGCGTGCATCAGCGTGGAGGAG 300
DB 281 GAGCTCATCGCGAGGCGATGGACCAAGGTCCGCAAGGCGTGCATCAGCGTGGAGGAG 340

QY 301 TCC 303
DB 341 TCC 343

RESULT 60

US-08-473-020A-7

; Sequence 7, Application US/08473020A
; Patent No. 5877273

GENERAL INFORMATION:

; APPLICANT: Hance, Allan J
; APPLICANT: Grandchamp-Desraux, Bernard
; APPLICANT: Levy-Frebault, Veronique

APPLICANT: Gicquel, Brigitte

; TITLE OF INVENTION: Nucleotide sequences of actinomycetales,
; TITLE OF INVENTION: applications to the synthesis or detection of nucleic
; TITLE OF INVENTION: acids, products of expression of such sequences and
; TITLE OF INVENTION: application as immunogenic compositions.

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,020A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/623,729

FILING DATE: 14-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H

REGISTRATION NUMBER: 24190

REFERENCE/DOCKET NUMBER: A54435

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 398-3249

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

; LENGTH: 343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-473-020A-7

Query Match 50.0%; Score 210.2; DB 2; Length 343;
Best Local Similarity 80.9%; Pred. No. 6.9e-32;
Matches 245; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 AAGAAGACCGACGACGTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 60
DB 41 AAGAAGACCGACGACGTCGCGGTGACGGTACGACACCGCGACCGTTCTCGCCCGAGCG 100

QY 61 CTGCTACGCGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 120
DB 101 TTGCTCAAGAGGCGCTCGCGCAACGTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 160

QY 121 GGCATCAGAGGCGCGTCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 180
DB 161 GGCATCAGAGGCGCGTCTCGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 220

QY 181 GAGACCAAGGAGGAGTCTCCACCGCTTCCATCTCCCGCGCGACACCGGATGGCTCTCAAGCGC 240
DB 221 GAGACCAAGGAGGAGTCTCCACCGCTTCCATCTCCCGCGCGACACCGGATGGCTCTCAAGCGC 280

QY 241 GAGCTCATCGCGAGGCGATGGACCAAGGTCCGCAAGGCGTGCATCAGCGTGGAGGAG 300
DB 281 GAGCTCATCGCGAGGCGATGGACCAAGGTCCGCAAGGCGTGCATCAGCGTGGAGGAG 340

QY 301 TCC 303
DB 341 TCC 343

Search completed: April 1, 2006, 17:06:27

Job time : 255.586 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: April 1, 2006, 22:17:36 ; Search time 1130.56 Seconds
 (without alignments)
 3072.051 Million cell updates/sec
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 Perfect score: 420
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 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 9793542 seqs, 4134689005 residues
 Total number of hits satisfying chosen parameters: 19587084
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 60 summaries
 Database : Published Applications NA Main:
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 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:
 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
 6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
 7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:
 9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:
 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420	100.0	420	8	US-10-824-527-43 Sequence 43, Appl
2	420	100.0	420	8	US-10-824-527-45 Sequence 45, Appl
3	412	98.1	420	8	US-10-824-527-58 Sequence 58, Appl
4	404	96.2	1623	6	US-10-156-761-3915 Sequence 3915, Ap
5	404	96.2	9025608	6	US-10-156-761-1 Sequence 1, Appl
6	396	94.3	420	8	US-10-824-527-47 Sequence 47, Appl
7	396	94.3	420	8	US-10-824-527-48 Sequence 48, Appl
8	394.4	93.9	420	8	US-10-824-527-3 Sequence 3, Appl
9	394.4	93.9	420	8	US-10-824-527-9 Sequence 9, Appl
10	394.4	93.9	420	8	US-10-824-527-11 Sequence 11, Appl
11	394.4	93.9	420	8	US-10-824-527-20 Sequence 20, Appl
12	392.8	93.5	420	8	US-10-824-527-15 Sequence 15, Appl
13	392.8	93.5	420	8	US-10-824-527-23 Sequence 23, Appl
14	392.8	93.5	420	8	US-10-824-527-55 Sequence 55, Appl
15	391.2	93.1	420	8	US-10-824-527-6 Sequence 6, Appl
16	391.2	93.1	420	8	US-10-824-527-16 Sequence 16, Appl
17	391.2	93.1	420	8	US-10-824-527-22 Sequence 22, Appl
18	388	92.4	420	8	US-10-824-527-24 Sequence 24, Appl
19	388	92.4	420	8	US-10-824-527-36 Sequence 36, Appl
20	388	92.4	420	8	US-10-824-527-61 Sequence 61, Appl
21	386.4	92.0	420	8	US-10-824-527-17 Sequence 17, Appl
22	386.4	92.0	420	8	US-10-824-527-32 Sequence 32, Appl
23	386.4	92.0	420	8	US-10-824-527-34 Sequence 34, Appl

24	386.4	92.0	420	8	US-10-824-527-38	Sequence 38, Appl
25	386.4	92.0	420	8	US-10-824-527-40	Sequence 40, Appl
26	386.4	92.0	420	8	US-10-824-527-46	Sequence 46, Appl
27	386.4	92.0	420	8	US-10-824-527-49	Sequence 49, Appl
28	386.4	92.0	420	8	US-10-824-527-57	Sequence 57, Appl
29	386.4	92.0	422	8	US-10-824-527-18	Sequence 18, Appl
30	384.8	91.6	420	8	US-10-824-527-8	Sequence 8, Appl
31	384.8	91.6	420	8	US-10-824-527-31	Sequence 31, Appl
32	384.8	91.6	420	8	US-10-824-527-35	Sequence 35, Appl
33	383.2	91.2	420	8	US-10-824-527-13	Sequence 13, Appl
34	383.2	91.2	420	8	US-10-824-527-19	Sequence 19, Appl
35	383.2	91.2	420	8	US-10-824-527-26	Sequence 26, Appl
36	383.2	91.2	420	8	US-10-824-527-37	Sequence 37, Appl
37	381.6	90.9	420	8	US-10-824-527-21	Sequence 21, Appl
38	381.6	90.9	420	8	US-10-824-527-25	Sequence 25, Appl
39	381.6	90.9	420	8	US-10-824-527-28	Sequence 28, Appl
40	381.6	90.9	420	8	US-10-824-527-29	Sequence 29, Appl
41	381.6	90.9	420	8	US-10-824-527-60	Sequence 60, Appl
42	380	90.5	420	8	US-10-824-527-14	Sequence 14, Appl
43	378.4	90.1	420	8	US-10-824-527-51	Sequence 51, Appl
44	378.4	90.1	420	8	US-10-824-527-52	Sequence 52, Appl
45	378.4	90.1	420	8	US-10-824-527-53	Sequence 53, Appl
46	378.4	90.1	420	8	US-10-824-527-54	Sequence 54, Appl
47	373.6	89.0	420	8	US-10-824-527-50	Sequence 50, Appl
48	372	88.6	420	8	US-10-824-527-27	Sequence 27, Appl
49	372	88.6	420	8	US-10-824-527-56	Sequence 56, Appl
50	372	88.6	420	8	US-10-824-527-56	Sequence 56, Appl
51	372	88.6	420	8	US-10-824-527-59	Sequence 59, Appl
52	370.4	88.2	420	8	US-10-824-527-5	Sequence 5, Appl
53	370.2	88.1	423	8	US-10-824-527-7	Sequence 7, Appl
54	368.6	87.8	423	8	US-10-824-527-30	Sequence 30, Appl
55	365.6	87.0	420	8	US-10-824-527-4	Sequence 4, Appl
56	362.4	86.3	420	8	US-10-824-527-33	Sequence 33, Appl
57	362.2	86.2	423	8	US-10-824-527-39	Sequence 39, Appl
58	360.8	85.9	420	8	US-10-824-527-10	Sequence 10, Appl
59	359.2	85.5	420	8	US-10-824-527-12	Sequence 12, Appl
60	322.4	76.8	604	8	US-10-500-586-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
 US-10-824-527-43
 ; Sequence 43, Application US/10824527
 ; Publication No. US20040265873A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIM, BUM-JOON
 ; APPLICANT: KIM, CHANG-JIN
 ; APPLICANT: KO, YOUNG HWAN
 ; APPLICANT: KOH, JONG-SAM
 ; APPLICANT: PARK, DONG-JIN
 ; APPLICANT: LEE, HYANG BUM
 ; APPLICANT: SEOUL, HONG KIM
 ; APPLICANT: KIM, SUN-HYUN
 ; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
 ; FILE REFERENCE: 05823_0260-00000
 ; CURRENT APPLICATION NUMBER: US/10/824,527
 ; CURRENT FILING DATE: 2004-04-15
 ; PRIOR APPLICATION NUMBER: KR 2003-24656
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: KR 2003-80580
 ; PRIOR FILING DATE: 2003-11-14
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: Patentin Ver. 3.2
 ; SEQ ID NO 43
 ; LENGTH: 420
 ; TYPE: DNA
 ; ORGANISM: Streptomyces scabiei
 US-10-824-527-43

Query Match 100.0% Score 420; DB 8; Length 420;

Db 241 GAGCTATCCCGGAGGCGATGGCAAGGTCGGCAAGGAGCGGTATCATCCCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGCTAC 360
Db 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGCTAC 360
QY 361 ATCTCGGCGTACTTCGCGCCACCGACATGGAGCGGATGGAGCGGTCGTCGACGACCCGCTAC 420
Db 361 ATCTCGGCGTACTTCGCGCCACCGACATGGAGCGGATGGAGCGGTCGTCGACGACCCGCTAC 420

RESULT 4

US-10-156-761-3915
; Sequence 3915, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3915
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1623)
US-10-156-761-3915

Query Match 96.2%; Score 404; DB 6; Length 1623;
Best Local Similarity 97.6%; Pred. No. 2.7e-94;
Matches 410; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCGCTCCCGGTGACGGTACGACACCGCGCGGTCTCCGCCAGGCG 60
Db 232 AAGAGACGAGCGCTCCCGGTGACGGTACGACACCGCGCGGTCTCCGCCAGGCG 291
QY 61 CTCGTACGCGAGGCGCTCGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
Db 292 CTCGTCCGCGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 351
QY 121 GGCATCGAAGGCGCTCGAGGCGGTCCTCGGCGGCTCTCGAGCAGCGCAAGGATGTC 180
Db 352 GGCATCGAAGGCGCTCGAGGCGGTCCTCGGCGGCTCTCGAGCAGCGCAAGGATGTC 411
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCACCCAGATCGGC 240
Db 412 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCACCCAGATCGGC 471
QY 241 GAGCTCATCGCGAGGCGATGACAAAGTGGCAAGGAGGCGTATCAACCGTCGAGGAG 300
Db 472 GAGCTCATCGCGAGGCGATGACAAAGTGGCAAGGAGGCGTATCAACCGTCGAGGAG 531
QY 301 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGCTAC 360
Db 532 TCCGAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGCTAC 591
QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGGCGTCTCGACGACCCGCTAC 420
Db 592 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGGCGTCTCGACGACCCGCTAC 651

RESULT 5

US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 96.2%; Score 404; DB 6; Length 9025608;
Best Local Similarity 97.6%; Pred. No. 1.6e-94;
Matches 410; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGAGACGAGCGCTCCCGGTGACGGTACGACACCGCGCGGTCTCCGCCAGGCG 60
Db 4855588 AAGAGACGAGCGCTCCCGGTGACGGTACGACACCGCGCGGTCTCCGCCAGGCG 4855529
QY 61 CTCGTACGCGAGGCGCTCGGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 120
Db 4855528 CTCGTCCGCGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCGATGGCTCTCAAGGCG 4855469
QY 121 GGCATCGAAGGCGCTCGAGGCGGTCCTCCGCGCGCTCTCGAGCAGCGCAAGGATGTC 180
Db 4855468 GGCATCGAAGGCGCTCGAGGCGGTCCTCCGCGCGCTCTCGAGCAGCGCAAGGATGTC 4855409
QY 181 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCACCCAGATCGGC 240
Db 4855408 GAGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGCGCGCGCACCCAGATCGGC 4855349
QY 241 GAGCTCATCGCGAGGCGATGGAAGGTCGCGCAAGGAGGCGTATCAACCGTCGAGGAG 300
Db 4855348 GAGCTCATCGCGAGGCGATGGAAGGTCGCGCAAGGAGGCGTATCAACCGTCGAGGAG 4855289
QY 301 TCCGAGACCTTCGGTCTGGAGCTCGAGCTCACCGAGGATATGCGCTTCGACAAAGGCGCTAC 360
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QY 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAGGCGTCTCGACGACCCGCTAC 420
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RESULT 6

US-10-824-527-47
; Sequence 47, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN

ORGANISM: Streptomyces acrimycini
US-10-824-527-3

Query Match 93.9%; Score 394.4; DB 8; Length 420;
Best Local Similarity 96.2%; Pred. No. 8.5e-92;

Mismatches 0; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCCCGGTGACGTACGACACCGCGGCTTCTCGCCCGAGGCG 60
DB 1 AAGAAGACGAGCAGCTCCCGGTGACGTACGACACCGCGGCTTCTCGCCCGAGGCG 60
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DB 61 CTGGTCAGGAGGCGCTCGGACGTCGCGCGGCTGCAACCCCGATGCTCTCAAGCGC 120
QY 121 GGCAATCAGAGGCGCTCGGACGTCGCGCGGCTGCAACCCCGATGCTCTCAAGCGC 180
DB 121 GGCAATCAGAGGCGCTCGGACGTCGCGCGGCTGCAACCCCGATGCTCTCAAGCGC 180
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DB 181 GAGACCAAGGAGCAGATCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGCTTCCAGGCGC 240
QY 241 GAGCTCATCGCGAGGCGATGACAAAGGTTCGCAAGGAGGCGTTCATCAACCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGCGATGACAAAGGTTCGCAAGGAGGCGTTCATCAACCGTCGAGGAG 300
QY 301 TCCGACACCTTCGCTCGGAGCTGAGCTCACCGAGGAGGCGTTCATCAACCGTCGAGGAG 360
DB 301 TCCGACACCTTCGCTCGGAGCTGAGCTCACCGAGGAGGCGTTCATCAACCGTCGAGGAG 360
QY 361 ATCTCGGCGTACTTCCGACCGACATGAGGCGGATGAGGCGGCTTCGACGACCGGTAC 420
DB 361 ATCTCGGCGTACTTCCGACCGACATGAGGCGGATGAGGCGGCTTCGACGACCGGTAC 420

RESULT 9

US-10-824-527-9

Sequence 9, Application US/10824527

Publication No. US20040265873A1

GENERAL INFORMATION:

APPLICANT: KIM, BUM-JOON

APPLICANT: KIM, CHANG-JIN

APPLICANT: KO, YOUNG HWAN

APPLICANT: KOH, JEONG-SAM

APPLICANT: PARK, DONG-JIN

APPLICANT: LEE, HYANG BURM

APPLICANT: SEOUL, HONG KIM

APPLICANT: KIM, SUN-HYUN

TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

FILE REFERENCE: 05823.0260-00000

CURRENT FILING DATE: 2004-04-15

PRIOR APPLICATION NUMBER: US/10/824,527

PRIOR FILING DATE: 2003-04-18

PRIOR FILING DATE: 2003-04-18

PRIOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 9

LENGTH: 420

TYPE: DNA

ORGANISM: Streptomyces alboniger

US-10-824-527-9

Query Match 93.9%; Score 394.4; DB 8; Length 420;
Best Local Similarity 96.2%; Pred. No. 8.5e-92;

Mismatches 0; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGAAGACGAGCAGCTCCCGGTGACGTACGACACCGCGGCTTCTCGCCCGAGGCG 60
DB 1 AAGAAGACGAGCAGCTCCCGGTGACGTACGACACCGCGGCTTCTCGCCCGAGGCG 60

Db 181 GAGACCAAGGAGCAGATCGCTCCACGGCTCCATCTCCGCCCGGACACCCAGATCGGC 240
Qy 241 GAGCTATATCCCGAGGCGATGGACAGGTGGCAAGAGGCGTTCATCAGCGTCGAGGAG 300
Db 241 GAGCTATATCCCGAGGCGCATGGACAGGTGGCAAGGTCGCAAGGAGGCGTTCATCAGCGTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGTTCGACAAAGGGGTAC 360
Db 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGTTCGACAAAGGGGTAC 360
Qy 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGCGTTCGACAAAGGGGTAC 420
Db 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGCGTTCGACAAAGGGGTAC 420

RESULT 11

US-10-824-527-20
; Sequence 20, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 20
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces chartreusis
US-10-824-527-20

Query Match 93.9%; Score 394.4; DB 8; Length 420;
Best Local Similarity 96.2%; Pred. No. 8.5e-92;
Matches 404; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 AAGNAGACGACGACGTCCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTCGCAAGCTCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTCAAGGAGGCGCTTCGCAAGCTAGCGCGCGCGCGCAACCGGATGGCGCTCAAGCGC 120
Qy 121 GGCAATCAGAAAGGCGCTCGAGCGCGCTCTCGCGCGCGCTTCGCGCGCGCGTTCGAGAGCGGCGAAGGATGTC 180
Db 121 GGTATCGAGCGTCCGCTCGAGCGCGCTCTCGCGCGCGCTTCGAGAGCGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCACCGCGCTTCATCTCCGCGCGCGCGACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCACCGCGCTTCATCTCCGCGCGCGCGACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGAGGCGTTCATCAGCGTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGAGGCGTTCATCAGCGTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGTTCGACAAAGGGGTAC 360
Db 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGTTCGACAAAGGGGTAC 360

Qy 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGCGTTCGACAAAGGGGTAC 420
Db 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGCGTTCGACAAAGGGGTAC 420

RESULT 12

US-10-824-527-15
; Sequence 15, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 15
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces bambergiensis
US-10-824-527-15

Query Match 93.5%; Score 392.8; DB 8; Length 420;
Best Local Similarity 96.0%; Pred. No. 2.2e-91;
Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 1 AAGAAGACGACGACGTCCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCCGCGGTGACGGTACGACACCGCGGACCGTTCGCGCCAGGCG 60
Qy 61 CTGCTACGCGAGGCGCTTCGCGCGGTGCCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTCAAGGAGGCGCTTCGCGCGGTGCCAACCGGATGGCGCTTCGCGCCAGGCG 120
Qy 121 GGCAATCAGAAAGGCGCTCGAGCGCGCTCTCGCGCGCGCTTCGCGCGCGCGTTCGAGAGCGGCGAAGGATGTC 180
Db 121 GGTATCGAGAGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGAGAGCGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCACCGCGCTTCATCTCCGCGCGCGCGACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCACCGCGCTTCATCTCCGCGCGCGCGACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGCGCTTCATCAGCGTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGACAGGTGGCAAGGTGGCAAGGCGCTTCATCAGCGTCGAGGAG 300
Qy 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGTTCGACAAAGGGGTAC 360
Db 301 TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGAGGGTATGCGTTCGACAAAGGGGTAC 360
Qy 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGCGTTCGACAAAGGGGTAC 420
Db 361 ATCTCGCGGTACTTCGCCACCGACATGGAGCGGTATGCGTTCGACAAAGGGGTAC 420

RESULT 13

US-10-824-527-23
; Sequence 23, Application US/10824527
; Publication No. US20040265873A1

; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: KIM, SUN-HUYN
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces cinereoruber
US-10-824-527-23

Query Match 93.5%; Score 392.8; DB 8; Length 420;
Best Local Similarity 96.0%; Pred. No. 2.2e-91;
Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCCGGTGACGGTACGACACCGCGACCGTTCGCCCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCCGGTGACGGTACGACACCGCGACCGTTCGCCCCAGGCG 60

QY 61 CTGCTACGAGAGCGCGTCGCGAAGCTGCGCGCGCGTGCACACCGTGCCTCTCAAGCGC 120
DB 61 CTGCTCGCGAGGCGCTTCGCAACGTCGCGCGCGCGTGCACACCGTGCCTCTCAAGCGC 120

QY 121 GGCATCGAGAGCGCGTCGAGCGCGCTTCGCGCGCGCGTTCGCGCGCGCGTTCGCGCGCGCGTTC 180
DB 121 GGCATCGAGAGCGCGTCGAGCGCGCTTCGCGCGCGCGTTCGCGCGCGCGTTCGCGCGCGCGTTC 180

QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240

QY 241 GAGCTCATCGCGAGCGGCGATCGAAGGTGCGGCAAGGAGGCGTTCATCAGGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGGCGATCGAAGGTGCGGCAAGGAGGCGTTCATCAGGTCGAGGAG 300

QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCAGCGGATGCGCTTCGACAGGGGCTAC 360
DB 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCAGCGGATGCGCTTCGACAGGGGCTAC 360

QY 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACAGCCCGTAC 420
DB 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACAGCCCGTAC 420

RESULT 14
US-10-824-527-55
; Sequence 55, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 55
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces bottropensis
US-10-824-527-55

Query Match 93.5%; Score 392.8; DB 8; Length 420;
Best Local Similarity 96.0%; Pred. No. 2.2e-91;
Matches 403; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCCGGTGACGGTACGACACCGCGACCGTTCGCCCCAGGCG 60
DB 1 AAGAAGACGACGACGTCGCCGGTGACGGTACGACACCGCGACCGTTCGCCCCAGGCG 60

QY 61 CTGCTACGCGAGGCGCTCGCAACGTCGCCCGCGGTGCACACCGTGCCTCTCAAGCGC 120
DB 61 CTGCTCGCGAGGCGCTTCGCAACGTCGCCCGCGGTGCACACCGTGCCTCTCAAGCGC 120

QY 121 GGCATCGAGAGCGCGTCGAGCGCGCTTCGCGCGCGCGTTCGCGCGCGCGTTCGCGCGCGCGTTC 180
DB 121 GGCATCGAGAGCGCGTCGAGCGCGCTTCGCGCGCGCGTTCGCGCGCGCGTTCGCGCGCGCGTTC 180

QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240

QY 241 GAGCTCATCGCGAGCGGCGATCGAAGGTGCGGCAAGGAGGCGTTCATCAGGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGCGGCGATCGAAGGTGCGGCAAGGAGGCGTTCATCAGGTCGAGGAG 300

QY 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCAGCGGATGCGCTTCGACAGGGGCTAC 360
DB 301 TCCAGACCTTCGGTCTGGAGCTGAGCTCAGCGGATGCGCTTCGACAGGGGCTAC 360

QY 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACAGCCCGTAC 420
DB 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGTTCGACAGCCCGTAC 420

RESULT 15
US-10-824-527-6
; Sequence 6, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HYANG BURM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

DB	121	G	T	T	A	T	C	G	A	A	G	G	C	G	T	C	T	C	G	C	G	C	T	T	C	G	C	G	C	C	T	T	C	G	C	C	A	A	G	A	G	A	T	G	T	C							
QY	181	G	A	G	A	C	A	A	G	A	G	C	A	G	A	T	C	G	T	T	C	A	C	G	G	C	T	T	C	A	T	C	C	G	C	G	C	C	A	C	A	C	C	A	G	A	T	C	G	C			
DB	181	G	A	G	A	C	A	A	G	A	G	C	A	G	A	T	C	G	T	T	C	A	C	G	G	C	T	T	C	A	T	C	C	G	C	G	C	C	A	C	C	A	G	A	T	C	G	C					
QY	241	G	A	G	C	T	C	A	T	C	G	C	G	A	G	G	C	G	A	T	G	A	C	A	G	G	C	T	T	C	A	A	G	C	G	T	C	A	A	G	C	G	T	C	A	C	C	T	C	G	A	G	A
DB	241	G	A	G	C	T	C	A	T	C	G	C	G	A	G	G	C	T	T	C	A	A	G	C	G	T	C	T	T	C	A	A	G	C	G	T	C	A	A	G	C	G	T	C	A	C	C	T	C	G	A	G	A
QY	301	T	C	C	A	G	A	C	T	T	C	G	G	T	C	T	G	A	G	T	C	A	C	C	G	A	G	G	T	A	T	G	C	G	T	T	C	G	A	C	A	A	G	G	G	C	T	A	C				
DB	301	T	C	C	A	G	A	C	T	T	C	G	G	T	C	T	G	A	G	T	C	A	C	C	G	A	G	G	T	A	T	G	C	G	T	T	C	G	A	C	A	A	G	G	C	T	A	C					
QY	361	A	T	C	T	C	G	G	C	T	A	C	C	G	A	C	A	T	G	A	G	C	G	G	A	T	G	A	G	C	G	T	C	G	T	C	G	A	C	A	C	C	C	G	T	A	C						
DB	361	A	T	C	T	C	G	G	C	T	A	C	C	G	A	C	A	T	G	A	G	C	G	G	A	T	G	A	G	C	G	T	C	G	T	C	G	A	C	A	C	C	C	G	T	A	C						

RESULT 18

```

US-10-824-527-24
; Sequence 24, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-246556
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces cirratus
US-10-824-527-24

```

Qy	301	TCCCAGACCTTCGGTCTGGAGCTCACCAGGAGGTATGCGCTTCGACCAAGGGCTAC	360
Db	301	TCCCAGACCTTCGGTCTGGAGCTCAGAGCTCACCAGAGGCGATGCGCTTCGACCAAGGGCTAC	360
Qy	361	ATCTCGGCGTACTTCGCCACCACGACATGAGAGCGGATGAGAGGCGTCTGCTCGACACCCGCTAC	420
Db	361	ATCTCGGCGTACTTCGCCACCACGACATGAGAGCGGATGAGAGGCGTCTGCTCGACACCCGCTAC	420

RESULT 19
 US-10-824-527-36
 ; Sequence 36, Application US/10824527
 ; Publication No. US20040265873A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIM, BUM-JOON
 ; APPLICANT: KIM, CHANG-JIN
 ; APPLICANT: KO, YOUNG HWAN
 ; APPLICANT: KOH, JEONG-SAM
 ; APPLICANT: PARK, DONG-JIN
 ; APPLICANT: LEE, HYANG BUM
 ; APPLICANT: SEOUL, HONG KIM
 ; APPLICANT: KIM, SUN-HUYN
 ; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
 ; TITLE OF INVENTION: groSL2 GENE
 ; FILE REFERENCE: 05823.0260-00000
 ; CURRENT APPLICATION NUMBER: US/10/824,527
 ; CURRENT FILING DATE: 2004-04-15
 ; PRIOR APPLICATION NUMBER: KR 2003-24656
 ; PRIOR FILING DATE: 2003-04-18
 ; PRIOR APPLICATION NUMBER: KR 2003-80580
 ; PRIOR FILING DATE: 2003-11-14
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 36
 ; LENGTH: 420
 ; TYPE: DNA
 ; ORGANISM: Streptomyces humiferus
 US-10-824-527-36

RESULT 20


```
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces galilaeus
US-10-824-527-32

Query Match
Best Local Similarity 92.0%; Score 386.4; DB 8; Length 420;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
QY 61 CTCGTACGCGAGGGCCCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
DB 61 CTCGTACGCGAGGGCCCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGT 120
QY 121 GGCATCGAGAGGGCCCTGCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGCGCGCG 180
DB 121 GGCATCGAGAGGGCCCTGCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGCGCGCG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCCTTCATCTCCGCGCGCGCACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCCTTCATCTCCGCGCGCGCACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGAGGGCGATGAGCAAGGTGCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGGCGATGAGCAAGGTGCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTCGAGCTGAGCTCACCAGGGGTATCGGTTGCAAGGGCTTAC 360
DB 301 TCCGAGACCTTCGGTCTCGAGCTGAGCTCACCAGGGGTATCGGTTGCAAGGGCTTAC 360
QY 361 ATCTCGGCGTACTTTCGCGCACGATGAGGCGGATGAGGCGGCTCGACGACCCGCTAC 420
DB 361 ATCTCGGCGTACTTTCGCGCACGATGAGGCGGATGAGGCGGCTCGACGACCCGCTAC 420

RESULT 24
US-10-824-527-38
; Sequence 38, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 38
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces minutiscleroticus
US-10-824-527-38

Query Match
Best Local Similarity 92.0%; Score 386.4; DB 8; Length 420;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
DB 1 AAGAAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCTCGCCCGAGGG 60
QY 61 CTCGTACGCGAGGGCCCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGC 120
DB 61 CTCGTACGCGAGGGCCCTGCGCAACGTCGCGCGCGGTGCGCAACCGGATGCTCTCAAGCGT 120
QY 121 GGCATCGAGAGGGCCCTGCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGCGCGCG 180
DB 121 GGCATCGAGAGGGCCCTGCGAGCGCTCTCGCGCGCGCTCTCGCGCGCGCTCTCGCGCGCG 180
QY 181 GAGACCAAGGAGCAGATCGCTTCCACGGCCTTCATCTCCGCGCGCGCACACCCAGATCGGC 240
DB 181 GAGACCAAGGAGCAGATCGCTTCCACGGCCTTCATCTCCGCGCGCGCACACCCAGATCGGC 240
QY 241 GAGCTCATCGCGAGGGCGATGAGCAAGGTGCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
DB 241 GAGCTCATCGCGAGGGCGATGAGCAAGGTGCGCAAGGAGGCGTTCATCCCGTCGAGGAG 300
QY 301 TCCGAGACCTTCGGTCTCGAGCTGAGCTCACCAGGGGTATCGGTTGCAAGGGCTTAC 360
DB 301 TCCGAGACCTTCGGTCTCGAGCTGAGCTCACCAGGGGTATCGGTTGCAAGGGCTTAC 360
QY 361 ATCTCGGCGTACTTTCGCGCACGATGAGGCGGATGAGGCGGCTCGACGACCCGCTAC 420
DB 361 ATCTCGGCGTACTTTCGCGCACGATGAGGCGGATGAGGCGGCTCGACGACCCGCTAC 420

RESULT 23
US-10-824-527-34
; Sequence 34, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces griseolus
US-10-824-527-34

Query Match
Best Local Similarity 92.0%; Score 386.4; DB 8; Length 420;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```

121 GGCAATCGAAGGCGCTCGAGGCGCTCTCCGGCGCCCTCTGCTGAGCAGGCGAAGGATGTC 180
121 GGTATCGAAGAGCGCTCGAGGCGCTCTCCGGTGCCCTGCTGAGCAGGCGAAGGAGCTC 180
181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCCGACACCCAGATCGGC 240
181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCCGAGGCTCCAGATCGGC 240
241 GAGCTCATCGCCGAGGCGATGGACAGGTGCGGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
241 GAGCTCATCGCCGAGGCGATGGACAGGTGCGGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420

RESULT 25

US-10-824-527-40
; Sequence 40, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 40
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces nodosus
US-10-824-527-40

Query Match 92.0%; Score 386.4; DB 8; Length 420;
Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
1 AAGAAGACGAGACGCTCGCGGCTGACGGTACGACCAACCGGACCGGCTCTCGCCCGAGCG 60
1 AAGAAGACGAGACGCTCGCGGCTGACGGTACGACCAACCGGACCGGCTCTCGCCCGAGCG 60
61 CTGCTACGCGAGGCGCTCGCGACAGCTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
61 CTGCTACGCGAGGCGCTCGCGACAGCTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
121 GGCAATCGAAGGCGCTCGAGGCGCTCTCCGGCGCCCTGCTGAGCAGGCGCAAGGATGTC 180
121 GGTATCGAAGGCGCTCGAGGCGCTCTCCACCGCGCTGCTGAGCAGGCGCAAGGAGCTC 180
181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCCGACACCCAGATCGGC 240
181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCCGACACCCAGATCGGC 240
241 GAGCTCATCGCCGAGGCGATGGACAGGTGCGGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
241 GAGCTCATCGCCGAGGCGATGGACAGGTGCGGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420

241 GAGCTCATCGCCGAGGCGATGGACAGGTGCGGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420

RESULT 26

US-10-824-527-46
; Sequence 46, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: LEE, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 46
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces scabiei
US-10-824-527-46

Query Match 92.0%; Score 386.4; DB 8; Length 420;
Best Local Similarity 95.0%; Pred. No. 9.7e-90;
Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
1 AAGAAGACGAGACGCTCGCGGCTGACGGTACGACCAACCGGACCGGCTCTCGCCCGAGCG 60
1 AAGAAGACGAGACGCTCGCGGCTGACGGTACGACCAACCGGACCGGCTCTCGCCCGAGCG 60
61 CTGCTACGCGAGGCGCTCGAGGCGCTCTCCGGCGCCCTGCTGAGCAGGCGCAAGGATGTC 120
61 CTGCTACGCGAGGCGCTCGCGACAGCTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGT 120
121 GGCAATCGAAGGCGCTCGAGGCGCTCTCCGGCGCCCTGCTGAGCAGGCGCAAGGATGTC 180
121 GGTATCGAAGGCGCTCGAGGCGCTCTCCACCGCGCTGCTGAGCAGGCGCAAGGAGCTC 180
181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCCGACACCCAGATCGGC 240
181 GAGACCAAGGAGCAGATCGCTTCCACGGCTTCCATCTCCGCCCGCCGACACCCAGATCGGC 240
241 GAGCTCATCGCCGAGGCGATGGACAGGTGCGGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
241 GAGCTCATCGCCGAGGCGATGGACAGGTGCGGCAAGGAGGCGTCAATCACCCTCGAGGAG 300
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
301 TCCGAGACCTTCGGCTCGAGCTGGAGCTCACCGAGGCTATGCGCTTCGACAAAGGCGTAC 360
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420
361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGGCGCTCTCGACGACCGCGTAC 420

RESULT 27

US-10-824-527-49
; Sequence 49, Application US/10824527
; Publication No. US20040265873A1

GENERAL INFORMATION:

; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN

; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; FILE REFERENCE: 970EL2 GENE

; CURRENT APPLICATION NUMBER: US/10/824,527

; PRIOR FILING DATE: 2004-04-15

; PRIOR APPLICATION NUMBER: KR 2003-24656

; PRIOR FILING DATE: 2003-04-18

; PRIOR APPLICATION NUMBER: KR 2003-80580

; PRIOR FILING DATE: 2003-11-14

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 49

; LENGTH: 420

; TYPE: DNA

; ORGANISM: Streptomyces scabiei

US-10-824-527-49

Query Match 92.0%; Score 386.4; DB 8; Length 420;

Best Local Similarity 95.0%; Pred. No. 9.7e-90;

Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy	1	AAGAAGACGGACGAGTCCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCACGCG	60
Db	1	AAGAAGACGGACGAGTCCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCACGCG	60
Qy	61	CTCGTACGCGAGGGCGTGGCAACGTCCGCGCGGTGCGCAACCGGACCGTTCTCGCCACGCG	120
Db	61	CTCGTACGCGAGGGCGTGGCAACGTCCGCGCGGTGCGCAACCGGACCGTTCTCGCCACGCG	120
Qy	121	GGCATCGAGAGCGCGTTCGAGCCGTCTCCGCGCGCTCTCGGACGAGCGCAAGATGTC	180
Db	121	GGCATCGAGAGCGCGTTCGAGCCGTCTCCGCGCGCTCTCGGACGAGCGCAAGATGTC	180
Qy	181	GAGACCAAGGACGAGATCGCTTCCAGCGCTTCATCTCCGCGCGGACACCCAGATCGGC	240
Db	181	GAGACCAAGGACGAGATCGCTTCCAGCGCTTCATCTCCGCGCGGACACCCAGATCGGC	240
Qy	241	GAGTCTATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGTCAATCACCCTCGAGGAG	300
Db	241	GAGTCTATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGTCAATCACCCTCGAGGAG	300
Qy	301	TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGGAGGTATGCGTTTCGACAGGGCTAC	360
Db	301	TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGGAGGTATGCGTTTCGACAGGGCTAC	360
Qy	361	ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGACAGCCCGTAC	420
Db	361	ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGACAGCCCGTAC	420

RESULT 28

US-10-824-527-57
; Sequence 57, Application US/10824527
; Publication No. US20040265873A1

GENERAL INFORMATION:

; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN

; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN

; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; FILE REFERENCE: 970EL2 GENE

; CURRENT APPLICATION NUMBER: US/10/824,527

; PRIOR FILING DATE: 2004-04-15

; PRIOR APPLICATION NUMBER: KR 2003-24656

; PRIOR FILING DATE: 2003-04-18

; PRIOR APPLICATION NUMBER: KR 2003-80580

; PRIOR FILING DATE: 2003-11-14

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 57

; LENGTH: 420

; TYPE: DNA

; ORGANISM: Streptomyces neyagawaensis

US-10-824-527-57

Query Match 92.0%; Score 386.4; DB 8; Length 420;

Best Local Similarity 95.0%; Pred. No. 9.7e-90;

Matches 399; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy	1	AAGAAGACGGACGAGTCCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCACGCG	60
Db	1	AAGAAGACGGACGAGTCCCGGTGACGGTACGACCAACCGGACCGTTCTCGCCACGCG	60
Qy	61	CTCGTACGCGAGGGCGTTCGCAACGTCCGCGCGGTGCGCAACCGGACCGTTCTCGCCACGCG	120
Db	61	CTCGTACGCGAGGGCGTTCGCAACGTCCGCGCGGTGCGCAACCGGACCGTTCTCGCCACGCG	120
Qy	121	GGCATCGAGAGCGCGTTCGAGCCGTCTCCGCGCGCTCTCGGACGAGCGCAAGATGTC	180
Db	121	GGCATCGAGAGCGCGTTCGAGCCGTCTCCGCGCGCTCTCGGACGAGCGCAAGATGTC	180
Qy	181	GAGACCAAGGACGAGATCGCTTCCAGCGCTTCATCTCCGCGCGGACACCCAGATCGGC	240
Db	181	GAGACCAAGGACGAGATCGCTTCCAGCGCTTCATCTCCGCGCGGACACCCAGATCGGC	240
Qy	241	GAGTCTATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGTCAATCACCCTCGAGGAG	300
Db	241	GAGTCTATCGCCGAGGCGATGGAACAAGTCCGCAAGGAGCGTCAATCACCCTCGAGGAG	300
Qy	301	TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGGAGGTATGCGTTTCGACAGGGCTAC	360
Db	301	TCCGAGACCTTCGGTCTCGGAGCTGAGCTCACCGGAGGTATGCGTTTCGACAGGGCTAC	360
Qy	361	ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGACAGCCCGTAC	420
Db	361	ATCTCGGCGTACTTCGCCACCGACATGAGCGGATGAGGGCGTCTCGACAGCCCGTAC	420

RESULT 29

US-10-824-527-18

; Sequence 18, Application US/10824527

; Publication No. US20040265873A1

GENERAL INFORMATION:

; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN

; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING

; FILE REFERENCE: 970EL2 GENE

; CURRENT APPLICATION NUMBER: US/10/824,527

; CURRENT FILING DATE: 2004-04-15

QY 61 CTCGTACGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTCGTCAAGAGGCGCTCGCAACGTCGCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCGGCGCGCTCGAGGCGCGGTGCGCAAGGATGTC 180
Db 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCGGCGCGCTCGAGGCGCGGTGCGCAAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGCACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGCACCCAGATCGGC 240
QY 241 GAGCTCATCGGAGGCGATGAGCAAGGTGCGCAAGGAGGCGCTCATCAAGGTGAGGAG 300
Db 241 GAGCTCATCGGAGGCGATGAGCAAGGTGCGCAAGGAGGCGCTCATCAAGGTGAGGAG 300
QY 301 TCCGACACCTTCGGTCTGAGCTGAGGCTCACCGGGGTATGCGCTTCGACGACCCGCTAC 420
Db 301 TCCGACACCTTCGGTCTGAGCTGAGGCTCACCGGGGTATGCGCTTCGACGACCCGCTAC 420
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGTATGCGCTTCGACGACCCGCTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGTATGCGCTTCGACGACCCGCTAC 420

RESULT 32

US-10-824-527-35
; Sequence 35, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-0000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 35
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces griseoviridis
US-10-824-527-35

Query Match 91.6%; Score 384.8; DB 8; Length 420;
Best Local Similarity 94.8%; Pred. No. 2.5e-89;
Matches 398; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 AAGAAGCGGACGATCGCGGTGACGGTACGACACCGGACCGGTCTCGCCGAGCGG 60
Db 1 AAGAAGCGGACGATCGCGGTGACGGTACGACACCGGACCGGTCTCGCCGAGCGG 60
QY 61 CTCGTACGAGGCGCTCGCAACCTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTGGTCAAGAGGCGCTCGCAACCTAGCGCGCGGTGCGCAACCCGATGGCTCTGAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCGCTCTCGAGGCGCGGTGCGCAAGGATGTC 180
Db 121 GGTATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCGCTCTCGAGGCGCGGTGCGCAAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGCACCCAGATGGCT 240

Db 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGCACCCAGATCGGC 240
QY 241 GAGCTCATCGGAGGCGATGAGCAAGGTGCGCAAGGAGGCGCTCATCAAGGTGAGGAG 300
Db 241 GAGCTCATCGGAGGCGATGAGCAAGGTGCGCAAGGAGGCGCTCATCAAGGTGAGGAG 300
QY 301 TCCGACACCTTCGGTCTGAGCTGAGGCTCACCGGGGTATGCGCTTCGACGACCCGCTAC 360
Db 301 TCCGACACCTTCGGTCTGAGCTGAGGCTCACCGGGGTATGCGCTTCGACGACCCGCTAC 360
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGTATGCGCTTCGACGACCCGCTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGTATGCGCTTCGACGACCCGCTAC 420

RESULT 33

US-10-824-527-13
; Sequence 13, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823-0260-0000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces anandii
US-10-824-527-13

Query Match 91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 AAGAAGCGGACGATCGCGGTGACGGTACGACACCGGACCGGTCTCGCCGAGCGG 60
Db 1 AAGAAGCGGACGATCGCGGTGACGGTACGACACCGGACCGGTCTCGCCGAGCGG 60
QY 61 CTCGTACGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGC 120
Db 61 CTGGTCCGCGAGGCGCTCGCAACGTCGCGCGGTGCGCAACCCGATGGCTCTGAAGCGC 120
QY 121 GGCATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCGCTCTCGAGGCGCGGTGCGCAAGGATGTC 180
Db 121 GGTATCGAGAAGGCGCTCGAGGCGCTCTCCGCGCGCTCTCGAGGCGCGGTGCGCAAGGATGTC 180
QY 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGCACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCACGGCTTCATCTCCGCGCGCGCACCCAGATCGGC 240
QY 241 GAGCTCATCGGAGGCGATGAGCAAGGTGCGCAAGGAGGCGCTCATCAAGGTGAGGAG 300
Db 241 GAGCTCATCGGAGGCGATGAGCAAGGTGCGCAAGGAGGCGCTCATCAAGGTGAGGAG 300
QY 301 TCCGACACCTTCGGTCTGAGCTGAGGCTCACCGGGGTATGCGCTTCGACGACCCGCTAC 360
Db 301 TCCGACACCTTCGGTCTGAGCTGAGGCTCACCGGGGTATGCGCTTCGACGACCCGCTAC 360

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QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420

RESULT 34
US-10-824-527-19
; Sequence 19, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces cellulosa
US-10-824-527-19

Query Match 91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGTTCGCGCCAGGCG 60

QY 61 CTGATACGCGAGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 120
Db 61 CTGATCAAGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 120

QY 121 GGCATCGAGAGGCGCTGCGAGCGCTCTCCGCGCGCTGCGCAACCGATGCTCTCAAGCGC 180
Db 121 GGTATCGAGAGGCGCTGCGAGCGCTCTCCGCGCGCTGCGCAACCGATGCTCTCAAGCGC 180

QY 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240
Db 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240

QY 241 GAGCTATCGCGAGCGGTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 300
Db 241 GAGCTATCGCGAGCGGTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 300

QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
Db 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360

QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420

RESULT 35
US-10-824-527-26
; Sequence 26, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces collinus
US-10-824-527-26

Query Match 91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGTTCGCGCCAGGCG 60

QY 61 CTGATACGCGAGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 120
Db 61 CTGATCAAGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 120

QY 121 GGCATCGAGAGGCGCTGCGAGCGCTCTCCGCGCGCTGCGCAACCGATGCTCTCAAGCGC 180
Db 121 GGTATCGAGAGGCGCTGCGAGCGCTCTCCGCGCGCTGCGCAACCGATGCTCTCAAGCGC 180

QY 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240
Db 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240

QY 241 GAGCTATCGCGAGCGGTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 300
Db 241 GAGCTATCGCGAGCGGTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 300

QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
Db 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360

QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420

RESULT 36
US-10-824-527-37
; Sequence 37, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces collinus
US-10-824-527-37

Query Match 91.2%; Score 383.2; DB 8; Length 420;
Best Local Similarity 94.5%; Pred. No. 6.4e-89;
Matches 397; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGTTCGCGCCAGGCG 60
Db 1 AAGAAGACGACGACGTCGCGGTGACGATACGACACCGCGACCGTTCGCGCCAGGCG 60

QY 61 CTGATACGCGAGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 120
Db 61 CTGATCAAGAGGCGCTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 120

QY 121 GGCATCGAGAGGCGCTGCGAGCGCTCTCCGCGCGCTGCGCAACCGATGCTCTCAAGCGC 180
Db 121 GGTATCGAGAGGCGCTGCGAGCGCTCTCCGCGCGCTGCGCAACCGATGCTCTCAAGCGC 180

QY 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240
Db 181 GAGACCAAGAGCAGATGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGC 240

QY 241 GAGCTATCGCGAGCGGTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 300
Db 241 GAGCTATCGCGAGCGGTGCGCAAGCTGCGCGCGGTGCGCAACCGATGCTCTCAAGCGC 300

QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
Db 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360

QY 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420
Db 361 ATCTCGCGTACTTCGCCACCGACATGAGCGGTGCGCTCGACGACCGGTAC 420
```


Db 1 AAGAGACGACGAGCGTCCGCGGTGACGGTACGACACACCGGACCGGTTCTCGCCAGGCC 60
Qy 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTAAGGAAGGCGCTGCGCAACGTCGCGCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAAGGCGCTGCGAGGCGCTCTCGGCGCGCTGCGAGGCGGCGAAGGATGTC 180
Db 121 GGTATCGAGCGCGCGCTGAGAGCGCGTCTCCGCGCGCTGCTGAGAGGCGGAAAGGACGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTCAATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTCAATCACCCTCGAGGAG 300
Qy 301 TCCAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
Db 301 TCCAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
Qy 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGCGGCTCCTTGACGACCGGCTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGCGGCTCCTTGACGACCGGCTAC 420

RESULT 39

US-10-824-527-28
; Sequence 28, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces diastaticus
US-10-824-527-28

Query Match 90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 AAGAGACGACGAGCGTCCGCGGTGACGGTACGACACACCGGACCGGTTCTCGCCAGGCC 60
Db 1 AAGAGACGACGAGCGTCCGCGGTGACGGTACGACACACCGGACCGGTTCTCGCCAGGCC 60
Qy 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGAGAGGCGGCGAAGGATGTC 180
Db 121 GGCATCGAGAAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGAGAGGCGGCGAAGGATGTC 180

Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTCAATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTCAATCACCCTCGAGGAG 300
Qy 301 TCCAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
Db 301 TCCAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360
Qy 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGCGGCTCCTTGACGACCGGCTAC 420
Db 361 ATCTCGGCGTACTTCGCCACCGACATGGAGCGGTATGGAGCGGCTCCTTGACGACCGGCTAC 420

RESULT 40

US-10-824-527-29
; Sequence 29, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 29
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces djakartensis
US-10-824-527-29

Query Match 90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 AAGAGACGACGAGCGTCCGCGGTGACGGTACGACACACCGGACCGGTTCTCGCCAGGCC 60
Db 1 AAGAGACGACGAGCGTCCGCGGTGACGGTACGACACACCGGACCGGTTCTCGCCAGGCC 60
Qy 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGCTAGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCCAAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAAGGCGCTGCGAGGCGCTCTCCGCGCGCTGCTGAGAGGCGGCGAAGGATGTC 180
Db 121 GGTATCGAGCGCGCGCTGAGAGCGGCTCTCCGCGCGCTGCTGAGAGGCGGCGAAGGATGTC 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGCGCGCGGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTCAATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGCGATGGAACAAGGTGCGCAAGGCGTCAATCACCCTCGAGGAG 300
Qy 301 TCCAGACCTTCGCTCGGAGCTGGAGCTCACCGAGGATGCGCTTCGACCAAGGCGTAC 360

Db 301 TCCAGACCTTCGGTCTGGAGCTGGAGCTACCGAGGGTATGCGTTCCGACAGGGCTAC 360
Qy 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATCGAGGCGTGGTTCGACGACCGCGTAC 420
Db 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGCGGTCTTCGACGACCGCGTAC 420

RESULT 41

US-10-824-527-60
; Sequence 60, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 60
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces acidiscabies
US-10-824-527-60

Query Match 90.9%; Score 381.6; DB 8; Length 420;
Best Local Similarity 94.3%; Pred. No. 1.7e-88;
Matches 396; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACACCGGACCGTTCGCCCCAGGGC 60
Db 1 AAGAAGACGAGCGATAGCGCGGACGCGACGACCGGACCGTTCGCCCCAGGGC 60
Qy 61 CTCGTACGCGAGGGCTCGCAACCTCGCGCGGCTGCCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGGTCCGCGAGGGCTTCGCAACCTCGCGCGGCTGCCAACCGGATGGCTCTCAAGCGC 120
Qy 121 GGCATCGAGAGCGCGTTCGAGCCGCTCTCCGCGCCCTCTGAGCAGCGCGAAGGATGTC 180
Db 121 GGCATCGAGAGCGCGTTCGAGCCGCTCTCCGCGCCCTCTGAGCAGCGCGAAGGATGTC 180
Qy 181 GAGACCAAGGACGATGCTTCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGATGCTTCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGCGGATGACAGGTTCGCAAGGAGGCGTTCATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGCGGATGACAGGTTCGCAAGGAGGCGTTCATCACCCTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGTTTCGACAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGTTTCGACAGGGCTAC 360
Qy 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGGGTGCGTTCGACGACCGCGTAC 420
Db 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGGGTGCGTTCGACGACCGCGTAC 420

RESULT 42

US-10-824-527-14

; Sequence 14, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces argenteolus
US-10-824-527-14

Query Match 90.5%; Score 380; DB 8; Length 420;
Best Local Similarity 94.0%; Pred. No. 4.3e-88;
Matches 395; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACACCGGACCGTTCGCCCCAGGGC 60
Db 1 AAGAAGACGAGCGTCCCGGTGACGGTACGACACCGGACCGTTCGCCCCAGGGC 60
Qy 61 CTCGTACGCGAGGGCTTCGCAACCTCGCGCGGCTGCCAACCGGATGGCTTCGAGCGC 120
Db 61 CTGGTCCGCGAGGGCTTCGCAACCTCGCGCGGCTGCCAACCGGATGGCTTCGAGCGC 120
Qy 121 GGCATCGAGAGGGCTTCGAGCCGCTCTCCGCGCCCTCTGAGCAGCGCGAAGGATGTC 180
Db 121 GGCATCGAGAGGGCTTCGAGCCGCTCTCCGCGCCCTCTGAGCAGCGCGAAGGATGTC 180
Qy 181 GAGACCAAGGACGATGCTTCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGACGATGCTTCACGGCTTCATCTCCGCGCGCGACACCCAGATCGGC 240
Qy 241 GAGCTCATCGCGAGGGATGACAGGTTCGCAAGGAGGCGTTCATCACCCTCGAGGAG 300
Db 241 GAGCTCATCGCGAGGGATGACAGGTTCGCAAGGAGGCGTTCATCACCCTCGAGGAG 300
Qy 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGTTTCGACAGGGCTAC 360
Db 301 TCCAGACCTTCGGTCTGGAGCTGAGCTACCGAGGGTATGCGTTTCGACAGGGCTAC 360
Qy 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGGGTGCGTTCGAGCAGCCGCTAC 420
Db 361 ATCTCGGGTACTTCCGCCACCGACATGAGCGGATGAGGGGTGCGTTCGAGCAGCCGCTAC 420

RESULT 43

US-10-824-527-51
; Sequence 51, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM

	241	GAGCTCATCCGCGGCATGGACAAGTCCGCAAGHAGCGCTCATTCACGGTCGAGGAG	300
Db			
	301	TCCAGACCTTTGGGTCTGGAGCTCACCGAGGATATGCGCTTTCGAAGAAGGGCTAC	360
Qy			
	301	TGCGAGACTTTCGGCTCGAGCTTGAGCTCACCGAGGGCATTGCGCTTTCGAAGAAGGGCTAC	360
Db			
	361	ATCTCGGGCTACTTTCGCCACCGACATGGAGCGGATGGAGGCGTTCGCTTCGACGACCCGCTAC	420
Qy			
	361	ATCTCGGGCTACTTTCGCCACCGACATGGAGCGGATGGAGGCGTTCGCTTCGACGACCCGCTAC	420
Db			

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RESULT 48
US-10-824-527-27
/ Sequence 27, Application US/10824527
/ Publication No. US20040265873A1
/ GENERAL INFORMATION:
/ APPLICANT: KIM, BUM-JOON
/ APPLICANT: KIM, CHANG-JIN
/ APPLICANT: KO, YOUNG HWAN
/ APPLICANT: KOH, JEONG-SAM
/ APPLICANT: PARK, DONG-JIN
/ APPLICANT: LEE, HYANG BUM
/ APPLICANT: SEOUL, HONG KIM
/ APPLICANT: KIM, SUN-HYUN
/ TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
/ TITLE OF INVENTION: GROEL2 GENE
/ FILE REFERENCE: 05823-0260-00000
/ CURRENT APPLICATION NUMBER: US/10/824,527
/ CURRENT FILING DATE: 2004-04-15
/ PRIOR APPLICATION NUMBER: KR 2003-24656
/ PRIOR FILING DATE: 2003-04-18
/ PRIOR APPLICATION NUMBER: KR 2003-80580
/ PRIOR FILING DATE: 2003-11-14
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 27
/ LENGTH: 420
/ TYPE: DNA
/ ORGANISM: Streptomyces corchorusii
US-10-824-527-27

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RESULT 49
US-10-824-527-44
; Sequence 44, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BUM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HUYN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; TITLE OF INVENTION: GROS2 GENE
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 44
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces scabiei
US-10-824-527-44

```

RESULT 50
US-10-824-527-56
; Sequence 56, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM

APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BUM
APPLICANT: SEOUL, HONG KIM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
TITLE OF INVENTION: gtoel2 GENE
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 56
LENGTH: 420
TYPE: DNA
ORGANISM: Streptomyces diastatochromogenes
US-10-824-527-56

Query Match 88.6%; Score 372; DB 8; Length 420;
Best Local Similarity 92.9%; Pred. No. 4.8e-86;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGATCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 60
Db 1 AAGAAGACGACGATCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 60
Qy 61 CTGATCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 120
Db 61 CTGATCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 120
Qy 121 GGATTCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 180
Db 121 GGATTCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCCGCACACCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCCGCACACCAGATCGGC 240
Qy 241 GAGTCTCATCTCCCGAGGCGATGGAACAAGGTGCGCAAGAAAGGGTGTCATCACCGTCGAGGAG 300
Db 241 GAGTCTCATCTCCCGAGGCGATGGAACAAGGTGCGCAAGAAAGGGTGTCATCACCGTCGAGGAG 300
Qy 301 TCCCAGACTTTCGGTTCGAGCTGAGGCTCACGAGGGTATGCGCTTCGACAAAGGGCTAC 360
Db 301 TCCCAGACTTTCGGTTCGAGCTGAGGCTCACGAGGGTATGCGCTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGCGGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGCTAC 420
Db 361 ATCTCGCGGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGCTAC 420

RESULT 51
US-10-824-527-59
Sequence 59, Application US/10824527
Publication No. US20040265873A1
GENERAL INFORMATION:
APPLICANT: KIM, BUM-JOON
APPLICANT: KIM, CHANG-JIN
APPLICANT: KO, YOUNG HWAN
APPLICANT: KOH, JEONG-SAM
APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BUM
APPLICANT: SEOUL, HONG KIM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
TITLE OF INVENTION: gtoel2 GENE
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 420
TYPE: DNA
ORGANISM: Streptomyces alanosinicus
US-10-824-527-5

APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BUM
APPLICANT: SEOUL, HONG KIM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
TITLE OF INVENTION: gtoel2 GENE
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 55
LENGTH: 420
TYPE: DNA
ORGANISM: Streptomyces diastatochromogenes
US-10-824-527-55

Query Match 88.6%; Score 372; DB 8; Length 420;
Best Local Similarity 92.9%; Pred. No. 4.8e-86;
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 1 AAGAAGACGACGATCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 60
Db 1 AAGAAGACGACGATCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 60
Qy 61 CTGATCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 120
Db 61 CTGATCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 120
Qy 121 GGATTCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 180
Db 121 GGATTCGAGAACGCGTCGCGGTGACGGTACGACCAACCGCAGCCGTTCTCGCCCCAGGCG 180
Qy 181 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCCGCACACCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCCAGCGGCTCCATCTCCGCCGCACACCAGATCGGC 240
Qy 241 GAGTCTCATCTCCCGAGGCGATGGAACAAGGTGCGCAAGAAAGGGTGTCATCACCGTCGAGGAG 300
Db 241 GAGTCTCATCTCCCGAGGCGATGGAACAAGGTGCGCAAGAAAGGGTGTCATCACCGTCGAGGAG 300
Qy 301 TCCCAGACTTTCGGTTCGAGCTGAGGCTCACGAGGGTATGCGCTTCGACAAAGGGCTAC 360
Db 301 TCCCAGACTTTCGGTTCGAGCTGAGGCTCACGAGGGTATGCGCTTCGACAAAGGGCTAC 360
Qy 361 ATCTCGCGGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGCTAC 420
Db 361 ATCTCGCGGTACTTTCGCCACCGACATGAGCGGATGAGGCGTTCGTCGACGACCCGCTAC 420

RESULT 51
US-10-824-527-59
Sequence 59, Application US/10824527
Publication No. US20040265873A1
GENERAL INFORMATION:
APPLICANT: KIM, BUM-JOON
APPLICANT: KIM, CHANG-JIN
APPLICANT: KO, YOUNG HWAN
APPLICANT: KOH, JEONG-SAM
APPLICANT: PARK, DONG-JIN
APPLICANT: LEE, HYANG BUM
APPLICANT: SEOUL, HONG KIM
APPLICANT: KIM, SUN-HUYN
TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
TITLE OF INVENTION: gtoel2 GENE
FILE REFERENCE: 05823.0260-00000
CURRENT APPLICATION NUMBER: US/10/824,527
CURRENT FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: KR 2003-24656
PRIOR FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: KR 2003-80580
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 420
TYPE: DNA
ORGANISM: Streptomyces alanosinicus
US-10-824-527-5

QY 178 GTGAGACCAAGGAGGAGATCGTTTCAAGGCTTCCATCTCCGCCCGGACACCCAGATC 237
|||
Db 181 GTGAGACCAAGGAGGAGATCGTTTCAAGGCTTCCATCTCCGCCCGGACACCCAGATC 240
|||
QY 238 GCGAGCTCATCCCGGCGGATGGACAAAGTCCGCAAGGAGGCGTTCATCCGTCGAG 297
|||
Db 241 GCGAGCTCATCCCGGCGGATGGACAAAGTCCGCAAGGAGGCGTTCATCCGTCGAG 300
|||
QY 298 GAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGCG 357
|||
Db 301 GAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGGTATGGCTTCGACAAAGGCG 360
|||
QY 358 TACATCTCGCGGTACTTTCGCAACCGACATGAGGCGGATGAGGCGTTCGACGACCCG 417
|||
Db 361 TACATCTCGCGGTACTTTCGCAACCGACATGAGGCGGATGAGGCGTTCGACGACCCG 420
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QY 418 TAC 420
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Db 421 TAC 423

RESULT 55

US-10-824-527-4
; Sequence 4, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces aculeolatus
US-10-824-527-4

Query Match 87.0%; Score 365.6; DB 8; Length 420;
Best Local Similarity 91.9%; Pred. No. 2.1e-84;
Matches 386; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 AAGAGACGAGGAGCGTCCCGGTGACGGTACGACACCGCGACCGTTCCTCCGCCAGGCG 60
|||
Db 1 AAGAGACGAGGAGCGTCCCGGTGACGGTACGACACCGCGACCGTTCCTCCGCCAGGCG 60
|||
QY 61 CTGCTACGCGAGGGCGCTCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
|||
Db 61 CTGGTCAAGGAGGGCGCTCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
|||
QY 121 GGCATCGAGAGGCGCTCGAGGCGCTTCGCGGCGCTTCGAGGAGGCGGAGGATGTC 180
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Db 121 GGCATCGAGAGGCGCTCGAGGCGCTTCGCGGCGCTTCGAGGAGGCGGAGGATGTC 180
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QY 181 GAGACCAAGGAGGAGATGCTTCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
|||
Db 181 GAGACCAAGGAGGAGATGCTTCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
|||
QY 241 GAGCTCATCGCGGCGGATGGCAAGGTCCGCAAGGAGGCGTTCATCCCGTTCGAGGAG 300
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Db 241 GAGCTCATCGCGGCGGATGGCAAGGTCCGCAAGGAGGCGTTCATCCCGTTCGAGGAG 300
|||
QY 301 TCCAGACCTTCGGTCTGGAGCTCACCAGGGGTATCGCTTCGACAAAGGCGTAC 360
|||
Db 301 TCCAGACCTTCGGTCTGGAGCTCACCAGGGGTATCGCTTCGACAAAGGCGTAC 360
|||
QY 361 ATCTCGGCTACTTTCGCCACCGACATGGAGCGCATGGAGGCGGAGCTTCGAGGACCCGTC 420
|||
Db 361 ATCTCGGCTACTTTCGCCACCGACATGGAGCGCATGGAGGCGGAGCTTCGAGGACCCGTC 420
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RESULT 56

US-10-824-527-33
; Sequence 33, Application US/10824527
; Publication No. US20040265873A1
; GENERAL INFORMATION:
; APPLICANT: KIM, BUM-JOON
; APPLICANT: KIM, CHANG-JIN
; APPLICANT: KO, YOUNG HWAN
; APPLICANT: KOH, JEONG-SAM
; APPLICANT: PARK, DONG-JIN
; APPLICANT: LEE, HYANG BURM
; APPLICANT: SEOUL, HONG KIM
; APPLICANT: KIM, SUN-HYUN
; TITLE OF INVENTION: IDENTIFICATION METHOD OF GENUS STREPTOMYCES BY USING
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 33
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces griseochromogenes
US-10-824-527-33

Query Match 86.3%; Score 362.4; DB 8; Length 420;
Best Local Similarity 91.4%; Pred. No. 1.4e-83;
Matches 384; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1 AAGAGACGAGGAGCGTCCCGGTGACGGTACGACACCGCGACCGTTCCTCCGCCAGGCG 60
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Db 1 AAGAGACGAGGAGCGTCCCGGTGACGGTACGACACCGCGACCGTTCCTCCGCCAGGCG 60
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QY 61 CTGCTACGCGAGGGCGCTCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
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Db 61 CTGGTCAAGGAGGGCGCTTCGCAACGTCGCGCGGTGCGCAACCCGATGCTCTCAAGCGC 120
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QY 121 GGCATCGAGAGGCGCTCGAGGCGCTTCCTCCGCGCGCTTCGAGGAGGCGGAGGATGTC 180
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Db 121 GGCATCGAGAGGCGCTCGAGGCGCTTCCTCCGCGCGCTTCGAGGAGGCGGAGGATGTC 180
|||
QY 181 GAGACCAAGGAGGAGATGCTTCACGGCTCCATCTCCGCGCGCGCAACCCAGATCGGC 240
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Db 181 GAGACCAAGGAGGAGATGCTTCACGGCTCCATCTCCGCGCGCGCAACCCAGATCGGC 240
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QY 241 GAGCTCATCGCGGCGGATGGCAAGGTCCGCAAGGAGGCGTTCATCCCGTTCGAGGAG 300
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Db 241 GAGCTCATCGCGGCGGATGGCAAGGTCCGCAAGGAGGCGTTCATCCCGTTCGAGGAG 300
|||
QY 301 TCCAGACCTTCGGTCTGGAGCTCACCAGGGGTATGCGCTTCGACAAAGGCGTAC 360
|||
Db 301 AGCAACACTTCGGTCTGGAGCTCAGGCTCACCAGGGGCGATGCGCTTCGACAAAGGCGTAC 360
|||
QY 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGGCGTTCGTCGACGACCCGTC 420
|||
Db 361 ATCTCGGCGTACTTCGCCACCGACATGAGGCGGATGAGGCGGCGTTCGTCGACGACCCGTC 420
|||

; TITLE OF INVENTION: groEL2 GENE
; FILE REFERENCE: 05823.0260-00000
; CURRENT APPLICATION NUMBER: US/10/824,527
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: KR 2003-24656
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: KR 2003-80580
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces aminophilus
US-10-824-527-12

Query Match 85.5%; Score 359.2; DB 8; Length 420;
Best Local Similarity 91.0%; Pred. No. 9.3e-83;
Matches 382; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 AAGAAGACGGACGACGTCGCGGTGACGGTAGCACCACCGCGGACCGGTTCTCGCCCGAGGCG 60
Db 1 AAGAAGACGGACGACGTCGCGGTGACGGTAGCACCACCGCGGACCGGTTCTCGCCCGAGGCG 60

Qy 61 CTCGTACGCGAGGGCTCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
Db 61 CTGGTCAAGGAGGGCTCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120

Qy 121 GGCATCGAGAACGCGTCGAGCGCCCTCTCCGCGCCCTCTGCGAGCAGGCGAAGGATGTC 180
Db 121 GGCATCGAGAACGCGTCGAGCGCCCTCTCCGCGCCCTCTGCGAGCAGGCGAAGGATGTC 180

Qy 181 GAGACCAAGGAGCAGATCGCTTCACGGGCTTCATCTCGCGCGCGACACCCAGATCGGC 240
Db 181 GAGACCAAGGAGCAGATCGCTTCACGGGCTTCATCTCGCGCGCGACACCCAGATCGGC 240

Qy 241 GAGCTCATCGCGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTCAATCAACCGTCGAGGAG 300
Db 241 GAGCTCATCGCGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTCAATCAACCGTCGAGGAG 300

Qy 301 TCCGAGACCTTCGGTCTGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
Db 301 TCCGAGACCTTCGGTCTGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360

Qy 361 ATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAGCGCTCGCTCGACGACCGCTAC 420
Db 361 ATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAGCGCTCGCTCGACGACCGCTAC 420

RESULT 60
US-10-500-586-34
; Sequence 34, Application US/10500586
; Publication No. US20050014157A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Bum-Joon
; APPLICANT: BIOMEDLAB CORPORATION
; TITLE OF INVENTION: PRIMERS FOR AMPLIFYING HSP 65 GENE OF MYCOBACTERIAL SPECIES, HSP
; TITLE OF INVENTION: 65 GENE FRAGMENTS AND METHOD OF IDENTIFYING MYCOBACTERIAL SPECIE
; TITLE OF INVENTION: WITH THE SAME
; FILE REFERENCE: OPP021096KR
; CURRENT APPLICATION NUMBER: US/10/500,586
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: KR 10-2002-0004297
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: KR 10-2002-0011648
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 34
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Mycobacterium phlei
US-10-500-586-34

Query Match 76.8%; Score 322.4; DB 8; Length 604;
Best Local Similarity 85.5%; Pred. No. 2.6e-73;
Matches 359; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 1 AAGAAGACGGACGACGTCGCGGTGACGGTAGCACCACCGCGGACCGTTCCTGCCCGAGGCG 60
Db 50 AAGAAGACGGACGATGTCGCGGTGACGGTAGCACCACCGCGGACCGTTCCTGCCCGAGGCG 109

Qy 61 CTCGTACGCGAGGGCTCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 120
Db 110 CTGGTCCGCGAGGGCTCGCAACGTCGCGCGGTCGCAACCGGATGGCTCTCAAGCGC 169

Qy 121 GGCATCGAGAACGCGTCGAGCGCCCTCTCCGCGCCCTCTGCGAGCAGGCGAAGGATGTC 180
Db 170 GGTATCGAGAACGCGTCGAGCGCCCTCTCCGCGCCCTCTGCGAGCAGGCGAAGGATGTC 229

Qy 181 GAGACCAAGGAGCAGATCGCTTCACGGGCTTCATCTCGCGCGCGACACCCAGATCGGC 240
Db 230 GAGACCAAGGAGCAGATCGCTTCACGGGCTTCATCTCGCGCGCGACACCCAGATCGGC 289

Qy 241 GAGCTCATCGCGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTCAATCAACCGTCGAGGAG 300
Db 290 GAGCTCATCGCGAGCGGATGACAAAGGTTCGCGCAAGGAGGCGTCAATCAACCGTCGAGGAG 349

Qy 301 TCCGAGACCTTCGGTCTGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 360
Db 350 AGCAACACCTTCGGGCTCGAGCTGAGGCTCACCGAGGGTATGCGCTTCGACAAGGGCTAC 409

Qy 361 ATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAGCGCTCGCTCGACGACCGCTAC 420
Db 410 ATCTCGGCTACTTCGGTACCGGACCGCGGTCAGGAAGCGGCTCTCGAGGATCCGTAC 469

Search completed: April 2, 2006, 01:14:41
Job time : 1134.56 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 22:19:05 ; Search time 1038.23 Seconds
(without alignments)
1615.302 Million cell updates/sec

Title: US-10-824-527-43

Perfect score: 420

Sequence: 1 asgaagacgacgacgtgc.....cgtcgctgacgacccgtac 420

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : Published Applications NA_New.*

- 1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 10: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200.4	47.7	555	14	US-11-055-637-99
2	157.2	37.4	1632	8	US-10-467-657-1019
3	157.2	37.4	1716	8	US-10-467-657-1021
4	148.2	35.3	2035	11	US-11-077-619-107
5	144.4	34.4	1638	11	US-11-232-406A-27
6	141.8	33.8	2032	11	US-11-077-619-33
7	141	33.6	552	14	US-11-055-637-111
8	132	31.4	552	14	US-11-055-637-108
9	131	31.2	1626	14	US-11-074-176-29
10	129.6	30.9	1620	11	US-11-232-406A-31
11	129	30.7	1654	11	US-11-201-916-3
12	127.2	30.3	1662	11	US-11-201-916-5
13	125	29.8	552	14	US-11-055-637-89
14	125	29.8	552	14	US-11-055-637-101
15	125	29.8	1665	11	US-11-201-916-1
16	122.4	28.1	1838	8	US-10-615-668-7
17	121.8	29.0	552	14	US-11-055-637-98
18	119.2	28.4	552	14	US-11-055-637-99

19	119.2	28.4	552	14	US-11-055-637-104
20	118.6	28.2	552	14	US-11-055-637-90
21	117.6	28.0	2047	11	US-11-077-619-35
22	117	27.9	552	14	US-11-055-637-87
23	115.4	27.5	552	14	US-11-055-637-92
24	114.4	27.2	552	14	US-11-055-637-103
25	107.4	25.6	552	14	US-11-055-637-91
26	106.4	25.3	553	14	US-11-055-637-107
27	105.2	25.3	1661	11	US-11-201-916-7
28	105.8	25.2	552	14	US-11-055-637-95
29	102.6	24.4	552	14	US-11-055-637-110
30	101	24.0	552	14	US-11-055-637-94
31	100.6	24.0	1620	8	US-10-793-626-789
32	100.6	24.0	3885	8	US-10-793-626-3883
33	100	23.8	552	14	US-11-055-637-105
34	97.6	23.2	555	14	US-11-055-637-113
35	95.8	22.8	1647	14	US-11-038-686-9525
36	95.8	22.8	1457619	14	US-11-038-686-8739
37	95.2	22.7	552	14	US-11-055-637-102
38	94.8	22.6	1719	9	US-10-932-182A-77733
39	94.8	22.6	1719	9	US-10-932-182A-77733
40	94.6	22.5	2211	14	US-11-128-061-526
41	94.6	22.5	2211	14	US-11-128-049-526
42	93.8	22.3	2175	14	US-11-136-527-3831
43	93.6	22.3	552	14	US-11-055-637-100
44	93.6	22.3	552	14	US-11-055-637-109
45	93	22.1	552	14	US-11-055-637-96
46	91	21.7	552	14	US-11-055-637-112
47	90.4	21.5	552	14	US-11-055-637-97
48	89.8	21.4	552	14	US-11-055-637-85
49	89.8	21.4	552	14	US-11-055-637-86
50	89.8	21.4	552	14	US-11-055-637-93
51	88.2	21.0	552	14	US-11-055-637-106
52	87.4	20.8	2258	14	US-11-000-688-1372
53	83.2	19.8	552	14	US-11-055-637-114
54	80.8	19.2	684	9	US-10-932-182A-4757
55	80.8	19.2	684	9	US-10-932-182A-4757
56	71.6	17.0	422	14	US-11-000-688-1371
57	59.8	14.2	1876	11	US-11-096-568A-1371
58	56.8	13.5	556	10	US-10-301-480-304422
59	56.8	13.5	556	10	US-10-301-480-917831
60	56.8	13.5	561	6	US-09-925-065A-218359

ALIGNMENTS

RESULT 1
US-11-055-637-99
; Sequence 99, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055.637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-99

Query Match 47.7%; Score 200.4; DB 14; Length 555;
Best Local Similarity 70.6%; Pred. No. 2.2e-42;
Matches 267; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 40 GCGACCGTCTCGCCACGCGCTCGTACGCGAGGGCTCGCAACGTCGCGCGCGGTGCC 99
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DB 1 GCGACGCTGCTGGCGGAGGCGATGATCGCGAGGGTCTGAAGAACGTCGCGCGTGGTGG 60
|||
QY 100 AACCCGATGCTCTCAAGCGCGGATCGAGAACGCGCTCGAGCCGCTCTCCGCGCCCTG 159
|||
DB 61 AACCCGATGCTCTCGCCGCGGCTTGAAGAGCGCTGACGCGTGGCGTGGAGGAGCTG 120
|||
QY 160 CTGGAGCAGCGGAGGATCTCGAACCAAGAGGAGATCGCTCCACGCGCTCATCTCC 219
|||
DB 121 AAGAAGATCGGAAGCGGCTCCAGGGCCGCAAGAACATCGCGAGGTTCGCGCCATCTCG 180
|||
QY 220 GCGCCGACACCCAGATCGCGGAGCTCATCGCGAGGCGATGACAGGTCGCGCAAGGAA 279
|||
DB 181 GCTGTTGCAACGAATCGGCGAGCTCATCGCGATGCGATGCGATGGAGGTTGGCAACGAC 240
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QY 280 GCGGTATCATCCGTCGAGGAGTCCAGACCTTCGCTGCTGAGCTGAGGCTCAACGAGGT 339
|||
DB 241 GCGGTGATCAACGTCGAGAGGTCGAAGGGCTTCACGACCGAGCTTGAGGTCTGCGAGGT 300
|||
QY 340 ATGCGCTTCGACAGGCGTACATCTCGCGCTACTTCGCCACCGACATGAGCGGATGCGAG 399
|||
DB 301 ATGCGATTCGACCGCGCTCATCTCGCGCTTACATGCTGAGCGAGCGCGGCAAGATGGAG 360
|||
QY 400 GCGTCTGTCGACGACCGC 417
|||
DB 361 GCTGCTGTCGACGACCGC 378
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RESULT 2

US-10-467-657-1019
; Sequence 1019, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1019
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1019

Query Match 37.4%; Score 157.2; DB 8; Length 1632;
Best Local Similarity 62.7%; Pred. No. 2.8e-31;
Matches 262; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCGCGCCGAGGCGCTC 63
|||
DB 238 AAAACCAACGACGTAGCGGCGACGGTACGACTACCGCCACCGTATTGGCAACAATCCATC 297
|||
QY 64 GTACCGAGGCGCTCGCAAGCTCGCGCGGTGCCAACCGATGGCTCTCAAGCGCGGC 123
|||
DB 298 GTTCCGGAAGGCATGAATACTGTTACCGCGCGCATGAACCCGACCGATCTGAACGCGGC 357
|||
QY 124 ATCGAAGGCGGTCGAGGCGCTCTCGCGGCGCTGCTGGAGCAGGCGAAGGATGTCGAG 183
|||
DB 358 ATCGAAGGCGGTCGCGCTTTGGTGAAGAGCTGAANAACATCGCCAAACCTTGGAT 417
|||

QY 184 ACCAAGGACGATCGCTTCCAGCGCTCCATCTCGC---CGCGACACCCAGATCGGC 240
|||
DB 418 ACTTCAAAGAAATCCCCCAAGTCGGCTCGATTTCGCCCACTCCGACGAACAAGTCGGC 477
|||
QY 241 GAGCTCATCGCGAGGCGATGGACAGGTCGCGCAAGGAAGGGTTCATCACCGTCGAGGAG 300
|||
DB 478 GCGATTATCGCGAGGCGATGGAAGAAGTCGCGAAGAGGCGTGATTACCGTTGAAGAC 537
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QY 301 TCCAGACCTTCGCTGAGCTGAGCTTCAACGAGGATGCGGTTCGACAAAGGGCTAC 360
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DB 538 GGCMAATCTTTGMAAAACGAGCTGGACGTGGTTGAAGGTATGCACTTCGACCGCGCTAC 597
|||
QY 361 ATCTCGCGCTACTTCGCCACCGACATGGAGCGGTGCGCTCGACGACCCGT 418
|||
DB 598 CTGTCCCTTACTTTATCAACGACGCGGAAAAAACAATCGCGGTCTGGACAATCCGT 655
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RESULT 3

US-10-467-657-1021/C
; Sequence 1021, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1021
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1021

Query Match 37.4%; Score 157.2; DB 8; Length 1716;
Best Local Similarity 62.7%; Pred. No. 2.7e-31;
Matches 262; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

QY 4 AAGACGACGACGTCGCGGTGACGGTACGACCAACCGGACCGTTCGCGCCGAGGCGTC 63
|||
DB 1428 AAAACCAACGACGTAGCGGCGGACGGTACGACTACCGCCACCGTATTGGCAACAATCCATC 1369
|||
QY 64 GTACCGAGGCGCTCGGCAAGCTCGCGCGGTGCCAACCGATGGCTCTCAAGCGCGGC 123
|||
DB 1368 GTTCCGGAAGGCATGAATACTGTTACCGCGCGCATGAACCCGACCGATCTGAACCGCGC 1309
|||
QY 124 ATCGAAGGCGCGTCGAGGCGCTCTCGCGCGCTCTCGAGCAGCGGAGGATGTCGAG 183
|||
DB 1308 ATCGAAGGCGCTTCGCGCTTTGGTGAAGAGCTGAANAACATCGCCAAACCTTGGAT 1249
|||
QY 184 ACCAAGGACGATCGCTTCCAGCGCTCCATCTCGC---CGCGACACCCAGATCGGC 240
|||
DB 1248 ACTTCAAAGAAATCCCCCAAGTCGGCTCGATTTCGCCCACTCCGACGAACAAGTCGGC 1189
|||
QY 241 GAGCTCATCGCGAGGCGATGGACAGGTCGCGCAAGAGGCGTTCATCCCGTCGAGGAG 300
|||
DB 1188 GCGATTATCGCGAAGCGATGGAAGAAGTCGGCAAGAGGCGTGATTACCGTTGAAGAC 1129
|||
QY 301 TCCAGACCTTCGCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360
|||
DB 1128 GGCMAATCTTTGMAAAACGAGCTGGAGCTGGTTGAAGGTATGCACTTCGACCGCGCTAC 1069
|||
QY 361 ATCTCGCGCTACTTCGCCACCGACATGGAGCGGATGAGGCGGTGCGTCGACGACCCGT 418
|||
DB 1068 CTGTCCCTTACTTTATCAACGACGCGGAAAAAACAATCGCGGTCTGGACAATCCGT 1011
|||

RESULT 4
US-11-077-619-107
; Sequence 107, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Feesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: DE 10242433.0
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107
; LENGTH: 2035
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2035)
; OTHER INFORMATION: groEL
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1835)
US-11-077-619-107

Query Match 35.3%; Score 148.2; DB 11; Length 2035;
Best Local Similarity 59.7%; Pred. No. 5.6e-29;
Matches 249; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 4 AAGACGAGCGCTGCGCGGTGACGCGTACGACACCGCGACCGTTCCTCCGCCAGGCGCTC 63
DB 435 AAAACAAACGATGTTCCCGGTGACGCGTACGACACGACGACGATTCCTAGCTCAGGCGATG 494
QY 64 GTACGCGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGCGCG 123
DB 495 ATTGCGAAGGCTTAAACAGTAACTGCGCGGCTTAACCTGTAGGCGTGCAGAGGT 554
QY 124 ATCGAGAAGCGCGTGCAGCGCGTCTCCGCGCGCTGCTGGAGCAGCGCGAAGGATGTGCGAG 183
DB 555 ATCGAGCAGGCTGTGGCTGTAGCTGTGAAAGCGCTGAAAGAAATCTCTAAACCAATTGAA 614
QY 184 ACCAAGGACGATGCTTCCAGGCGCTCACTCCGCGCGCGACACCCAGATCGCGGAG 243
DB 615 GGCAGAGATCAATCGCAAGTGTCTCAATCTCCGCTGCGAGCGAAGAGTTCGGAAGC 674
QY 244 CTCATCGCGAGCGGATGACAAAGTTCGCAAGGAGGCGTCACTACCGTTCGAGGAGTCC 303
DB 675 CTGATCGCTGAAGCAATGAGCGCGTTCGCAACGACGCGTGTATACAGATCGAAGATCC 734
QY 304 CAGACCTTCGGTCTGGAGCTGAGCTCACCGAGGATATCGCTTCGACAAAGGCGTACATC 363
DB 735 AAAGGATTCACACAGAGCTTGAAGTGTGGAAGTATGCACTTCGACCGCGGATATCGG 794
QY 364 TCGGCGTACTTCGCCACCGACATGAGCGGATGAGGCGTCTCGACGACCGCGTAC 420
DB 795 TCTCCTTACATGCTGACGCGATTCGATAGATGGAAGCGGTTCTTGAGAATCCGTAC 851

RESULT 5
US-11-232-406A-27
; Sequence 27, Application US/11232406A

; Publication No. US20060030011A1
; GENERAL INFORMATION:
; APPLICANT: USUDA, Yoshihiro
; APPLICANT: NISHIO, Yosuke
; APPLICANT: YASUEDA, Hieaehi
; APPLICANT: SUGIMOTO, Shinichi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING POLYPEPTIDES INVOLVED IN THE STRESS RES;
; FILE REFERENCE: 232744USO
; CURRENT APPLICATION NUMBER: US/11/232,406A
; CURRENT FILING DATE: 2005-09-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Methylophilus methylotrophus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1638)
US-11-232-406A-27

Query Match 34.4%; Score 144.4; DB 11; Length 1638;
Best Local Similarity 60.8%; Pred. No. 5.4e-28;
Matches 254; Conservative 0; Mismatches 161; Indels 3; Gaps 1;
QY 4 AAGACGAGCGCTGCGCGGTGACGCGTACGACACCGCGACCGTTCCTCCGCCAGGCGCTC 63
DB 238 AAAACCAACGACATCGCTGGTACGCGTACGACGATTCGAGCTGTGTTGGCACACGCGATC 297
QY 64 GTACGCGAGGCGCTGCGCAACGTCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGCGCG 123
DB 298 ATCCGCGAAGGCATGAATCTGTGGCTGTGGCATGAACCCCAATGGACCTGAAGCGCGGT 357
QY 124 ATCGAGAAGCGCGTGCAGCGCGTCTCCGCGCGCTGCTGGAGCAGCGCGAAGGATGTGCGAG 183
DB 358 ATCGCAAGCGGTTGAAGCGCGCATGTCTGAATTTGAAGTGCAATCCAAACCTGTACG 417
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCCGC---CGCGACACCCAGATCGGC 240
DB 418 ACCAAGAAATGCGCCAGTAGTGTCTATCTCTGCTTACTTCGACACTTCTGTGGC 477
QY 241 GAGCTATCGCGAGCGCATGGAAGGTTCGCAAGGAGGCGTTCATCACTCGAGGAG 300
DB 478 CAAATTAATGCTGATGCGATGGAAGTAAAGGAGGCGTATCATCTGTGAAGAC 537
QY 301 TCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATATCGCTTCGACAAAGGCGTAC 360
DB 538 GGTTCGTGGCTTGAGCAACGAGCTGGACGTTGAGGCTATGCAATTTGATCGCGGTTAC 597
QY 361 ATCTCGCGGTACTTCGCCACCGACATGAGCGGATGGAGGCGTCTCGACGACCGGT 418
DB 598 TTGTCCTCATCTTCATCAACACCGACGCGCAAAATTTGCTGCTGCAATCTCT 655

RESULT 6
US-11-077-619-33
; Sequence 33, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Feesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09

Db 1 GCTACAGTCTTCTCAAGCGATGATTCGCGAAGGCTTGAAAAACGTAAACAGCGGTGCA 60
QY 100 AACCCGATGCTCTCAAGCGCGCATCGAAGGCGGTGAGGCGGTCTCCGCGCCCTG 159
Db 61 AACCCGATGGTTATGCGCAAGGTATCGAAGGCGAGTTCGTCGACAGTAGAAGACTG 120
QY 160 CTGAGGAGCGGAAGGATGTCGAGACCAAGGAGCAGATCGTTCCACGGCTCCATCTCC 219
Db 121 CATGCGATTTCTAAACCAATCGAAGGTAAAGATCTATCGCACAGTAGCAGCTATTCT 180
QY 220 GCGCGCGACACCCAGATCGCGAGCTCATCGCGAGCGATGACACAGGTGCGCAAGGAA 279
Db 181 GCTGCTGATGAGAAATCGGCCAACTGATGCTGGAAGCTATGGAAGATAGGAAAGAT 240
QY 280 GCGCTCATCACCGTCGAGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GCGGTATCACAGTAGAAGATCAAGGCTTCACACAGACTGATGTTGTAGAGGT 300
QY 340 ATGCGCTTCGACAAAGGCTACATCTCGGCGTACTTCGCCACCGACATGAGCGGATGGAG 399
Db 301 ATGCAATTCGACCGCGATACGCTTCTCCATACATGATCACGATACGTAAGATGGAA 360
QY 400 GCGTCTCGACACCGCTA 419
Db 361 GCAGTCTTGATAATCCGTA 380

RESULT 9

US-11-074-176-29
; Sequence 29, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; TITLE OF INVENTION: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1626)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 406; GroEL - 60 kDa chaperonin
US-11-074-176-29

Query Match 31.2%; Score 131; DB 14; Length 1626;
Best Local Similarity 57.0%; Pred. No. 1.5e-24;
Matches 239; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 2 AGAAGCGACGACGTGCGCGGTGACGTACGACACCGGACCGTCTCGGCCAGGGCG 61
Db 233 AAAGACTAACGACATGCGCGGTGACGTACTACTACTGTTGACTCAAGCAA 292
QY 62 TGTAGCGAGGCGCTTGGCAAGCTGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGG 121
Db 293 TTGCTGTGAAGGTATGAAGAACGTTACTGCTGGTGTCTAACCTGTGAGCATTCGTCGG 352
QY 122 GCATCGAAGAGGCGCTCGAGGCGGTCTCGCGCGCGCTGCTGAGCAGCGGAGGATGTG 181

Db 353 GTATTGAAGAGCAACTAAGGCTGCTGTGTGATGAATTAACAAGATTAGCCACAAGTTG 412
QY 182 AGACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCGCGCGCGACACCCAGATCGGG 241
Db 413 AATCAAGGAGCAAAATGCTTAACGATGCTGCTGTTTCTTTCAGATCTAAAGAGTTGG 472
QY 242 AGCTCATCGCGAGCGATGGCAAGGTGCGCAAGGAGGCGTCACTACCGTCGAGGAGT 301
Db 473 AATTGATCGCTGACGCTATGGAAGGTTGGTCACGATGGTGTATTACTATCGAAGATT 532
QY 302 CCCAGACCTTCGCTTCGAGCTGAGGCTCACCGAGGATGCGCTTCGACAAAGGCTACA 361
Db 533 CACGTGGTATCAATATCTGAATTTTCAGTAGTTGAAGGATGCAATTCGATCGTGGTACT 592
QY 362 TCTCGCGGTACTTCGCCACCGACATGAGCGATGAGCGCTCGCTTCGACGACCCGTAC 420
Db 593 TGTCAATATACATGTTAACTGACACGACAGATGGAAGACACTTGTATAACCCATAC 651

RESULT 10

US-11-232-406A-31
; Sequence 31, Application US/11232406A
; Publication No. US20060030011A1
; GENERAL INFORMATION:
; APPLICANT: USUDA, Yoshihiro
; APPLICANT: NISHIO, Yosuke
; APPLICANT: YASUEDA, Hisaaki
; APPLICANT: SUGIMOTO, Shinichi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING POLYPEPTIDES INVOLVED IN THE STRESS RES:
; TITLE OF INVENTION: ENVIRONMENTAL CHANGES IN METHYLOPHILUS METHYLOTROPHUS
; FILE REFERENCE: 232744US0
; CURRENT APPLICATION NUMBER: US/11/232,406A
; CURRENT FILING DATE: 2005-09-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent version 3.1
; SEQ ID NO 31
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Methylophilus methylotrophus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1620)
US-11-232-406A-31

Query Match 30.9%; Score 129.6; DB 11; Length 1620;
Best Local Similarity 58.7%; Pred. No. 3.5e-24;
Matches 244; Conservative 0; Mismatches 169; Indels 3; Gaps 1;
QY 4 AAGACGACGACGTGCGCGGTGACGCTACGACACCGGACCGTTCGCGCCAGCGCTC 63
Db 238 AAACAGCTGACGTGGCGCGGTGACGCTACGACTACCGTCTCGCTCAGGCGATT 297
QY 64 GTACGCGAGGCGCTGCGCAACGTGCGCGCGGTGCAACCGGATGGCTCTCAAGCGCGC 123
Db 298 GTACAAAGAGGATGAAGTCAGTCCGCTCCGCGCATGAATCCACCGACTAAACCGTGG 357
QY 124 ATCGAAGAGCGCTGAGGCGCTCTCGCGCGCGCTGCTGGAGCAGCGGAGGATGTCGAG 183
Db 358 ATTGATAAAGCGGTGACAGCGCTTGGTGTGATGAGCTTAAATCCATGTCGCAAGCTATCAC 417
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTTCATCTCGCGC---CGCGCACACCCAGATCGGC 240
Db 418 ACCCATAAAGAAATTTGCCCAAGTCGGTCCGATTTTCGCAACTCTGACCATGTCATTGGC 477
QY 241 GAGCTCATGCGCGAGCGCATGGAAGGTGCGCAAGGAGGCGTCACTACCGTCGAGGAG 300
Db 478 CAGATCATCGCGCATGCCATGCAAAAAGTCGTAAGAAAGGCGTGTATTCGTTGGAAGAA 537
QY 301 TCCAGACCTTCGCTGAGCTCACGAGGATGCGCTTACGAGGATGCGCTTCGACAAAGGCTAC 360
Db 538 GGTAACTCAGTGCATAAATGAATCTCGAGTGTGCGAGGCGATGCACTTTGACCGCGCTAT 597

QY 124 ATCGAGAGGCGCTCGAGGCGCTCTCGGCGCCCTGCTGAGGAGCGGAGGATGTCGAG 183
Db 372 ATGACAAAGCTGTGCGCTCGCTGTTGAAGAACTGAAAGCGCTGTCCGTACCGTCTCT 431
QY 184 ACCAAGGAGCAGATCGCTTCCAGCGCTCCATCTCCGC---CGCCGACACCCAGATCGGC 240
Db 432 GACTTAAGCCATGCTCAGGTAGGTACCACTTCGCTAACTCCGACGAAACCGTAGGT 491
QY 241 GAGCTCATCGCCGAGGCGATGGAACAAGGTGCGCAAGAGGCGCTCATCACCGTCGAGGAG 300
Db 492 AAACCTGATCGCGAAGCGATGGAATAAGTCGTAAGAGGCGGTGATCACCCTGTAAGAC 551
QY 301 TCCAGACCTTCGCTGAGGCTGAGGCTCACCGAGGATGCGCTTCGACAAAGGCTAC 360
Db 552 GGTACCGGCTGGAAGACGAACTGGAAGGTTGAAGGTATGCAAGTTGCAACCGCGTTAC 611
QY 361 ATCTCGGCGTACTTCGACCGACGATGAGCGCGATGAGGCGCTCGACGACCGGTAC 420
Db 612 CTGTCCCATCTTCATCAACAGCCAGAACTGGCGCTGTGAGCTGGAAAGCCCGTTTC 671

RESULT 13

US-11-055-637-89
; Sequence 89, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-89

Query Match 29.8%; Score 125; DB 14; Length 552;
Best Local Similarity 58.0%; Pred. No. 5.8e-23;
Matches 221; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 40 GCGACGTTCTCGCCAGGCGCTCGTACGAGGCGCTCGCAAGTCCGCGCGGTGCC 99
Db 1 GCGACAGTTCTAGCTCAGGCGATGATTCGCAAGGCTTTAAAGACGTAATCGCGCGCT 60
QY 100 AACCCGATGCTCTCAAGCGCGCATCGAGAGGCGCTCGAGCGCTCTCCGCGCGCTG 159
Db 61 AACCTGTAGGCGTGGCAAGGATTCGAGCGAGCTGTGCTGTAGCTGTGAAGCCCTG 120
QY 160 CTGAGCAGCGAAGGATGTCAGACCAAGAGGAGCATCGCTTCCACGCGCTCTCCATCTCC 219
Db 121 AAGAAATCTCTAAACCAATTGAAGGCAAGAAATCAATCGCACAGTTGCTTCAATCTCC 180
QY 220 GCGCGCACACCCAGATCGGCGATCATCGCGAGCGCATCGCAAGTTCGCGCAAGNA 279
Db 181 GCTGCAGACGAAGAGTTCGAAAGCCCTGATCGCTGAAGCAATGAGCGCGTTCGCAACCGAC 240
QY 280 GCGCTCATCAGCTCGAGGAGTCCAGACCTTCGCTCTGAGCTGAGCTCACCGAGGT 339
Db 241 GGTGTATCAGATCGAAGATCCAAAGGATTCACACAGAGCTTGAAGTGTGAAGT 300
QY 340 ATGCGCTTCGACAAAGGCTTACATCTCGCGCTTCTCCACCGCATCGAGCGGATGGAG 399

RESULT 15

US-11-201-916-1
; Sequence 1, Application US/11201916
; Publication No. US20060039922A1
; GENERAL INFORMATION:

Db 301 ATGCAAGTTCCAGCGCGATATCGTCTCTTACATGTCGACGATTCGATAAGATGGAA 360
QY 400 GCGTCGCTCGACGACCCGTAC 420
Db 361 GCGGTTCTTGAGAAATCCGTAC 381
RESULT 14
US-11-055-637-101
; Sequence 101, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-101

Query Match 29.8%; Score 125; DB 14; Length 552;
Best Local Similarity 58.0%; Pred. No. 5.8e-23;
Matches 221; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 40 GCGACGTTCTCGCCAGGCGCTCGTACGAGGCGCTCGCAAGTCCGCGCGGTGCC 99
Db 1 GCAACCGTACTAGCGCAAGCGATGATCGTGAAGGTCTAAAAACGTAACATCCGCTGCG 60
QY 100 AACCCGATGCTCTCAAGCGCGCATCGAGAGGCGCTCGAGCGCTCTCCGCGCGCTG 159
Db 61 AACCCAGTAGGCTTCGCGCGGATTTGAAGCAACCGAGTCTGCTACTCAGGAATTT 120
QY 160 CTGAGCAGGCGAAGGATGTCAGACCAAGAGGAGCATCGCTTCCACGCGCTCTCCATCTCC 219
Db 121 CGCAAAATCTCTAAGCCAATCGAAGCGCGAGTCCATTTCTCAGGTAGCTTCCATCTCT 180
QY 220 GCGCGCACACCCAGATCGGCGATCATCGCGAGGCGATCGCAAGTTCGCGCAAGNA 279
Db 181 GCTTCCGATACGAAGTTCGCGCGCTGATTCGTAAGCGATGAGCGCGTAGGAACCGAT 240
QY 280 GCGCTCATCAGCTCGAGGAGTCCAGACCTTCGCTCTGAGCTGAGCTCACCGAGGT 339
Db 241 GCGTTATTAACAATTGAAGATCTAAGGTTTCAATACAGAACTAGAGTGTGTAAGT 300
QY 340 ATGCGCTTCGACAAAGGCTTACATCTCGCGCTTCTCCACCGCATCGAGCGGATGGAG 399
Db 301 ATGCAAGTTCCAGCGCGCTATGCTTCTCCATACATGTTTACAGACCGAGTAAAAATGGAA 360
QY 400 GCGTCGCTCGACGACCCGTAC 420
Db 361 GCGGTTCTTGAGATTCCTTAC 381

APPLICANT: Mizzen, Lee
APPLICANT: Wisniewski, Jan
TITLE OF INVENTION: STREPTOCACAL HEAT SHOCK PROTEINS OF THE
TITLE OF INVENTION: MSP60 FAMILY
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/201,916
FILING DATE: 11-AUG-2005
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,737
FILING DATE: 31-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 870109.408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1649
US-11-201-916-1

Query Match 29.8%; Score 125; DB 11; Length 1665;
Best Local Similarity 59.4%; Pred. No. 5.4e-23;
Matches 231; Conservative 0; Mismatches 155; Indels 3; Gaps 1;
QY 4 AAGACGACGACGCTGCGCGGTGACGGTACGACACCGCGACCGCTTCTCGCCCGAGCGCTC 63
DB 252 AAGCGAAGCAGCGCTGCGGTGACGGTACCGACCGCGACCGTACTGGCTCAGTCCATC 311
QY 64 GTACCGAGGCGCTGCGCGAAGCGTCCGCGCGGTGCCAACCGGATGGCTCTCAAGCGCGGC 123
DB 312 ATCACTGAAGCGCTGAAAGCGGTGCTGCGGGCATGAACCGGATGCGATCTGAAACGCTGT 371
QY 124 ATGAGAGGCGCTGAGGCGCTCTCGCGCGCTGCGGCGGCGGAGGAGGATGTCGAG 183
DB 372 ATCGACAAAGCTGCTGCTGCTGCTGTTGAAGAACTGAAAGCACTGTCGTACCGTGCTCC 431
QY 184 ACCAAGGACGACGCTGCTCCACCGCTCCATCTCCGC---CGCCGACACCGAGATCGGC 240
DB 432 GACTCTAAGACTATGCTCAGGTGGTACCATCTCCGCTAACTCCGACGAAACCGTAGGT 491
QY 241 GAGCTATCGCGAGGCGATGGACAAGGTGCGGCAAGGAAGGCGTCAATCAGCTCGAGGAG 300
DB 492 AAACGTGCTGAGCGATGGAACAAAGTCGGTAAAGAGGCGGTGATCAGCTGTTGAAGAC 551
QY 301 TCCGACACCTTGGTCTGAGCTGAGCTACCGGAGGTATGCGCTTCGACAGGCGTAC 360
DB 552 GGTACCGGTCTGACGAGACGAACCTGACGCTGTTGAAGGTATGACGATTCGACCGGTGCTAC 611
QY 361 ATCTCGCGGTACTTTCGCGCACCGCATGGA 389

Db 612 CTGCTCTCTTACTTCATCAACAAGCCGGA 640

RESULT 16

US-10-615-668-7
; Sequence 7, Application US/10615668
; Publication No. US20050276819A1
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; APPLICANT: Bugnoli, Massimo
; APPLICANT: Telford, John
; APPLICANT: Macchia, Giovanni
; APPLICANT: Rappuoli, Rino
; TITLE OF INVENTION: Helicobacter Pylori CAI Antigen Polynucleotides
; FILE REFERENCE: CHIR0337
; CURRENT APPLICATION NUMBER: US/10/615,668
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 08/471,491
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/256,848
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: 09/410,835
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1838
; TYPE: DNA
; ORGANISM: Helicobacter pylori
US-10-615-668-7

Query Match 29.1%; Score 122.4; DB 8; Length 1838;
Best Local Similarity 57.4%; Pred. No. 2.5e-22;
Matches 241; Conservative 0; Mismatches 176; Indels 3; Gaps 1;
QY 4 AAGACGACGACGCTGCGCGGTGACGGTACGACACCGCGCGGTCTTCGCGCGAGCGCTC 63
DB 292 AAAACCGCTGATGCTGCGCGGTGACGGTACGACACCGCGCGGTGCTAGCTTATAGCAT 351
QY 64 GTACGCGAGGCGCTGCGCAAGCTGCGCGCGGTGCCAACCGGATGGCTCTCAAGCGCGGC 123
DB 352 TTTAAAGAAAGGTTTGAGGAATATCACGCGTGGGGCTAACCCCTATTGAAGTGAACAGGC 411
QY 124 ATCGAAGAAGCGCTGCGAGCGCTCTCGCGCGCGCTGCGAGCAGCGGAGGATGTCGAG 183
DB 412 ATGATTAAGCTGCTGAGCGATCATTAATGAGCTTAAAAAGCGAGCAAAAAGTAGGC 471
QY 184 ACCAAGGACGACGCTTTCACGGCTCCATCTCCGC---CGCCGACACCGAGATCGGC 240
DB 472 GGTAAAGAAAGAAATCAACCAAGTGGCGCACTTTCTGCAAACTCCGATCAATAATCGGG 531
QY 241 GAGCTCATCGCGAGGCGATGGACAAGGTGCGCAAGGAGGCGTCAATCAGCTCGAGGAG 300
DB 532 AAACCTATCGCTGACGCTATGGAAGGAGTGGGTAAAGACGCGGTGATCACCGTTGAGGAA 591
QY 301 TCCGACACCTTGGCTGCGAGCTGAGCTCACCGAGGATGCGCTTCGACAAAGGCGTAC 360
DB 592 GCTAAGGCAATTGAAGATGAATTGGATGCTGTAAGAGCATGCAATTTGATAGAGGCTAC 651
QY 361 ATCTCGCGGTACTTTCGCGCACCGCATGAGCGGATGAGGCGGTGCTTCGACGACCGGTAC 420
DB 652 CTCTCCCTTATTTTGTAGCAAGCGCTGAGAAATGACCGCTCAATTGGATATGCTTAC 711

RESULT 17

US-11-055-637-88
; Sequence 88, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-88

Query Match 29.0%; Score 121.8; DB 14; Length 552;
Best Local Similarity 57.5%; Pred. No. 3.8e-22;
Matches 219; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGCGCTCGTACGCGAGGCGCTGCGCAACCTGCGCGCGGTGCC 99
DB 1 GCGACAGTTCTTCCGACAGCAATGATCCGTGAAGGCTTAAACACGTAAACAGAGCGCT 60
QY 100 AACCCGATGGCTCTCAAGCGCGCATCGAGAGCGCGTTCGAGGCGCTCTCCGCGCGCTG 159
DB 61 AATCTGTAGGCTTCGTAAGGTATGAAAGCTGTAGCGTTCGATCGAAACTTA 120
QY 160 CTGAGCAGCGGAGAGATGTCGAGCAAGAGAGCAGATCGTTCCAGCGCTCCATCTCC 219
DB 121 AAGAAATTTCTAAGCAATCGAAGGCAAGAGTCTATCGCTCAGGTTCGCGATCTCT 180
QY 220 GCGCGGACACCCAGATCGCGAGCTCATCGCGAGGCGCATGCAAGGTGCAAGTTCGCAAGGAA 279
DB 181 GCTGCTGATGAGAGTTCGAAGCCTTATCGCTGAAGCAATGGAAGCGGTAGCGCAACGAC 240
QY 280 GCGTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
DB 241 GGGTTATCACAATCGAAGTCTAAGGCTTCACAACGTGAGCTTGAAGTTGTTGAGGT 300
QY 340 ATGCGCTTCGACAGGCTTACATCTCGGCTACTTCGCGGCTACTTCGCCACCGACATGAGGCGATGGAG 399
DB 301 ATGCAATTCGACCGCGGATGCGTCTCTTACATGTTAACTGACTCTGTAAGATGGAA 360
QY 400 GCGTCGCTCGACCGGTAC 420
DB 361 GCGTTCTTGACAATCTTAC 381

RESULT 18
US-11-055-637-98
; Sequence 98, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 552
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-98
Query Match 28.4%; Score 119.2; DB 14; Length 552;
Best Local Similarity 57.1%; Pred. No. 1.8e-21;
Matches 217; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGCGCTCGTACGCGAGGCGCTGCGCAACCTGCGCGCGGTGCC 99
DB 1 GCGACCGTTCTCGCCAGCGCAATGATCCGTGAAGGCTTGAACACGTAAACAGAGCGCA 60
QY 100 AACCCGATGGCTCTCAAGCGCGCATCGAGAGGCGCTGAGGCGCTCTCCGCGCGCTG 159
DB 61 AACCCGTTGGCATCCGCAAGGGATTGAAAAGCGTTGCGGCTGCTGTTGAAGATTA 120
QY 160 CTGAGCAGCGGCAAGAGATGTCGAGACCAAGAGGAGCAGATCGTTCCAGCGCTCCATCTCC 219
DB 121 AAAGCCATTTGAAACCAATCGAAGGCAAGCTTCATCGCCCAAGTTGCTGCAATTTCC 180
QY 220 GCGCGGACACCCAGATCGCGAGCTCATCGCGAGGCGCATGCAAGGTGCAAGTTCGCAAGGAA 279
DB 181 TCTGCTGACGAAGAGTTGGCGAATTCGCTGAAGCAATGGAACGCGTGGGCAACGAC 240
QY 280 GCGTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
DB 241 GCGCTCATTAACATTGAAGATCAAAAGCTTCTCAACGGAATGGAAGTTGTTGAGGG 300
QY 340 ATGCGCTTCGACAGGCTTACATCTCGGCTACTTCGCCACCGACATGAGGCGGATGGAG 399
DB 301 ATGCAATTCGACCGTGGCTTATGCAATCGCTTACATGTTAACTGATTCGCAAAATGGAA 360
QY 400 GCGTCGCTCGACCGGTAC 419
DB 361 GCTGTTCTGATAACCCCTTA 380

RESULT 19
US-11-055-637-104
; Sequence 104, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-104

Query Match 28.4%; Score 119.2; DB 14; Length 552;
Best Local Similarity 57.1%; Pred. No. 1.8e-21;
Matches 217; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGCGCTCGTACGCGAGGCGCTGCGCAACCTGCGCGCGGTGCC 99
DB 1 GCAACAGTTCTTGTCTCAGGCAATGATCCGTGAAGGCTTAAAGACGTAACTGACGTTGCT 60

QY 100 AACCCGATGCTCTCAAGCGCGGCATCGAAGGCCGTCGAGCGCGTCTCGGCGCCCTG 159
|||||
Db 61 AACCAATGGCATCCGCAAGGATTTGAAAGCGGTTTCTACTGCTGTTGAGAGTTA 120
|||||
QY 160 CTGGAGCAGCGGAAGGATGTCGAGACCAAGGAGCAGATCGTCTCCACGGCTCCATCTCC 219
|||||
Db 121 AAGCTATTTCAAAACCTATCGAAACCAAGAAATCTATCGACAGGTTGCTGCTATTCT 180
|||||
QY 220 GCGCCGACACCCAGATCGGGAGCTCATCGCGAGGGATGACCAAGGTCGGCAAGGAA 279
|||||
Db 181 GCTGCTGACATGAATGAATGGCCAGCTGATCGCTGAAGCAATGGAGCGCGTTGGCAACGAT 240
|||||
QY 280 GCGGTCTATCAACCGTCGAGGAGTCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGT 339
|||||
Db 241 GGTGTTATCAATCGAAGATCTAAAGGTTTCAACTGAGCTTGATGTTGTAAGGT 300
|||||
QY 340 ATGCGTCTGACAGGCTTACATCTCGCGCTACTTCGCCACCGACATGCGAGCGATGGAG 399
|||||
Db 301 ATGCAATTCGACGCGGATAGCTTACCATATACATGTTACAGATCTTGATAAGATGAA 360
|||||
QY 400 GCGTGGCTCGACGACCCGTA 419
|||||
Db 361 GCGGTTCTTGAACCCCTTA 380
|||||

RESULT 20

US-11-055-637-90
; Sequence 90, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array

US-11-055-637-90
Query Match 28.2%; Score 118.6; DB 14; Length 552;
Best Local Similarity 57.0%; Pred. No. 2.6e-21;
Matches 217; Conservative 0; Mismatches 164; Indels 0; Gaps 0;
QY 40 GCGACCGTTCTCGCCAGCGGCTCGTACGCGAGGGCTCGGCAACAGTGGCGCGCGTGGCC 99
|||||
Db 1 GCGACTGTACTTGGCAGGCTATGATCGCGAAGGCTTAAACAGTAACTGCGGGGCT 60
|||||
QY 100 AACCCGATGCTCTCAAGCGCGGCATCGAAGGCCGTCGAGCGCGTCTCGGCGCCCTG 159
|||||
Db 61 AACCTGTGCGGTGCGTAAGGATGTAAGCAAGCCGTGACTGTAGCAATCGAAAACTTA 120
|||||
QY 160 CTGAGCAGGCGGAAGGATGTCGACCAAGGAGCAGATCGTCTCCAGGCGCTCATCTCC 219
|||||
Db 121 AAGAAATTTCTAAGCCGATCGAAGCAAGAGTCTATCGCTCAGGTTGCTGCGATCTCT 180
|||||
QY 220 GCGCCGACACCCAGATCGGGAGCTCATCGCGAGGGATGGAAGAAGTTCGGCAAGGAA 279
|||||
Db 181 GCTGCTGATGAGGAAGTCGAAGCCTTATCGCTGAAGCAATGGAGCGCGCTAGGAACGAC 240
|||||
QY 280 GCGGTCTACCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339
|||||

Db 241 GCGGTCTATCACATCGAAGTCTAAAGGTTTCACAACTGAGCTTGAAGTGT 300
|||||
QY 340 ATGCGCTTTCGAAGAAGGCTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
|||||
Db 301 ATGCAATTTGACCGCGGATATGCGTCTCCTTACATGCTGACTGACTCTGATAAGATGAA 360
|||||
QY 400 GCGTGGCTCGACGACCCGTAC 420
|||||
Db 361 GCGGTTCTTGAACAATCCTTAC 381
|||||

RESULT 21

US-11-077-619-35
; Sequence 35, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Fessche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juerger, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: DE 10242433.0
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 2047
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2047)
; OTHER INFORMATION: grol
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1847)

US-11-077-619-35
Query Match 28.0%; Score 117.6; DB 11; Length 2047;
Best Local Similarity 56.7%; Pred. No. 4.3e-21;
Matches 238; Conservative 0; Mismatches 179; Indels 3; Gaps 1;
QY 4 AAGACGGACGACGTCGCGGTGACGGTACGACACCGCGACCGTTCGCGCCAGGCGCTC 63
|||||
Db 438 AAAGCAAAACGACGTCGCGAGCGGATGACCACTGCAACCGCTACTGGCTCAGGCTATC 497
|||||
QY 64 GTACGCGAGGCTTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGG 123
|||||
Db 498 ATCACTGAAGGTCTGAAGCTGTGTGTCGCGGGATGAACCCGATGGAACCTGGAACGTTG 557
|||||
QY 124 ATCGAAGGCGCGTCGAGGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGG 183
|||||
Db 558 ATCGAAGGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTC 617
|||||
QY 184 ACCAAGGAGCAGATCGCTTCCACGCGCTCATCTCGCG-----CGCGGACACCCAGATCGGC 240
|||||
Db 618 GACTCTAAAGCGATGCTCAGGTTGGTACCATCTCGCTAACTCCGACGAAACCGTAGGT 677
|||||
QY 241 GAGCTCATCGCGAGCGGATGGAAGGTCGCGAAGGAGGCGTCATCAGCGTCGAGGAG 300
|||||
Db 678 AACTGATCGCTGAAGCGATGGAAGGTCGTAAGAGGCGGTTATCACCGTTGAAGAC 737
|||||
QY 301 TCCGACACCTTCGCTGCGAGCTGGAGCTCACCGAGGATGCGCTTCGACAAAGGGCTAC 360
|||||

Db 738 GGTACCGTCTCGAGGAGCAACTGGAGCTGGTTGAAGGTANGCAGTTTCGACCGTGCTAC 797
Qy 361 ATCTCGCGTACTTTCGCCACCGACATGGAGCGGATGAGCGCTCGCTCGACGACCGCTAC 420
Db 798 CTGTCTCTTACTTCTCATCAACAGCCGGAACCTGGCGCAGTAGAACTGGAAAGCCCGTTC 857

RESULT 22

US-11-055-637-87
; Sequence 87, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-87

Query Match 27.9%; Score 117; DB 14; Length 552;
Best Local Similarity 56.7%; Pred. No. 6.6e-21;
Matches 216; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

Qy 40 GCGACCGTTCGCGCCAGCGCTCGTACGCGAGGGCTCGCAACGTCGCGCGCGTGCC 99
Db 1 GCAACAGTTCTTGGCGCAAGCATGATCCGTGAAGGCTTAAAAACGTAAACAGCGCGT 60
Qy 100 AACCGATGCTCTCAAGCGCGCATCGAGAGGCGCTCGAGCGCTTCCGCGCGCTG 159
Db 61 AACCTGTAGGGCTGCGTAAAGGATGGAACAGCTGTAGCGTTCGATCGAATACTTA 120
Qy 160 CTGAGCAGCGAAGATCTCGAGCAAGGACGATCGCTTCCAGCGCTCCATCTCC 219
Db 121 AAAGAAATTTCTAAGCCATCGAAGCAAGAGTCTATCGCTCAGGTTGCTCGATCTCT 180
Qy 220 GCGCGCGACACCCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTTCGCAAGGAA 279
Db 181 GCTGCTGATGAGGAGTCTGAAGCCTTATCGTGAAGCAATGGAGCGGTAGAAACGAC 240
Qy 280 GCGCTCATCCGTCGAGGAGTCCAGACCTTTCGCTTGGAGCTGGAGCTCAACGAGGT 339
Db 241 GCGCTTATCACAATCGAAGTCTAAAGGCTTCAAACTGAGCTTGAAGTGTGAAGT 300
Qy 340 ATGCGCTTCGACAGGCTACATCTCGGCTACTTCGCCACCGACATGGAGCGGATGG 399
Db 301 ATGCAATTCGACCGCGATATCGCTCTCTTACATGTTAACTGACTCTGTATAAGATGAA 360
Qy 400 GCGTCTGCTCGACCGCTGAC 420
Db 361 GCGGTTCTTGATATCTTAC 381

RESULT 23

US-11-055-637-92
; Sequence 92, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland

; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-92

Query Match 27.5%; Score 115.4; DB 14; Length 552;
Best Local Similarity 56.4%; Pred. No. 1.7e-20;
Matches 215; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

Qy 40 GCGACCGTTCGCGCCAGCGCTCGTACGCGAGGGCTCGCAACGTCGCGCGCGTGCC 99
Db 1 GCGACTGTGCTTGCAAGGCTATGATCCGGAAGGCTTAAAAACGTAACTCGGGAGCT 60
Qy 100 AACCGATGCTCTCAAGCGCGCATCGAGAGGCGCTCGAGCGCTTCCGCGCGCTG 159
Db 61 AATCTGTGCGCTGCTAAAGGTATGGAACAAGCGCTAACCGTGCATCGAAAACTTA 120
Qy 160 CTGAGCAGCGAAGATCTCGAGCAAGGACGATCGCTTCCAGCGCTCCATCTCC 219
Db 121 AAAGAAATTTCTAAGCCATCGAAGCAAGAGTCTATCGCTCAGGTTGCTCGAATCTCT 180
Qy 220 GCGCGCGACACCCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTTCGCAAGGAA 279
Db 181 GCTGCTGATGAGGAGTCTGAAGCCTTATCGTGAAGCAATGGAGCGGTAGAAACGAC 240
Qy 280 GCGCTCATCCGTCGAGGAGTCCAGACCTTTCGCTTGGAGCTGGAGCTCAACGAGGT 339
Db 241 GCGCTTATCACAATCGAAGTCTAAAGGCTTCAAACTGAGCTTGAAGTGTGAAGT 300
Qy 340 ATGCGCTTCGACAGGCTACATCTCGGCTACTTCGCCACCGACATGGAGCGGATGG 399
Db 301 ATGCAATTCGACCGCGATATCGCTCTCTTACATGTTAACTGACTCTGTATAAGATGAA 360
Qy 400 GCGTCTGCTCGACCGCTGAC 420
Db 361 GCGGTTCTTGATATCTTAC 381

RESULT 24

US-11-055-637-103
; Sequence 103, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 103
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-103

Query Match      27.2%; Score 114.4; DB 14; Length 552;
Best Local Similarity 56.3%; Pred. No. 3.1e-20;
Matches 214; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

Qy  40 GCGACCGTCTCGGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db  1 GCAACAGTTCTAGCGCAAGCAATGATCCGTTGAAGGCTTTAAAAACGTAACAGCTGGTGCA 60

Qy  100 AACCCGATGGCTCTCAAGCGCGGCATCGAGAGGCGCTCGAGCCGCTCTCCGGCGCCCTG 159
Db  61 AACCTGTGTGGCGTTTCGTAAGGGATCGAAGAGCAAGTGAAGTACACTTTGAAGGCTTG 120

Qy  160 CTGGAGCAGCGGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCC 219
Db  121 CAGGAGATTTCTAAACCAATCGAAGCAAGAATCAATTCCTCAAGTTGGTCTATTCT 180

Qy  220 GCGCCGACACCCAGATCGCGGAGCTCATCGCCGAGCGATGGAACAAGGTTCGCAAGGAA 279
Db  181 GCAGCAGATGAAGAAGTTGGAAGCCGTGCTGTAAGCAATGAGCGTGTAGTAAAGCA 240

Qy  280 GGGCTCATACCGTCGAGGAGTCCAGACCTTCGGTCTGAGAGCTGAGACTCACCAGGGT 339
Db  241 GGGCTGATCACAATCGAAGAACTTAAGGGTTTCAAACTGAGCTTGAAGTGAAGGA 300

Qy  340 ATGCGCTTCGACAAAGGCTACATCTCGGCGTACTTCGCCACGACATGGAGCGGATGGAG 399
Db  301 ATGCGTTTGACCGCGGATATGCTTACCATAATGTCGAGCTTGTATAAGATGGAA 360

Qy  400 GCGTCTCGACGACCGCGTAC 420
Db  361 GCGGTTCTTGAATAATCCTTAC 381

RESULT 26
US-11-055-637-107
; Sequence 91, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT FILING DATE: 2005-02-11
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-107

Query Match      25.3%; Score 106.4; DB 14; Length 553;
Best Local Similarity 55.0%; Pred. No. 3.5e-18;
Matches 209; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

Qy  40 GCGACCGTCTCGGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db  1 GCGACTTCTAGCTCAAGCGATGATTCGTGAAGGCTTTAAAAACGTAACATCTGGTGGC 60

Qy  100 AACCCGATGGCTCTCAAGCGCGGCATCGAGAGGCGCTCGAGCCGCTCTCCGGCGCCCTG 159
Db  61 AACCAATGGGTATCCGTAAAGGGATTTGAAAAAGCAACAGCTCTGCGGTTCACAGACTT 120

Qy  160 CTGGAGCAGCGGAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCC 219
Db  121 AAAATATTTCGAACCAATCGAAGCAAGAATCAATTCGCAAGTTGGGTGCTAATCA 180

Qy  220 GCGCCGACACCCAGATCGCGGAGCTCATCGCCGAGCGATGGAACAAGGTTCGCAAGGAA 279
Db  40 GCGACCGTCTCGGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
```

```
; SEQ ID NO 103
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-103

Query Match      27.2%; Score 114.4; DB 14; Length 552;
Best Local Similarity 56.3%; Pred. No. 3.1e-20;
Matches 214; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

Qy  40 GCGACCGTCTCGGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db  1 GCAACAGTTCTAGCGCAAGCAATGATCCGTTGAAGGCTTTAAAAACGTAACAGCTGGTGCA 60

Qy  100 AACCCGATGGCTCTCAAGCGCGGCATCGAGAAGCGCTCGAGGCGCTTCGCGCGCCCTG 159
Db  61 AACCTGTGTGGCGTTTCGTAAGGGATCGAAGAGCAAGTGAAGTACACTTTGAAGGCTTG 120

Qy  160 CTGGAGCAGCGGAAGGATGTCGAGACCAAGGAGCAGATCGCTTCCACGGCTCCATCTCC 219
Db  121 CAAGAAATCTCCATGAATCGAAGGAAAGAGAGATTGCACAAGTCGATCTATTCT 180

Qy  220 GCGCCGACACCCAGATCGCGGAGCTCATCGCGAGGCGATGGAACAAGGTTCGCAAGGAA 279
Db  181 TCTGAGCAGCAAGAGTTGGAAACTTATTCGTAAGCAATGAGCGCGTTGGCAACGAT 240

Qy  280 GGGCTCATACCGTCGAGGAGTCCAGACCTTCGGTCTGAGAGCTGGAAGCTCACCGAGGT 339
Db  241 GGTGTCACTATCGAAGTCAAAAGGCTTCAGACTGAATAGAGCTTGTGAAGGA 300

Qy  340 ATGCGCTTCGACAAAGGCTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db  301 ATGCAATTTGACCGCGTTATGCACTCGCATACATGCAACGCGATACAGACAAAATGGAA 360

Qy  400 GCGTCTCGACGACCGCGTA 419
Db  361 GCGTCTTCGACATCCGTA 380

RESULT 25
US-11-055-637-91
; Sequence 91, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT FILING DATE: 2005-02-11
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-91

Query Match      25.6%; Score 107.4; DB 14; Length 552;
Best Local Similarity 55.1%; Pred. No. 2e-18;
Matches 210; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

Qy  40 GCGACCGTCTCGGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
```


Db 181 GCAGCTGACGAGGAGTTGGACAAATATTGCGAGAGCAATGGAACGTGTGGAAAGCAC 240
QY 280 GGGCTCATCAACCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGAGCTCAACCGAGGGT 339
Db 241 GGGCTTATTACAATCGAAGAAATCAAAAGGTTTCTCTACTGAAATTAGAAAGTAGTAGAGGT 300
QY 340 ATGGCTTCGACAGGGCTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTCGATCGTGGTTTCGTTCTCCATACATGTTAAACCGATTCTTGCAAAATGGAA 360
QY 400 GCGTCGCTCGACGACCCGTA 419
Db 361 GCAGTTCCTGAAATCCATA 380

RESULT 27
US-11-201-916-7
; Sequence 7, Application US/11201916
; Publication No. US2006003992A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: STREPTOCOCCAL HEAT SHOCK PROTEINS OF THE
; TITLE OF INVENTION: HSP60 FAMILY
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/201,916
; FILING DATE: 11-AUG-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,737
; FILING DATE: 31-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 870109.408
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1649
; US-11-201-916-7

Query Match 25.3%; Score 106.2; DB 11; Length 1661;
Best Local Similarity 53.5%; Pred. No. 3.7e-18;
Matches 222; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 4 AAGACGAGGAGCGTCCCGGTGACGCTAGCACACCGGACCGGTTCCTCGCCGAGCGGCTC 63
Db 249 AAAACCAATGATTTGCTGTGATGGACGACTACTGCAACAGTTTGTGACACAAGCCATT 308
QY 64 GTACGGAGGGCGCTGGCAACCTCGCGCGGTGCGCAACCCGATGGCTCTCAAGCGCGGC 123

Db 309 GTTCATGAAGGACTAAAAATGTGACAGAGGTGTAAATCCAATTGGTATCCGTGAGGC 368
QY 124 ATCGAGAGCGCGTCCGAGGCGCTCTCCGGCGCCCTCTCGAGCAGCGAGGATGTGCGAG 183
Db 369 ATTGAACAGCAACAGCAACAGCTGTGGAAGCTTGAAGCCATTGCTCACTGTATCT 428
QY 184 ACCAAGGACGATCGCTTCCAGCGCTCAATCTCCGCCCGGACACCCAGATCGGCGAG 243
Db 429 GGCAGGAAGCTATTGCTCAGGTCTGAGTATCATCAGCTCTGAAAAAGTTGAGAG 488
QY 244 CTCATCGCGGCGGATGCAAGGTCCGCAAGGAGCGGTATCACTCGAGGAGTCC 303
Db 489 TATATCTCAGAAAGCTATGAGCGGTGTGGCAACGATGGTGTGATTACCATCGAAGATCT 548
QY 304 CAGACCTTCGCTCTGGAGCTGAGCTCACCGAGGGTATCGCTTCGACAAAGGCTACATC 363
Db 549 CGAGGTATGGAACAGAACTTGAAGTGTGGAAGCATGCAATTTGACCGTGGTTACCTG 608
QY 364 TCGGGTACTTCGCCACCGACATGAGCGGATGGAGCGGTCTCGACGACCGGT 418
Db 609 TCTCAATACATGCTCAGACAAATGAAAAAATGGTTGACAGCTTGAAGAACCCAT 663

RESULT 28
US-11-055-637-95
; Sequence 95, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-3305
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
; US-11-055-637-95

Query Match 25.2%; Score 105.8; DB 14; Length 552;
Best Local Similarity 54.9%; Pred. No. 5.1e-18;
Matches 209; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 40 GCGACCGTTTCGCCGAGCGCTGTACGCGAGGCGCTCGCAACGTCGCCCGCGGTGCC 99
Db 1 GCAACAGTTTTAGCGCAAGCAATGATCCGCAAGGATTGAAAAAGCTTACAGCTGGCGCT 60
QY 100 AACCGATGGCTCTCAACGCGGCGCATCGAAGAGCGGCTCGAGGCGCGTCTCCGGCGCCCTG 159
Db 61 AACCAATGGGCATCCGTAAAGGTATTGAAAAAGCGGTGCTGTGGCAGTAGAAGATTA 120
QY 160 CTGGAGCAGGCGAAGGATGTGAGACCAAGAGCAGATCGCTTCCACGCGCTTCACTCC 219
Db 121 AAAGCAATCTCAACCAATTCAGGTTAAGATCGATGTCTCAAGTTGACGAGTCTCT 180
QY 220 GCCCGCACCCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTCCGCAAGGAA 279
Db 181 GGGCTGAGGAAGATTGGTCAATTAATCGCAGAGCAATGGAACGCGTTGGCAACGAT 240
QY 280 GGGCTCATCAGCGTGGAGGATCCAGACCTTCGTCCTGGAGCTCGAGGCTCAACGAGGT 339
Db 241 GGTGTATCATTAGAAGAAATCGAAAGGCTTCGCAACGGAATTAGATGTTGTTCGAAGGT 300

Qy 340 ATGCGCTTCGACGAGGCTACATCTCGCGGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGACCGTGGTTATGTATCTCCATCATGATCAGATACAGAAAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTGTGAAATCCATAC 381

RESULT 29

US-11-055-637-110
; Sequence 110, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-3305
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-110

Query Match 24.4%; Score 102.6; DB 14; Length 552;
Best Local Similarity 54.3%; Pred. No. 3.4e-17;
Matches 207; Conservative 0; Mismatches 174; Indels 0; Gaps 0;
Qy 40 GCGACCGTTCTCGCCGAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db 1 GCAACTGTATTAGTCTAGTCCATGATTCGTGAAGTCTTAAACAGTAGCATCGGTGCT 60
Qy 100 AACCCGATGGCTTCAAGCGCGGATCGAGAGCGGCTCGAGGCGGTCTCGGCGCGCTG 159
Db 61 AACCCCTGTGTGTTCCGCGCGGAATCGAAAAAGCTGTTGAAGTAGCAGTAAAGAACTA 120
Qy 160 CTGGAGCAGCGGAGGATGTCGAGACCAAGSAGCAGATCGTCCACGGCTCCATCTCC 219
Db 121 AAAAATATTTCCAAAGTCAATCGAAAGCAAGAAATCTATTGCTCAAGTAGCAGAGTTCT 180
Qy 220 GCCCGCGACACCCAGATCGGCGAGCTCATCGCGAGGCGATGGAAGGTCGCAAGGTCGCAAGGAA 279
Db 181 TCTGACGATGAGAGTTGGTAGTTAATTTCTGAACCAATGGAACGTGTTGGTAGCAG 240
Qy 280 GGCGTCAATACCGTCGAGGAGTCCAGACCTTGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GGAGTTATTAATTTGAAGAATCAAAAGGTTTCAACACAGAGCTAGAAGTAGTTGAAGGT 300
Qy 340 ATGGCGTTCGACAGGCTACATCTCGCGGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGACCGTGGATGCTTCTCCATACATGTTAAGCAAGCAAGCAAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTGTGAAATCCGTAC 381

RESULT 30

US-11-055-637-94
; Sequence 94, Application US/11055637

Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-3305
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-94

Query Match 24.0%; Score 101; DB 14; Length 552;
Best Local Similarity 54.1%; Pred. No. 8.7e-17;
Matches 206; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
Qy 40 GCGACCGTTCTCGCCGAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db 1 GCTACAGTTCCTTGTTCAGGCTATGATTCGTGAAGTCTTAAAAACGTAACCGCAGCGCT 60
Qy 100 AACCCGATGGCTTCAAGCGCGGATGTCGAGACCAAGSAGGCGCTCGAGCGGCTCTCCGCGCGCTG 159
Db 61 AACCCCTGTAGGCGGTTCGTAAGGTATGGAACCAAGCTGTAAACGATTCGCAATTCAAAAACCTT 120
Qy 160 CTGGAGCAGCGGAGGATGTCGAGACCAAGGAGCAGATCGTTCACGCGGCTCCATCTCC 219
Db 121 CAAGAATCTCTAAACCGATCGAGAGAAAGATCTATGCTCAGGTTGCTGCGATTCT 180
Qy 220 GCCCGCGACACCCAGATCGGCGAGCTCATCGCGAGGCGATGGAAGGTCGCAAGGTCGCAAGGAA 279
Db 181 GCTGCTGATGAAAAAGTTCGGAAGCTGATTGCTGAAGCGATGAGCGCGTTGGAACGAC 240
Qy 280 GGCGTCAATACCGTCGAGGATCCAGACCTTGGTCTGGAGCTGGAGCTCACCGAGGT 339
Db 241 GGCGTTATCAGATCGAAGAACTTAAAGGTTTCAACACTGAGCTTGAAGTTGTTGAAGGT 300
Qy 340 ATGGCGTTCGACAAAGGCTACATCTCGCGGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAAGTTCGACCGCGGATATGCAATCTCTTACATGTTAACTGATCTGATAAGATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCGGTTCTGGAATCCCTTAC 381

RESULT 31

US-10-793-626-789
; Sequence 789, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 789
; LENGTH: 1620

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-789

Query Match      24.0%; Score 100.6; DB 8; Length 1620;
Best Local Similarity 52.5%; Pred. No. 1e-16;
Matches 220; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 1 AAGAGACGACGACGCTGCGCGGTGACGGTACGACACACCGCGCGCTTCGCGCCGAGCG 60
   |||||
Db 232 AATAAACAAATGAATCGCTGGGACGGTACAACTACAGCAACAGTTTATAGCACAAATCA 291
   |||||

QY 61 CTCGTACGCGAGGCGCTGCGCAACGCTGCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGC 120
   |||||
Db 292 ATGATTACGAGAGGCTCTTAAGATGTTACAAAGTGTGCAATCTCTAGGCTTAAGACAA 351
   |||||

QY 121 GGCATCAGAAAGCGCTGAGCGGCTCTCGCGCGCGCTGCTGAGCAGCGGCAAGGATGTC 180
   |||||
Db 352 GGTATTGACAAAGCAGTGCAGTGGCTATAGAAAGCGCTTCATGAGATTTCTCAAAAGGTT 411
   |||||

QY 181 GAGACCAAGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGCACCCAGATCGGC 240
   |||||
Db 412 GAAATAAGAACCGAGATAGCGCAAGTTGAGGCTATTTCAGCAGCAGATGAAGAAATCGGT 471
   |||||

QY 241 GAGCTCATCCCGAGGCGATGACAAAGTTCGCAAGGAGGCGCTCATCCCGTCGAGGAG 300
   |||||
Db 472 CGTACATTTCTGAGCAATGGATAAGTAGGTAAAGTGGCGGTATCACTATTGAAGAA 531
   |||||

QY 301 TCCAGACCTTCGGTCTGAGCTGAGGCTCACCAGGGGTATGCGTTTCGACAGGCGCTAC 360
   |||||
Db 532 TCAATGGGTTTAAATACAGAAATAGAAAGTATGTTGAAGGAATGCAATTTGATCGCGTTAT 591
   |||||

QY 361 ATCTCGCGTACTTCGCCACGACATGAGCGGATGAGGCGTGCCTCGACGACCCGTA 419
   |||||
Db 592 CAATCACCATATATGTTAACTGACTCAGATAAAATGATAGCTGAATTAGAAGCTCCATA 650
   |||||

RESULT 32
US-10-793-626-3883/c
; Sequence 3883, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3883
; LENGTH: 3885
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3883

Query Match      24.0%; Score 100.6; DB 8; Length 3885;
Best Local Similarity 52.5%; Pred. No. 9.8e-17;
Matches 220; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 1 AAGAGACGACGACGCTGCGCGGTGACGGTACGACACACCGCGCGCTTCGCGCCGAGCG 60
   |||||
Db 2639 AATAAACAAATGAATCGCTGGGACGGTACAACTACAGCAACAGTTTATAGCACAAATCA 2580
   |||||

QY 61 CTCGTACGCGAGGCGCTGCGCAACGCTGCGCGCGGTGCGCAACCGCATGGCTCTCAAGCGC 120
   |||||
```

```
Db 2579 ATGATTTCAGGAAGGCTTTAAGAAATGTTACAAGTGGTGCAAAATCCCTGTAGGCTTAAGACAA 2520
QY 121 GGCATCAGCAAGGCGCTTCAGGCGCGCTCCGCGCGCGCTTCGAGCAGCGCAAGGATGTC 180
   |||||
Db 2519 GGTATTGACAAAGCAGTGCAGTGGCTATAGAAGCGCTTCATGAGATTTCTCAAAAGGTT 2460
   |||||

QY 181 GAGACCAAGAGCAGATCGCTTCCACGGCTCCATCTCCGCGCGCGACACCCAGATCGGC 240
   |||||
Db 2459 GAAATAAAGAACGAGATAGCGCAAGTTGGAGCTATTTCAGCAGCAGATGAAGAAATCGGT 2400
   |||||

QY 241 GAGCTCATCCCGAGGCGATGACAAAGTTCGCAAGGAGGCGCTCATCCCGTCGAGGAG 300
   |||||
Db 2399 CGGTACATTTCTGAAGCAATGGATAAAGTAGGTAAAGTGGCGTTATCTCATTTGAAGAA 2340
   |||||

QY 301 TCCAGACCTTCGGTCTGAGCTGAGGCTCACCAGGGGTATGCGTTTCGACAGGCGCTAC 360
   |||||
Db 2339 TCAATGGGTTTAATACAGAAATAGAGTAGTTGAAGGAATGCAATTTGATCGCGTTAT 2280
   |||||

QY 361 ATCTCGCGCTACTTCGCCACCGACATGAGGCGGATGAGGCGTGCCTCGACGACCCGTA 419
   |||||
Db 2279 CAATCACCATATATGTTAACTGACTCAGATAAAATGATAGCTGAATTAGAAGCTCCATA 2221
   |||||

RESULT 33
US-11-055-637-105
; Sequence 105, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jaron
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-330S
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-105

Query Match      23.8%; Score 100; DB 14; Length 552;
Best Local Similarity 53.9%; Pred. No. 1.6e-16;
Matches 205; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 40 GCGACCGTTCTGCGCCAGCGCTCGTACGCGAGGCGCTTCGCGCAACGCTCGCGCCGCGTCC 99
   |||||
Db 1 GCTACTGTCTTGCACAAAGCTATGATTCGTGAAGGCGCTGMAAAACGTAACGCGCTCGCGCG 60
   |||||

QY 100 AACCGATGGCTCTCAAGCGGCGCATCGAAGGCGCGTTCGAGGCGCGTCTTCGCGCGCGCTG 159
   |||||
Db 61 AATCTATATGGGCAATTCGTAAGGGGATTGAAAAGCTGTGAAAAGCTGCAATTAGTGAGTTA 120
   |||||

QY 160 CTGAGCAGGCGGAGGATGTCGAGACCAAGAGCAGATCGCTTCCACCGCGCTCCATCTCC 219
   |||||
Db 121 CAGCTATCTTAACCAATCGAAACAAAGAGTCTATTGCAACAAGTTGACAGCAATCTCA 180
   |||||

QY 220 GCGCGCAGACCCAGATCGGAGCTCATCGCGAGGCGATGGAACAAGTTCGCGCAAGGAA 279
   |||||
Db 181 GCTTCTGACGAAGAGTGGTCAATTAATTCGTAAGCAATGGAACGGGTTCGCAACGAC 240
   |||||

QY 280 GCGCTCATCAGCTCGAGGAGTCCAGACCTTCGCTCGTTCGAGCTCGAGGCTCAACGAGGT 339
   |||||
Db 241 GGTGTATACAAATTTGAAGAGTCTAAAGGATTTCTCACTGAATTTGAGCTAGTAGAGGT 300
   |||||
```

Qy	340	ATCGCGTTCGACAAAGGGCTACATCTCGGGTATTCTTCGCCACCGACATGGAGCGGATGAG	399
Db	301	ATGCAGTTTCGACCGTGGATATGCACTCTGCTTATGTTAAACAAACCCAGATAAAATGGAA	360
Qy	400	GCCTCGCTCGACGACCCGTA	419
Db	361	GCAGTCTTGGAAATCCATA	380

RESULT 34
 US-11-055-637-113
 ; Sequence 113, Application US/11055637
 ; Publication No. US20050280619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BROUSSEAU, Roland
 ; APPLICANT: DUBOIS, Jason
 ; APPLICANT: EDGE, Tom
 ; APPLICANT: MASSON, Luc
 ; APPLICANT: TREVORS, Jack T.
 ; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
 ; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
 ; FILE REFERENCE: 2139-33US
 ; CURRENT APPLICATION NUMBER: US/11/055,637
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: US 60/543,288
 ; PRIOR FILING DATE: 2004-02-11
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO 113
 ; LENGTH: 555
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe for DNA array
 US-11-055-637-113

Query Match	23.2%	Score 97.6;	DB 14;	Length 555;
Best Local Similarity	55.2%;	Pred. No. 6.5e-16;		
Matches	212;	Conservative	0;	Mismatches 169; Indels 3; Gaps 1;

Qy	40	GCACCGCTTCTCGCCAGGCGCTGCTACGCGAGGGGCTCGCCAAAGCTCGCCCGGTGCC	99
Db	1	GCACCGTACTGCTCAGGCTATCATCTGAAGGCTCTGAAGGCTGTTGCTGCGGCGATG	60
Qy	100	AACCGATGCTCTAAGCGCGCATCGAAGAGCGCGTCTCGAGCGCGTCTTCGGCGCCCTG	159
Db	61	AACCGATGACCTGAAAGCTGGTATCGAAGAGCGGTTACCGCTGCAGTTGAAGAATG	120
Qy	160	CTGACGACGCGAAGGNTGTGAGACCAAGGAGCGATCGCTTCCACGCGCTCCATCTCC	219
Db	121	AAAGCGTGTGTCGTAACATGCTCTGACTCTAAAGCGATTTGCTCAGGTTGTATCACTCC	180
Qy	220	GC---CGCCGACACCCAGATCGCGGAGCTCATCGCGAGGCGCATGGAAGTTCGGCAAG	276
Db	181	GCTAACTCCGACGAACCGTAGTAACTGATCGCTGAAGCGATGGAACAAAGTTCGGTAA	240
Qy	277	GAAGGCGTCATCAACCGTCGAGGAGTCCCAGACCTTCGGTCTCGAGCTGAGGCTCAACGAG	336
Db	241	GAAGGCGTTATCACCGTTGAAGACGGTACCGGCTCTGACGAGCGAACTGGACGCTGGTTGAA	300
Qy	337	GGTATGCGCTTCGCAAGGCTACATCTGGGCTACTTCGCCACCGACATGGAGCGGATG	396
Db	301	GGTATGAGTTCGACCGTGGCTACCTGTCTCTTACTTATCAACAGCCGGAACCTGGC	360
Qy	397	GAGGCGTCTGCTCGACGACCCGTAC	420
Db	361	GCAGTAGAATCGGAAGCCCGTT	384

RESULT 35
 US-11-098-686-9525
 ; Sequence 9525, Application US/11098686

```
; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739

Query Match      22.8%; Score 95.8; DB 14; Length 1457619;
Best Local Similarity 53.5%; Pred. No. 1.2e-15;
Matches 224; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

QY 4 AAGACGGACGACCTCGCGGTGAGGTAGACACACCGCGACCGCTTCGCGCCAGCGCTC 63
DB 771162 AAAAATAGCGATATTGCTGGTGATGGAACCTACACACGACACAGTCTCTGACAAAGCTATT 771221

QY 64 GTACGGAGGCGCTCGCAACGTCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCT 123
DB 771222 TATCGTGAAGGTGTAACCTTTGAGCAGCTGGTGGTAACTCTATGGCCATTAACGGTGC 771281

QY 124 ATCGAGAAGCGCTCGAGGCGCTCTCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCT 183
DB 771282 ATAGATAAAGCTGTGTTGCTGTTACTTAAGAACTAAGCGACATTAAAGGCTACTCTGT 771341

QY 184 ACCAAGGAGCAGATCGTTCCAGCGCTTCACGCGCTTCATCTCCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 771342 GACCAAAAAGAAATAGCTCAAGTTGGAACCAATTTCTGCAAACTCTGTACAACTAGGT 771401

QY 241 GAGCTCATCGCGAGCGGTGACACAGGTGCGCAAGGCGGTGATCGCTTCGCAAGGCGCTAC 300
DB 771402 AATATCATAGCTGAAGCTATGCTGCTTAAAGTTGGAAGGAGGTGTTATCAGTTGAGGAA 771461

QY 301 TCCGACGACCTTCGCTCGAGCTGAGCTCACCGGCTGATGCGCTTCGCAAGGCGCTAC 360
DB 771462 GCTAAGGCTTGAAGCTATGATGCTGCTGAGGAGTGAAGTTGACCGTGGCTAC 771521

QY 361 ATCTCGGCTACTTCGCCACCGACATGAGCGCGGTGCGCTTCGCAAGGCGCTAC 419
DB 771522 CTCTCTCCATCTTTGTAATCTCTGAAATGTTGTAAGTCTGTAACCTTGAACCTTGAACCTTGA 771580

RESULT 37
US-11-055-637-102
; Sequence 102, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-3305
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-102

Query Match      22.7%; Score 95.2; DB 14; Length 552;
Best Local Similarity 53.2%; Pred. No. 2.7e-15;
Matches 202; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 40 GCGACGTTCTCGCGCCAGCGCTCGTACCGCGAGGCGCTCGCGCAAGCTCGCGCGCGCTCGCGCGCGCT 99
DB 1 GCAACTGTTCTGCTCAAGCAATGATCCGTGAAGTCTTAAAGAGTTACAGCTGCTGCA 60
QY 100 AACCCGATGCTCTCAAGCGCGGCTACGAGAGGCGCTCGAGGCGCTCTCGCGCGCGCTG 159
```


ORGANISM: Cricetulus griseus
US-11-128-049-526

Query Match 22.5%; Score 94.6; DB 14; Length 2211;
Best Local Similarity 54.6%; Pred. No. 3.6e-15;
Matches 206; Conservative 2; Mismatches 166; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGCTGCGGTGACGGTACGACACCGCGACCGTTCGCGCCAGGG 60
DB 349 AATAACACAAATGAAGAGCTGGGGATGGCRCTACCACTGCTACTGCTGCGCACGTTCT 408

QY 61 CTGCTAGCGGAGGCGCTGCGCAACGTCGCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
DB 409 ATTGCCAAGGAGGCTTTGGAAGATCAGCAAGGGGCTAATCCAGTAGAATCCGGAGA 468

QY 121 GGCATCGAGAGCGCCGTCGAGCGGCTCTCGGCGCCCTGCTGGAGCAGCGAAGGATGTC 180
DB 469 GGTGTGATGTTGGCTGTTGATGCTGTAATTTGCTGAATGAAAAACAATCTAAACCTGTG 528

QY 181 GAGACCAAGGACAGATCGTTCCACGGCTCATCTCCGC---CGCCGACACCCAGATC 237
DB 529 ACAACCCCTGAAGAAATTTGCTCAGGTTGCTACAAATTTCTCGCAATGGAGACAAAGACATT 588

QY 238 GCGAGCTCATCGCGAGCGGATGAGCAAGGTGCGCAAGGAGGCTCATCCGCTCGAG 297
DB 589 GGAACATCATCTCTGATGCAATGAAGAAAGGTTGGAAGGAAAGCGCTCATCAGTGAAG 648

QY 298 GAGTCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTCGACAGGCGC 357
DB 649 GATGGAAGAAACCTGATGATGAGTTAGAAATTTATGGAAGGCATGAAGTTGACAGAGA 708

QY 358 TACATCTCGGCTACTT 374
DB 709 TATATTTCCCGATATT 725

RESULT 42
US-11-136-527-3831
; Sequence 3831, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 3831
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3831

Query Match 22.3%; Score 93.8; DB 14; Length 2175;
Best Local Similarity 54.9%; Pred. No. 5.7e-15;
Matches 207; Conservative 0; Mismatches 167; Indels 3; Gaps 1;

QY 1 AAGAAGACGACGCTGCGGTGACGGTACGACACCGCGGTCGCAACCGATGGCTCTCAAGCGC 60
DB 313 AATAACACAAATGAAGAGCTGGGATGGACCAACCACTGCCACTGTTCTGCGCACGGTCT 372

QY 61 CTGCTAGCGGAGGCTCGCGCAACGTCGCGCGCGGTGCGCAACCGATGGCTCTCAAGCGC 120
DB 373 ATTGCCAAGGAGGCTTTGAGAAGATCAGCAAGGGGGCTAATCCAGTGGAAATCCGGAGA 432

QY 121 GGCATCGAAGCGCTGAGGCGCTCTCGGCGCCCTGCTGGAGCAGCGGAGGATGTC 180
DB 433 GGTGTGATGTTGGCTGTTGATGCTGTAATTTGCTGAACCTTAAGAAACAATCTAAACCTGTG 492

QY 181 GAGACCAAGGACGACGATCGCTTCCACGGCTTCATCTCCGC---CGCCGACACCCAGATC 237
DB 493 ACAACCCCTGAAGAAATTTGCTCAGGTTGCTACAAATTTCTGCAACCGAGACAAAGACATT 552

QY 238 GCGGAGCTCATCGCGAGCGGATGACAGGTCGCGCAGGAGGCGTTCATCCCGTCCGAG 297
DB 553 GGAACATCATTTCTGATGCAATGAAGAGGTTGGAAGAAAGGGTGTCTACACAGTGAAG 612

QY 298 GAGTCCAGACCTTCGGTCTGAGCTGAGCTCACCGAGGCTACCGGCTTCGACAGGCGC 357
DB 613 GATGGAAGAAACCTGATGATGAGCTAGAAATTTATGGAAGGCATGAAGTTTGATAGAGA 672

QY 358 TACATCTCGGCTACTT 374
DB 673 TATATTTCCCATATT 689

RESULT 43
US-11-055-637-100
; Sequence 100, Application US/11055637
; Publication No. US2005026019A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-100

Query Match 22.3%; Score 93.6; DB 14; Length 552;
Best Local Similarity 52.9%; Pred. No. 7e-15;
Matches 201; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 40 GCGACCGTTCGCGCCAGCGCTCGTACGCGAGGCGCTTCGCGCAACGTCGCGCGCGGTGCC 99
DB 1 GCAACTGTTCTTGCAACAGCAATGATCGTGAAGGCTTGAAGAAACGTAACCTGCTGGAGCT 60

QY 100 AACCGATGGCTTCAGCGCGGATCGAGAGGCGCTGAGGCGCTCTCCGGCGCCCTG 159
DB 61 AATCCTGTTGGCTTAAAAAAGGGATGGAAGAGGAGTTGCAACACGAGTAACTGAGCTA 120

QY 160 CTGAGCAGGCGAAGGATGTCGACACCAAGGACGATCGCTTCACCGGCTCCCATCTCC 219
DB 121 CAACATCTCAAAACAATTTGAAGTAAGATCAATGCTCAAGTTGCATCTATTCT 180

QY 220 GCGCGCAGACCCAGATCGCGAGCTCATCGCGAGGCGATGGAACAAGTCGCGCAAGAA 279
DB 181 TCTGTGACGAAGAAGTTGGCCAATTAATAGCTGAAGCAATGGAACGTTGTTGGTAATGAT 240

QY 280 GCGCTCATCCGTCGAGGAGTCCAGACCTTCGCTGAGGCTGAGAGCTCACCGAGGT 339
DB 241 GCGCTTATTACAAATGAAGAGTCTCGTGGTTTCTACTACAGAGCTTGAAGTTGTAGAAGA 300

QY 340 ATGCGCTTCGCAAGGGCTACATCTCGCGCTACTTGGCCCGCATCGAGCGGATGGAG 399
DB 301 ATGCAAGTTGAGCGGTGTTATGCAATCTCTTATATGTTAAACAGATTTGTATAAATGAA 360

QY 400 CGCTCGCTCGACGACCCGTA 419

Db 361 GCTGCTGCTGAATCCATA 380
|| ||| || ||| ||

RESULT 44

US-11-055-637-109
; Sequence 109, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-109

Query Match 22.3%; Score 93.6; DB 14; Length 552;
Best Local Similarity 52.9%; Pred. No. 7e-15;
Matches 201; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 40 GCGACCGTTCGCGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db 1 GCAACAGTTTTCGCGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTTGCTTCGAGCA 60
Qy 100 AACCCGATGGCTTCAAGCGCGGATCGAAGCGCGTTCGAGGCGGTCTCGCGCGCGCTG 159
Db 61 AACCCCTCGGTGTCGCGCGTGAATTTGAAAAGCTGTTGAAAGTTCGAGTACGAGCTT 120
Qy 160 CTGAGCAGGCGAGGATTCGACCAAGGCGAGTCCGCTCCAGCGCTCCATCTCC 219
Db 121 AGAAAAATTCACAAAAGTGAAGATAAAGATCAATCGCTCAAGTTCGAGCTATTCA 180
Qy 220 GCGCGCACACCCAGATCGCGAGCTCATCGCGAGGCGATGGACAAAGGTTCGCAAGGAA 279
Db 181 GCAATGCGAGAGTAGGTCAATTAATCGCTGAAGCATGGAGCGGTGGTATGAT 240
Qy 280 GGCTCATACCGTCGAGGAGTCCAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGT 339
Db 241 GGTGTAATTAAGTGAAGATCAAGAGGATTCAGCACTGAATTTGAAGTAGTAGAAGT 300
Qy 340 ATGCGCTTCGACAGGCGTACATCTCGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGACCGCGATATCTTCCATATATGTTATCTGACCAAGATAAGATGAA 360
Qy 400 GCGTCGCTCGACGACCGCTA 419
Db 361 GCACTGCTTGAAGATCCATA 380

RESULT 45

US-11-055-637-96
; Sequence 96, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-96

Query Match 22.1%; Score 93; DB 14; Length 552;
Best Local Similarity 52.8%; Pred. No. 1e-14;
Matches 201; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 40 GCGACCGTTCGCGCCAGGCGCTCGTACGCGAGGCGCTCGCAACGTCGCGCGCGGTGCC 99
Db 1 GCAACAGTTTTCGCGCCAGGCGCTCGTACGAGAGGCTTTAAAAAACGTAACGCGTGTGCT 60
Qy 100 AACCCGATGGCTTCAAGCGCGGATCGAAGCGCGTTCGAGGCGGTCTCGCGCGCGCTG 159
Db 61 AACCCCAATGGTATCGGTAAAGGTATGGAAGGCGAGTAGCTGTAGCGGTGGAAGAACTA 120
Qy 160 CTGAGCAGGCGAGGATGTGAGACCAAGGAGCAGATCGCTTCCACGCGCTCCATCTCC 219
Db 121 AAGCAATCTCTAACAACATTCAGGTAAAGATTCAATTGCTCAAGTAGGGCTATCTCA 180
Qy 220 GCGCGCACACCCAGATCGCGAGCTCATCGCGAGGCGATGACAAAGGTTCGCAAGGAA 279
Db 181 GCACTGACGAGAGTAGGTCAATTAATTCGTGAAGCAATGGAGCGGTGGTAAACGAC 240
Qy 280 GCGTTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGAGCTGGAGCTCACCGAGGT 339
Db 241 GCGTTCATCACCTTGAAGAAATCAAAAGGTTTCAACTGAATTGAAGTGGTAGAAGT 300
Qy 340 ATGCGCTTCGACAAAGGCTACATCTCGGGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCACTTTCGCGCGTGGATATGATCTCTTACATGTAATGATTCAGTAAATGGA 360
Qy 400 GCGTCGCTCGACGACCGCTAC 420
Db 361 GCTGATTAGATGATCATA 381

RESULT 46

US-11-055-637-112
; Sequence 112, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 552
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

US-11-055-637-112

Query Match 21.7%; Score 91; DB 14; Length 552;

Best Local Similarity 52.5%; Pred. No. 3.3e-14;

Mismatches 199; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 40 GCGACGGTCTCGCCAGGCGCTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCC 99

DB 1 GCAACAGTTTGGACACAAGCCATTGTTTCATGAGGACTTAAATAATGTGACAGAGTGTCT 60

QY 100 AACCGGATGCTCTCAAGCGCGGATCGAGAGCGCGTCAAGCGCGTCTCGCGCGCGCTG 159

DB 61 AATCCAAATTGGTATCGTTCGAGGCAATTGAAACAGCAACAGCAACAGCGCTTGAAGCCTTG 120

QY 160 CTGGAGCAGCGAGGATGTCGAGACCAAGGAGCAGATCGCTTCCAGGCGCTCATCTCC 219

DB 121 AAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCTATTGCTCAGGTGCGTCGAGTATCA 180

QY 220 GCGCGCGACACCCAGATCGCGGAGCTCATCGCGAGGCGATGCAACAGGTGCGCAAGGAA 279

DB 181 TCAGGCTCTGAAAAGTTGAGAGTATATCTGAGAGCTATGAGGCTGTGGGCAACGAT 240

QY 280 GCGGTCAATCCTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339

DB 241 GGTGTGATTACCATCGAAGAAATCTCGAGGTATCGAAGAAAGAACTTGAAGTGGTTGAAGGC 300

QY 340 ATGCGCTTCGACAAGGCTACATCTCGGCTACTTCGCCACCGACATGGAGCGGATGGAG 399

DB 301 ATGCAATTTGACCGTGTACCTGTCTCAATACATGCTCAGACACAATGAAAAATGGTT 360

QY 400 GCGTCTGCTCGACACCGT 418

DB 361 GCAGACCTTGAAACCCAT 379

RESULT 47

US-11-055-637-97

; Sequence 97, Application US/11055637

; Publication No. US20050260619A1

; GENERAL INFORMATION:

; APPLICANT: BROUSSEAU, Roland

; APPLICANT: DUBOIS, Jason

; APPLICANT: EDGE, Tom

; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.

; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND

; FILE REFERENCE: 2139-33US

; CURRENT APPLICATION NUMBER: US/11/055,637

; PRIOR FILING DATE: 2005-02-11

; PRIOR APPLICATION NUMBER: US 60/543,288

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 97

; LENGTH: 552

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

US-11-055-637-97

Query Match

Best Local Similarity 21.5%; Score 90.4; DB 14; Length 552;

Mismatches 199; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 40 GCGACGGTCTCGCCAGGCGCTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCC 99

DB 1 GCAACTGTATTAGCGCAAGCTATGATTCGTGAAGGTCTTTAAACACGTAAACAGCTGTGCT 60

QY 100 AACCCGATCGCTCTCAAGCGCGGCAATCGAGAAAGCGCTCGAGGCGGTCTTCGCGCGCCCTG 159

DB 61 AACCCAAATCGGCTCTCGTAAAGGTATCGAAAAAGCTGTACTGCTGCAATTTGAAGAATTA 120

QY 160 CTGGAGCAGCGAGGATGTCGAGACCAAGGAGCAGATCGCTTCCAGGCGCTCATCTCC 219

DB 121 AAACGATTTCTTAAACCAATCGAAGGCAAAATCTTATCGCAAGTAGCTGCTATTTCT 180

QY 220 GCGCGCGACACCCAGATCGCGGAGCTCATCGCGAGGCGATGCAACAGGTGCGCAAGGAA 279

DB 181 CGAGCTGACGAAGAGTAGTCAATTAATCGCTGAGCAATGAGGCGCTTGGTAACGAC 240

QY 280 GCGGTCAATCAGCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339

DB 241 GCGGTATTTACTTTAGAAGAGTCTAAAGGATTCACAAAGATTTAGACGCTAGTAGAAGGT 300

QY 340 ATGCGCTTCGACAAGGCTACATCTCGGCTACTTCGCCACCGACATGAGCGGATGGAG 399

DB 301 ATGCAATTTGATCGTGGATATGCATCTCTTACATGATTAATGATTTCTGACAAAATGGAA 360

QY 400 GCGTCTGCTCGACACCGT 419

DB 361 GCAGTCTTGATAACCCATA 380

RESULT 48

US-11-055-637-85

; Sequence 85, Application US/11055637

; Publication No. US20050260619A1

; GENERAL INFORMATION:

; APPLICANT: BROUSSEAU, Roland

; APPLICANT: DUBOIS, Jason

; APPLICANT: EDGE, Tom

; APPLICANT: MASSON, Luc

; APPLICANT: TREVORS, Jack T.

; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND

; FILE REFERENCE: 2139-33US

; CURRENT APPLICATION NUMBER: US/11/055,637

; PRIOR FILING DATE: 2005-02-11

; PRIOR APPLICATION NUMBER: US 60/543,288

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 85

; LENGTH: 552

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe for DNA array

US-11-055-637-85

Query Match

Best Local Similarity 21.4%; Score 89.8; DB 14; Length 552;

Mismatches 199; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 40 GCGACGGTCTCGCCAGGCGCTCGTACGCGAGGCGCTGCGCAACGTCGCGCGCGGTGCC 99

DB 1 GCAACTGTATTAGCGCAAGCTATGATTCGTGAAGGTCTTTAAACACGTAAACAGCTGTGCG 60

QY 100 AACCCGATGCTCTCAAGCGCGGCAATCGAGAAAGCGCTCGAGGCGGTCTTCGCGCGCCCTG 159

DB 61 AACCCAAATGGGCTCTCGTAAAGGTATCGAAAAAGCTGTACTGCTGCAATTTGAAGAATTA 120

QY 160 CTGGAGCAGCGAGGATGTCGAGACCAAGGAGCAGATCGCTTCCAGGCGCTCATCTCC 219

DB 121 AAACGATTTCTTAAACCAATCGAAGGCAAAATCTTATCGCAAGTAGCTGCTATTTCT 180

QY 220 GCGCGCGACACCCAGATCGCGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 279

DB 181 GCAGCTGACGAAGAGTAGTCAATTAATGCTGAGCAANTGAGCGGCTTGGTAACGAC 240

QY 280 GCGGTCAATCAGCGTCGAGGAGTCCAGACCTTCGGTCTGGAGCTGGAGCTCACCGAGGT 339

Db 241 GCGCTTATTACTTTAGAGAGTCTAAAGGATTCACACAGATTAGACGTAGTAGAAGGT 300
Qy 340 ATGGCGTTCGACAGGCGTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGATCGTGATATGCATCTCTTACATGATTACTGATTCTGCAAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTTCTTGATAACCCATAC 381

RESULT 49

US-11-055-637-86
; Sequence 86, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-86

Query Match 21.4%; Score 89.8; DB 14; Length 552;
Best Local Similarity 52.2%; Pred. No. 6.7e-14;
Matches 199; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 40 GCGACCGTTCGCGCCGAGGCGCTCGTAGCGGAGGCGCTCGCACGCTCGCGCGCGGTGCC 99
Db 1 GCAACTGTATTAGCGCAAGCTATGATTCGTGAAGGTCTTAAACACGTAAACAGCTGGTGG 60
Qy 100 AACCCGATGGTCTCAAGCGCGCATCGAGAAGGCGCTCGAGGCGGTCTCGGCGCGCGCTG 159
Db 61 AACCAATGGGTCTTCGTAAGGTATCGAAAAGGTCTTAAAGGCTTAAACACGTAAACAGCT 120
Qy 160 CTGGAGCAGGCGAAGGATGTGAGACCAAGGAGGAGGAGTCTTCCACGCGCTCATCTCC 219
Db 121 AAAACGATTTCTAAACCAATCGAAGGTAAATCTTCAATCGCACAGTAGCTGCTATTCT 180
Qy 220 GCGCGCGACACCCAGATCGCGGAGCTCATCGCGGAGCGATGACAAAGGTGCGCAAGGAA 279
Db 181 GCGCTGACGAGAGTAGTCAATTAATCGCTGAAGCAATGAGCGCGTGGTAGACAC 240
Qy 280 GCGCTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGT 339
Db 121 AAAACGATTTCTAAACCAATCGAAGGTAAATCTTCTATCGCACAGTAGCTGCTATTCT 180
Qy 220 GCGCGCGACACCCAGATCGCGGAGCTCATCGCGGAGCGATGACAAAGGTGCGCAAGGAA 279
Db 181 GCTGCTGACGAGAGTAGTCAATTAATCGCTGAAGCAATGAGCGCGTGGTAGACAC 240
Qy 280 GCGCTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGT 339
Db 241 GCGCTTATTACTTTAGAGAGTCTAAAGGCTTCAACAGATTAGACGTAGTAGAAGGT 300
Qy 340 ATGGCGTTCGACAGGCGTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGATCGTGATATGCATCTCTTACATGATTACTGATTCTGCAAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTTCTTGATAACCCATAC 381

RESULT 50

US-11-055-637-93
; Sequence 93, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-93

Query Match 21.4%; Score 89.8; DB 14; Length 552;
Best Local Similarity 52.2%; Pred. No. 6.7e-14;
Matches 199; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 40 GCGACCGTTCGCGCCGAGGCGCTCGTAGCGGAGGCGCTCGCACGCTCGCGCGCGGTGCC 99
Db 1 GCAACTGTATTAGCGACAGCTATGATTCGTGAAGGTCTTAAACACGTAAACAGCTGGTGG 60
Qy 100 AACCCGATGGTCTCAAGCGCGCATCGAGAAGGCGCTCGAGGCGCTTCGCGCGCGCGCTG 159
Db 61 AACCAATGGGTCTTCGTAAGGTATCGAAAAGGTGATGTTGCTGCAGTAGAAGAAATTA 120
Qy 160 CTGGAGCAGGCGAAGGATGTGAGACCAAGGAGGAGGAGTCTTCCACGCGCTCATCTCC 219
Db 121 AAAACGATTTCTAAACCAATCGAAGGTAAATCTTCAATCGCACAGTAGCTGCTATTCT 180
Qy 220 GCGCGCGACACCCAGATCGCGGAGCTCATCGCGGAGCGATGACAAAGGTGCGCAAGGAA 279
Db 181 GCGCTGACGAGAGTAGTCAATTAATCGCTGAAGCAATGAGCGCGTGGTAGACAC 240
Qy 280 GCGCTCATCACCGTCGAGGAGTCCAGACCTTCGGTCTGAGGCTGGAGCTCACCGAGGT 339
Db 241 GCGCTTATTACTTTAGAGAGTCTAAAGGATTCACAAAGATTAGATGTAGTAGAAGGT 300
Qy 340 ATGGCGTTCGACAGGCGTACATCTCGGCGTACTTCGCCACCGACATGGAGCGGATGGAG 399
Db 301 ATGCAATTTGATCGTGATATGCATCTCTTACATGATTACTGATTCTGCAAAATGGAA 360
Qy 400 GCGTCGCTCGACGACCGGTAC 420
Db 361 GCAGTTCTTGATAACCCATAC 381

RESULT 51

US-11-055-637-106
; Sequence 106, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637

; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-106

Query Match 21.0%; Score 88.2; DB 14; Length 552;

Best Local Similarity 52.0%; Pred. No. 1.7e-13;
Matches 198; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 40 GCGACGGTCTCGCCAGGCGCTCGTAGCGGGGCTGGCAACCTCGCGCGGTCGC 99
DB 1 GCAACTGTATTACGCGAAGCTATGATTCGTGAAGGCTTTAAACACGTAAACAGCTGGTCA 60
QY 100 AACCCGATGCTCTCAAGCGCGGCATCGAAGCGCGTCCGAGCGGCTCTCGCGCGCCCTG 159
DB 61 AACCCATGGCTCTCGTAAAGTATCGAAGAGCTGTACTGCTCAATTGAAGATTA 120
QY 160 CTGAGAGCGGAGGATGTCGAGACCAAGGACAGATCGCTTCCAGCGCCTCCATCTCC 219
DB 121 AAAGCGATTCTAAACCAATCGAAGGTAATCTTCTATCGCAAGTAGCTGCTATTCT 180
QY 220 GCGCGACACCCAGATCGCGAGCTCATCGCGAGCGGATGGAAGGTGCGCAAGAA 279
DB 181 TCGGCTGAGCAAGATGAGTCAATTAATCGTGAAGCAATGAGCGGCTTGGTAACGAC 240
QY 280 GCGCTCATACCGCTGAGAGTCCAGACCTTCGGTCTCGAGCTGAGCTCACCGAGGT 339
DB 241 GCGCTTACTTTAGAGATCTAAGGATTCAGAGATTCAGAGATTCAGAGATTCAGAGAT 300
QY 340 ATGCGCTTCGACAAAGGCTACATCTCGGCTACTTCGCCACCGACATGAGCGGATGGAG 399
DB 301 ATGCAATTTGATCGTGGATATGCACTCTCTTACATGATTACTGATTTCTGACAAATGGAA 360
QY 400 GCGTCTGACGACCCGTAC 420
DB 361 GCAGTTCTTGATAACCCATAC 381

RESULT 52

US-11-000-688-1372
; Sequence 1372, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOUTGATTE, Remi
; APPLICANT: BIRBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1372
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc feature
; LOCATION: (1)..(2258)
; OTHER INFORMATION: heat shock 60kda protein 1
; OTHER INFORMATION: (chaperonin) (HSPD1) gene.

Query Match 19.8%; Score 83.2; DB 14; Length 552;

Best Local Similarity 51.6%; Pred. No. 3.3e-12;
Matches 190; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 46 GTTCTCGCCAGGCGCTCGTAGCGGAGGCGCTCGGCAACCGTCGCGCGGTGCCAACCGG 105
DB 7 GTTCTTCACAAAGGTTTATTGCTGAGGGTGTCAAGGTGGTGGCTGCTGGTGCACAAACCT 66
QY 106 ATGGCTCTCAAGCGCGGATCGAGAGCCGTCGAGGCGGCTCTCGGCGCCCTGCTGGAG 165
DB 67 GTATTGATCACTAGAGGCAATTGAGAAAGAGGCTTTGGTAGCGGAGCTCAAGAAA 126

US-11-000-688-1372

Query Match 20.8%; Score 87.4; DB 14; Length 2258;
Best Local Similarity 53.8%; Pred. No. 2.5e-13;
Matches 203; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 1 AAGAAGACGACACGCTCGCCGCTGACCGGTACGACACCGCGCGGTCGCCACCGATGCTCTCAAGCG 60
DB 363 AATAACACAAATGAAGAGCTGGGATGGCACTACCACTGCTACTGTACTGGCAGCTCT 422
QY 61 CTCGTACGCGAGGCGCTCGGCAACCTCGCGCGGTCGCCACCGATGCTCTCAAGCG 120
DB 423 ATAGCAAGGAAGGCTTCGAGAAGATTAGCAAAAGGTGCTAAATCCAGTGGAAATCCAGGAGA 482
QY 121 GGCATCGAGAGGCGGCTCGAGGCGCTCTCGCGCGGCTCGTGGAGCAGCGGAAGGATGTC 180
DB 483 GGTGTGATGTAGCTGTTGATGCTGTAAATGCTGAACCTTAAAGAGAGTCTAAACCTGTG 542
QY 181 GAGACCAAGGACAGATCGCTTCCAGCGCTCCATCTCCGCGC---CGCCGACACCCAGATC 237
DB 543 ACCACCCCTGAAGAAATTCACAGGTTCCTACGATTTCTGCAACCGAGACAAAGAAAT 602
QY 238 GCGGAGCTCATCGCGAGCGGATGACAGAGTGGCGAAGGAGGCTCATCCGTCGAG 297
DB 603 GGCATATATCATCTCTGATGCAATGAAAGAGTTGGAAGAAAGGCTGTCTATCAGTAAAG 662
QY 298 GAGTCCAGACCTTCGGTCTGGAGCTGAGCTCACGAGGGTATCGCTTCGACAAAGGC 357
DB 663 GATGAAACCACTGATGATGATTAATTTTGAAGCAATGAGTTGATCGAGSC 722
QY 358 TACATCTCGGCTACTT 374
DB 723 TATATTTCTCCATCTT 739

RESULT 53

US-11-055-637-114
; Sequence 114, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-114

Query Match 19.8%; Score 83.2; DB 14; Length 552;

Best Local Similarity 51.6%; Pred. No. 3.3e-12;
Matches 190; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

166	Qy	CAGGCGAAGGATGTCGAGACACAGAGACAGATGCGTTCCAGGGCTCCATCTCCGCGGCC	225
167			
168			
169			
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171			
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182			
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186	Db	ATGTCCTAAGAGAGTTGAAGACAGTGAAGTTGAGATGGCAGCGCTTAGTGC CGGTAAAC	186
187			
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226	Qy	GACACCCAGATCGCGAGCTCATCCGAGGCGATGACAAAGTTCGGCAAGGAAGCGTC	285
227			
228			
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231			
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234			
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242			
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245			
246	Db	AATGCAGAAATTGGAAGCATGNTTCTGAGCANTGACAGAGTGGCAGGAAGGCTGTG	246
247			
248			
249			
250			
251			
252			
253			
254			
255			
256	Qy	ATCACCGTCGAGAGTCCACAGCTTCGCGTCTGAGCTTGGAGTCCACCGAGGTTATCGCG	345
257			
258			
259			
260			
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264			
265			
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RESULT 54

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US-10-932-182A-4757
; Sequence 4757, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 137023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4757
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (659)..(659)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-10-932-182A-4757

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RESULT 56

US-11-000-688-1371
; Sequence 1371, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois

```
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1371
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(422)
; OTHER INFORMATION: 5' terminal sequence from clone
; OTHER INFORMATION: image:563819. heat shock 60kda protein 1
; OTHER INFORMATION: (chaperonin) (HSPD1) gene.
US-11-000-688-1371

Query Match      17.0%; Score 71.6; DB 14; Length 422;
Best Local Similarity 53.0%; Pred. No. 3.3e-09;
Matches 177; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 1 AAGAGAGGACGACGCTGCGGCTGAGCGGTACGAGGACGACGCGGACCGCTTCTCGGCCAGGGG 60
DB 1 AAGAGAGGACGACGCTGCGGCTGAGCGGTACGAGGACGACGCGGACCGCTTCTCGGCCAGGGG 60
QY 61 CTGCTAGCGGAGGCGCTCGCAACGCTGCGCGCGGTGCGCAACCGCGATGGCTCTCAAGCGC 120
DB 147 ATAGCCAAAGGAGCTTCGAGAGATTAGCAAAAGGTGCTAATCCAGTGGAAATCAGAGA 206
QY 121 GGCATCGAGAAGCGCGTCTGAGGCGGCTCTCGGCGCCCTCTGTCGAGCAGCGAAGATGTC 180
DB 207 GGTGTGATGTAGCTGTGATGCTGTAATGCTGAACTTAAAGGCACTTAAAGCGAGTCTAA 266
QY 181 GAGACCAAGGAGCAGATGCTTCCAGCGCTCCATCTCCGC---CGCGACACCCAGATC 237
DB 267 ACCACCCCTGAAGAAATGACAGGTGCTGACGATTTCTGCAACCGGAGCAAAAGAAAT 326
QY 238 GCGAGCTCATCCCGGAGGCGATGAGCAAGGTGCGCAAGGAAGGCGTCTATCCCGTCGAG 297
DB 327 GGCATATCATCTCTGATGCAATGAAAAGTTGGAAGAAAGGTTCTCATCAGTAAG 386
QY 298 GAGTCCGAGACCTTCGGTCTGAGCTGAGCTCA 331
DB 387 GATGGAAGAAACACTGAATGATGAATTAGAAATTA 420

RESULT 57
US-11-096-568A-22123
; Sequence 22123, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22123
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1876)
; OTHER INFORMATION: Ceres Seq. ID no. 12407639
```

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US-11-096-568A-22123

Query Match      14.2%; Score 59.8; DB 11; Length 1876;
Best Local Similarity 47.9%; Pred. No. 3.3e-06;
Matches 172; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 57 GCGCTCTGTACGAGGCGCTTGGCAACGTCGCGCGCGGTGCGCAACCCGATGCTCTCAA 116
DB 477 GGTGGCATCCGGAGGTGCTCGCCAGCGCTCCGCGCTCTTGGTCTATGGAGTACGC 536
QY 117 GCGCGCATCGAGAGCGCGTGGAGCGCGTCTCCGCGCGCGTCTCGAGCAGCGGAGGA 176
DB 537 GCGCGCGGCGGAGCTTTCGCCAAGGTGGCGCGCGCGCTCGACGAGGACCAACCGCG 596
QY 177 TGTGAGAGACAAAGGAGCAGATCGCTTTCACGCGCTCCATCTCCGCGCGCGACACCCAGAT 236
DB 597 CGCTACTTTCAGAGAGTGGTCCGCGCGCTCGGCTTCTGCCACCGCGCGGTGCGGCA 656
QY 237 CGCGAGCTCATCGCGAGCGGATGCAAGAGTTCGGCAAGGAGGCGTCTATCCCGTCGA 296
DB 657 CGGGACCTCAAGCCCGAGAACCTGCTGTCGAGCAGGCGCGGCGGCTCAAGTCAACCGA 716
QY 297 GGAGTCCGAGACCTTCGGTCTGAGCTGAGCTCACCGAGGATGCGCTTTCGACAAGGG 356
DB 717 CTTGGGCTGGCGCGCGCTGCCCGAGCAGCTGCGGCCACGACGAGCGCTGCTCCACAGCGATG 776
QY 357 CTACATCTCGGCTACTTTCGCCACCGACATGAGCGGATGAGGCGGTGCTCGACGACC 415
DB 777 CGGCACCCCGGTACTGCGCCCGAGGTGCTCAGGAAGCGGCTACGACGCGCGCC 835

RESULT 58
US-10-301-480-304422
; Sequence 304422, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1228818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304422
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-304422

Query Match      13.5%; Score 56.8; DB 10; Length 556;
Best Local Similarity 50.6%; Pred. No. 2.1e-05;
Matches 164; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

QY 22 GGTGAGGTGACGACCAACCGGACCGCTTCTCGCCAGGCGCTCGTACGGAGGCGCTTCCGC 81
DB 57 GGGGATGCACTATCACTGCTGCTGATGTTGTTCTCTATTTCCAAATTAAGCTTCCAG 116
QY 82 AACGTGCGCGCGGTGCCAACCCGATGCTCTCAAGCGCGGCGATCGAGAAGGCGCGTCCAG 141
DB 117 AAGGTTAGCAAGGTGCTAATCCAGTGGAAATCAAGAGAGGTGCTGATGTTAGTGTGAT 176
QY 142 GCGGTCTCGGCGCGCTGCTGGAGCAGCGAGGATGTTCGAGACCAAGGAGCAGATCGCT 201
DB 177 GCTGTAATGCTGAACCTTAAAGGAGTCTAAACCTGTGACCAACCTGGAAGAAATGCA 236
QY 202 TCCAGGCGCTCATCTCCGCC---GCCGACACCCAGATCGGCGAGCTCATTCGCGAGGG 258
DB 237 CAGGTTGCTACAAATTTCTGCAAAATGGAGACAAAGAAATTTGGTAACATCATCTCTGATGCA 296
```

QY 259 ATGACAAAGCTCGCAGGAGGCGTCCATCACCCTGAGGAGTCCAGACCTTCGGTCTG 318
Db 297 ATGAAAAAGTTTGAAGAAAGGGCATCATCACATAAGGATGGAAAAACACTGATGAT 356
QY 319 GAGCTGAGCTCACCGAGGGTATG 342
Db 357 GAATTAGAAATTATTGAGGCNTG 380

RESULT 59

US-10-301-480-917831
; Sequence 917831, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917831
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-917831

Query Match 13.5%; Score 56.8; DB 10; Length 556;
Best Local Similarity 50.6%; Pred. No. 2.1e-05;
Matches 164; Conservative 0; Mismatches 157; Indels 3; Gaps 1;
QY 22 GGTGACGGTAGCACCACCGGACCGTTCGCCCCAGGCGCTCGTACCGAGGGCGCTCGCG 81
Db 57 GGGGATGGCACTATCACTGCTGTCTACTGTATGCTCTATTTCCAAATAAGCCCTCCAG 116
QY 82 AACCTCGCGCGGTGCCAACCCGATGCTCTCAAGCGCGCATCGAGAAAGCGCGTCGAG 141
Db 117 AAGTTAGCAAGGTGCTATCACTGGAATCAAGAGAGGTGTGATGTTAGCTGTTGAT 176
QY 142 GCGGTCTCCGCGCCCTCGTGGACGCGGAGGATGTGAGACCAAGAGGCGATCGCT 201
Db 177 GCTGTAATTGTAACCTTAAAGACGCTTAAACCTGTGACCAAAACCTGAAGAAATTGCA 236
QY 202 TCCAGCGCTCCATCTCCGCC---GCCGACACCCAGATCGCGAGCTCATCGCGAGGCG 258
Db 237 CAGTTGCTACAATTTCTGCAATGGAGAAAGGGCATCATCACATAAGGATGGAAAAACACTGATGAT 296
QY 259 ATGACAAAGTTCGCAAGGAGGCGTCCATCACCCTGAGGAGTCCAGACCTTCGGTCTG 318
Db 297 ATGAAAAAGTTTGAAGAAAGGGCATCATCACATAAGGATGGAAAAACACTGATGAT 356
QY 319 GAGCTGAGCTCACCGAGGGTATG 342
Db 357 GAATTAGAAATTATTGAGGCNTG 380

RESULT 60

US-09-925-065A-218359
; Sequence 218359, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218359
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-218359

Query Match 13.5%; Score 56.8; DB 6; Length 561;
Best Local Similarity 50.6%; Pred. No. 2.1e-05;
Matches 164; Conservative 0; Mismatches 157; Indels 3; Gaps 1;
QY 22 GGTGACGGTAGCACCACCGGACCGTTCGCCCCAGGCGCTCGTACCGAGGGCGCTCGCG 81
Db 57 GGGGATGGCACTATCACTGCTGTCTACTGTATGCTCTATTTCCAAATAAGCCCTCCAG 116
QY 82 AACCTCGCGCGGTGCCAACCCGATGCTCTCAAGCGCGCATCGAGAAAGCGCGTCGAG 141
Db 117 AAGTTAGCAAGGTGCTATCACTGGAATCAAGAGAGGTGTGATGTTAGCTGTTGAT 176
QY 142 GCGGTCTCCGCGCCCTCGTGGACGAGGCGAAGGATGTGAGACCAAGAGGCGATCGCT 201
Db 177 GCTGTAATTGCTGAACCTTAAAGACGATCTAAACCTGTGACCAAAACCTGAAGAAATTGCA 236
QY 202 TCCAGCGCTTCATCTCCGCC---GCCGACACCCAGATCGCGAGCTCATCGCGAGGCG 258
Db 237 CAGTTGCTACAATTTCTGCAATGGAGAAAGGGCATCATCACATAAGGATGGAAAAACACTGATGAT 296
QY 259 ATGACAAAGTTCGCAAGGAGGCGTCCATCACCCTGAGGAGTCCAGACCTTCGGTCTG 318
Db 297 ATGAAAAAGTTTGAAGAAAGGGCATCATCACATAAGGATGGAAAAACACTGATGAT 356
QY 319 GAGCTGAGCTCACCGAGGGTATG 342
Db 357 GAATTAGAAATTATTGAGGCNTG 380

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Job time : 1043.23 secs